STIC-Biotech/ChemLib



From: Sent: To:

Fredman, Jeffrey Monday, October 01, 2001 3:42 PM

STIC-Biotech/ChemLib Lacourciere, Karen

FW: Sequence search approval 09/757100

I Approve.

Subject:

Cc:

Jeff Fredman

----Original Message-----

Fr m:

Lacourciere, Karen

Sent:

Monday, October 01, 2001 3:06 PM

T:

Fredman, Jeffrey

Subject:

Sequence search approval 09/757100

Jeff, could you approve this sequence search? Each sequence is ~20 nt's long and they are antisense targeted to one sequence. Thank-you!

Karen

Please search the following SEQ ID NO:'s for 09/757,100 in both the commercial databases and the pending files (interference)

3, 4, 6-12,14-18, 20, 23, 30, 31 and 33.

Please limit the length of oligos to less than 50 nucleotides long. Thank-you!

Karen A. Lacourciere Ph.D. CM1 11D09 GAU 1635 🗸 (703) 308-7523

> Point of Contact: **Toby Port** Technical Info. Specialist CM1 1E01 TEL: 308-3534

Point of Comact: Toby Port Technical Info. Specialist CM1 1E01 TEL: 308-3534

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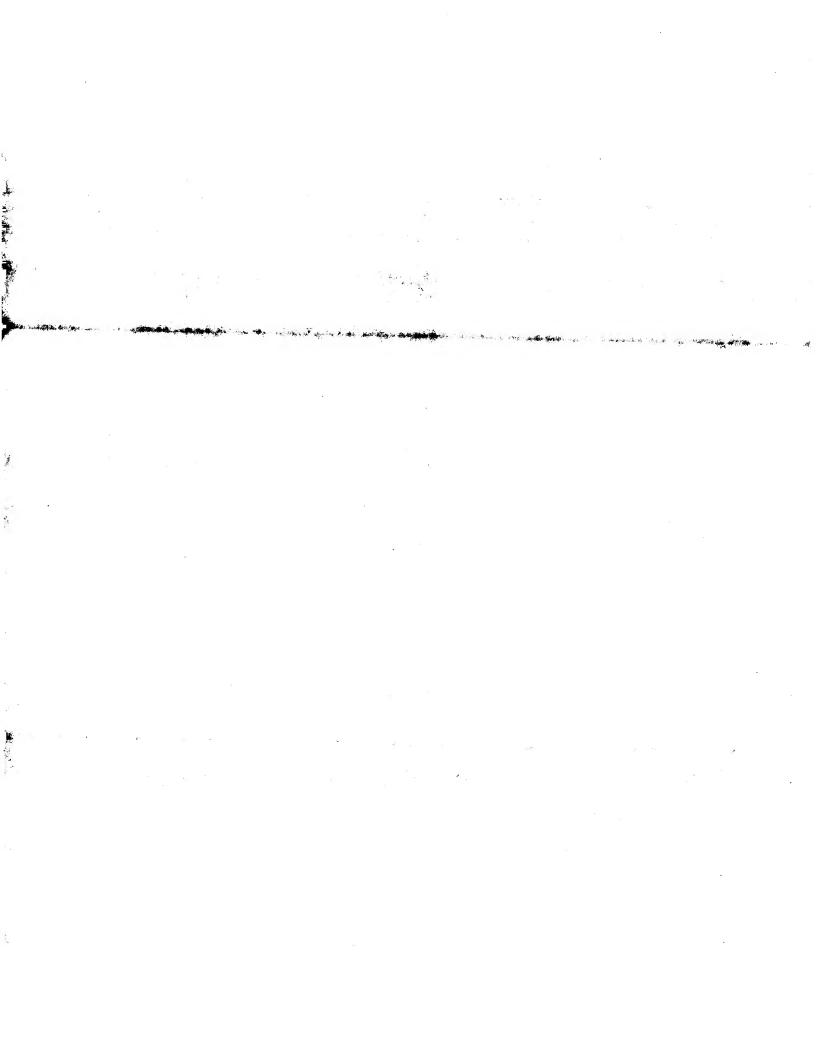
SEARCH REQUEST FORM

Appens DB#______

Scientific and Technical Information Center

| Re Full Nome: | · | Evaminar # . | Data |
|--|---|--|---------------------------------------|
| Requester's Full Name: Phone Nu | mber 30 | Serial Number: | _ Date |
| Mail Box and Bldg/Room Location: | Res | ults Format Preferred (circle | PAPER DISK E-MAI |
| If more than one search is submit | ted, please prioriti | ze searches in order of n | eed. ******** |
| Please provide a detailed statement of the se Include the elected species or structures, key utility of the invention. Define any terms th known. Please attach a copy of the cover she | /words, synonyms, acro at may have a special m | nyms, and registry numbers, and leaning. Give examples or releva | combine with the concept or |
| Title of Invention: | | | |
| Inventors (please provide full names): | | | |
| Earliest Priority Filing Date: | | | · · · · · · · · · · · · · · · · · · · |
| *For Sequence Searches Only* Please include appropriate serial number. | all pertinent information | (parent, child, divisional, or issued | patent numbers) along with the |
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| STAFF USE ONLY | Type of Search | | t where applicable |
| Searcher: 1084 TORT | NA Sequence (#) 19 | STN | |
| Searcher Phone #: 308-3534 | AA Sequence (#) | Dialog | |
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| Date Searcher Picked Up | Bibliographic | Dr.Link | |
| Date Completed: | Litigation | Lexis/Nexis | |
| Searcher Prep & Review Time | Fulltext - | Sequence Systems | <u> </u> |
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PTO-1590 (1-2000)



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Database

Searched:

Run on:

182248 Sequence 32 190782 Sequence 32 120218 Human kerat 164891 Sequence 7 B13249 Oligonucleo AR004965 Sequence 140158 Sequence

A10280 oligonucleo

A10280 182248 190782 HUMKRT10AG

I64891 E13249 AR004965 I40158

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Rothnagel, J.J., Dominey, A., Fisher, M., Axtell, S., Pittelkow, M.; Anton-Lamprecht, I., Hohl, D. and Roop, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HUMKRT10AG 45 bp DNA PRI 06-JAN-1995
Human Keratin 10 (KRT10) gene, partial cds including polymorphism.
L20218.1 GI:307087
Keratin; keratin 10; polymorphism; suprabasal keratin.
Homo sapiens Adult Blood DNA.
              10-JUN-1998
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); Mismatches 2;
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1 (bases 1 to 29)
Murphy.T.F.

Vaccine for branhamelia catarrhalis
Patent: US 5725862-A 32 10-MAR-1998;
Location/Qualifiers
                                                                                                              Murphy, T.F.
Vaccine for branhamella catarrhalis
Patent: US 5712118-A 32 27-JAN-1998;
Location/Qualifiers
          182248 29 bp DNA
Sequence 32 from patent US 5712118.
182248
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E14337 Primer. 7/1
A42578 Sequence 95
A42579 Sequence 91
A88768 Sequence 91
A04127 Synthetic o
AR071515 Sequence
AR075963 Sequence
AR075963 Sequence
AR089824 Sequence
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I61215 Sequence 22
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161220 Sequence 27
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AR090906 Sequence
AR034456 Sequence
AR070401 Sequence
AR026654 Sequence
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AX076373 Sequence
A03829 Artificial
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AR038266 Sequence
AR075196 Sequence
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/organism="synthetic construct"
/db_xref="taxon:32630"
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Location/Qualifiers
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AR016116
AR019114
AR030906
AR034456
AR070401
AR026654
AX067989
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AR089824
HUM66RVA
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E14337
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A04127
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121766
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synthetic construct. synthetic construct artificial sequence. 1 (bases 1 to 20)

ORGANISM

REFERENCE AUTHORS 1 tttcaaccagatggtc 16

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RESULT

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BASE COUNT ORIGIN

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JOURNAL

FEATURES

20 bp

A10280

DEFINITION

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TITLE

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/organism='Artificial sequences'
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Pred. No. 1e+05;
0; Mismatches 1; Indels
                    E13249 41 bp DNA PAT
Oligonucleotide for microgene construction.
E13249
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C12N15/09,C07H21/04//C12N9/00;
strandedness: Single;
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Wei,Y. and Sutton,G.G. III.
Human AlkB polypeptide
Patent: US 5747312-A 4 05-MAY-1998;
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Sequence 4 from patent US 5747312.
AR004965 GI:3965844
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/organism="unidentified"
/db_xref="taxon:32644"
10 c 15 g
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JP 1997154585-A/9
17-JUN-1997
06-DEC-1995 JP 1995318396
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<1. >45
<1. codon="RRT10"
/note="helix-initiation motif of 1A segment of rod domain"
/codon_start=1</pre>
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Identification of mutational hot spots in the suprabasal keratin genes from patients with epidermolytic hyperkeratosis Unpublished (1993)
                                                                                                                                                                                                                                                                                                                                                                   /note="polymorphism results in an Arg->His mutation at
amino acid position #10 in the HK10 rod; G00-118-828"
//phenotype="wild-type (G)"
/replace="g"
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Pred. No. 6.2e+04;
); Mismatches 2; Indels (
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                                                                                                                                                                                                                                                     /function="intermediate filament precursor"
/db_xref="GDB:G00-118-828"
/product="keratin 10"
/protein_id="AAB59438_1"
/db_xref="G1:307088"
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                                                    1..45
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_type="Lymphocyte"
/dev_stage="Adult"
/tissue_type="Blood"
/map="17921-923"
/note="from EHK patient"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 35)
Kuhajda,F.P. and Pasternack,G.R.
Cancer related antigen
Patent: US 5665874-A 7 09-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence 7 from patent US 565874.
164891
164891,1 GI:2481785
                                         Location/Qualifiers
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12 c 6 g
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/gene="KRT10"
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87.5%;
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Best Local Similarity 87.5
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Gaps
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Svendsen,A., Patkar,S.Anant, Gormsen,E., Okkels,J.Sigurd and Thellersen,M.
Lipase variants
Patent: US 5869438-A 38 09-FEB-1999;
Location/Qualifiers
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Pred. No. 1.3e+05;
0; Mismatches 3; Indels
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First, M.Kent and Agoulnik, A.I.
Male infertility Y-deletion detection battery
Patent: US 5783390-A 4 21-JUL-1998;
Location/Qualifiers
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Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
Methods of assaying differential expression
Patent: US 5994076-A 1026 30-NOV-1999;
                                                                                                                                                                                                                                                                                         PAT
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Pred. No. 1.3e+05;
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Sequence 1026 from patent US 5994076.
AR090906
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                                                                  /organism="unknown"
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AR034456.1 GI:5950061
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3 TTCTACCAGGTCGTCAT 19
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Best Local Similarity 82.4'
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Best Local Similarity 82.4
Matches 14; Conservative
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Pred. No. 1.3e+05;
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First, M. Kent, Agoulnik, A.I. and Muallem, A.
Male infertility y-deletion detection battery
Patent: US 5776682-A 4 07-JUL-1998;
Location/Qualifiers
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Pred. No. 1e+05;
0; Mismatches 1;
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Wei Y. and Sutton G.G. III.
DNA encoding human Alke
Patent: US 5618717-A 4 08-APR-1997;
Location/Qualifiers
                                              140158 30 bp DNA
Sequence 4 from patent US 5618717.
140158 13:2083163
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Sequence 4 from patent US 5776682.
AR016116 GI:3972393
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Sequence 4 from patent US 5783390.
AR019114 GI:3974228
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/organism="unknown"
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92.9%;
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Best Local Similarity 82.4%;
Matches 14; Conservative
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1 (bases 1 to 20)
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Best Local Similarity 92.9
Matches 13; Conservative
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KEYWORDS

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synthetic construct.
synthetic construct
artificial sequence.
1 (bases 1 to 29)
Levin,J.Z., Bauer,M.W. and Zheng,F.
Herbicide target genes and methods
Patent: WO 0077185-A 34 21-DEC-2000;
Novartis AG (CH); Novartis-Erfindungen Verwaltungsgesellschaft
                                                                                                                                                                                                                                                                                     60.0%; Score 12; DB 10; Length 29
75.0%; Pred. No. 1.6e+05;
.ive 0; Mismatches 5; Indels
                                                                                                                                                                   Sequence 34 from Patent WO0077185.
AX067989
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                              AX067989.1 GI:12329803
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Fukuchi,N., Yamamoto,H., Nagano,M., Kito,M., Tanaka,A., Ishii,K., Kobayashi,T. and Yoshimoto,R.
Peptide having anti-thrombus activity and method of producing the
       Gaps
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Unclassified.
Unclassified.
I (bases 1 to 33)
Svendsen.A. Patkar.S. Anant. Gormsen.E., Clausen.I.Groth,
Okkels,J.Sigurd and Thellersen.M.
Lipase variants
Patent: US 5892013-A 38 06-APR-1999;
Location/Qualifiers
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Pred. No. 1.3e+05;
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      3;
      Mismatches
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Sequence 38 from patent US 5892013.
AR070401. GI:7221289
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Sequence 9 from patent US 5856126.
AR026654 GI:5937494
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7 c 3 g
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      14; Conservative
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AR070401
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AR026654/c
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo , Ph.D. | CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CEAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html | Trace considered overall poor quality Insert Length: 1015 Std Error: 0.00 Seq primer: -40UP from Gibco High quality sequence stop: 1. | | /Jab_host="DH10B" //Jab_host="DH10B" //Octo="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; lst strand cDNA was prepared from mRNA obtained from Clontech Laboratories / Inc., and primed with a Not I - oligo(dT) primer [5' TGTTACAATCTGAAGGGGGCGCCCAATTTTTTTTTTTTT | (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. " 5 a 8 c 4 g 8 t | Match 62.0%; Score 12.4; DB 17; Length 25; Local Similarity 92.9%; Pred. No. 4.4e+04; Samilarity 0; Gaps 0; | 4 caaccagatggtca 17 | AZ429959 39 bp DNA GSS 03-OCT-2000 IM0214NO8F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0214NO8 F. DNA sequence. | AZ429959 AZ429959.1 GI:10553972 GSS. house mouse. | <pre>mus muscutta Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bukaryota; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 39) Dunn, D., Aoyaqi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly</pre> | .M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts Unpublished (2000) Contact: Robert B. Weiss | University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 |
|---|--|---|---|--|---|---|--|---|--|---|---|--|
| JOURNAL | | REATINES | source | | BASE COUNT | Query Matc) Best Local Matches | Oy 4 Db 20 | RESULT 2 AZ429959/C LOCUS DEFINITION | ACCESSION VERSION KEYWORDS SOURCE | OKGANISM REFERENCE AUTHORS | TITLE JOURNAL COMMENT | |
| IES Description | | ALS68255 AL125432, AL311307, AL453625 AL653664 | AA26681 AA07590 AA27590 A109607 AA3169 | AZ475536 IM0293P23 AA75536 IM0293P23 AA700915 z344c07.s AU104136 AU104136 AU104138 AU104138 AZ317925 IM036G20 AZ449662 IM0248B06 | A2427' BG504 A26504 T80630 AA07532 AV5053 | AZ3964 AZ4511 AA9955 AZ3862 AZ3862 | H55075 (AW28556) AW28556 AZ46371: AZ78016. | | | EST 29-NOV-1998 omc sapiens cDNA clone IMAGE:1836621 553 TUBULIN ALPHA CHAIN ;, mRNA | | is Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 to 25) http://www.ncbi.nlm.nih.gov/ncicgap. Cancer Institute, Cancer Genome Anatomy Project (CGAP), |
| SUMMARIES Query re Match Length DB ID | .4 62.0 25 17 4 62.0 39 24 .2 61.0 50 10 .2 61.0 50 10 | 12 60.0 49 16 12 60.0 49 24 6 58.0 31 24 6 58.0 34 24 6 58.0 35 24 | .6 58.0 36 4 .6 58.0 43.2 .2 56.0 34 16.24 .2 56.0 42.13 | 2 56.0 44 2 56.0 44 2 56.0 50 11 55.0 24 11 55.0 25 | 11 55.0 28 24, 11 55.0 35 11, 155.0 35 25, 11 55.0 45 18, 11 55.0 49 10, 11 55.0 50 31, 11 55.0 | .8 54.0 29 24 .8 54.0 34 24. .8 54.0 42 14. .8 54.0 42 24. | .8 54.0 44 151 .8 54.0 50 11. .6 53.0 26 24. .6 53.0 26 24. | .6 53.0 26 24; .6 53.0 34 131.6 53.0 34 131.6 53.0 34 124. | | AI208968 25 bp mRNA qg29f11.x1 Soares_testis_NHT Homo 3' similar to SW:TBA_LXTPI P02553 | sequence. A1208968 A1208968.1 GI:3770910 EST. human. | Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 25) NCI-CGAP http://www.ncbi.nlm.n National Cancer Institute, Can Tumor Gene Index |
| Result No. Scor | 20 12 12 12 12 12 12 12 12 12 12 12 12 12 | 111 | | 0 17 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 | 25 25 26 27 30 30 | 90000 | 36 10 37 10 38 10 | 22222 | | RESULT 1 AI208968/C LOCUS DEFINITION C | ACCESSION A VERSION A KEYWORDS D SOURCE D | REFERENCE AUTHORS TITLE |

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1 (bases 1 to 50)

2 (Suzuki, Y., Tsunoda, T., Taira, H., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Nakamura, Y., Morishita, S., Okubo, K., Suyama, A. and Sugano, S.
Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshicomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and
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Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0214 row: N column: 08
Seq primer: CGTTGTAAAACGACGGCCAGT
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0214N08"
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Location/Qualifiers
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AUTHORS
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COMMENT
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AU104028
                                                                                                                                     FEATURES
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EUKaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 50)
Suzuki Y., Tsunoda, T., Taira, H., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Nakamura, Y., Morishita, S., Okubo, K., Suyama, A. and Sugano, S.
Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Yutaka Suzuki
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Bemail: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched con library. Gene 200 (1-2), 149-156 (1997).
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AU104139 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HEP1348, mRNA sequence.
AU104139 GI:13553660
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AZ388563
AZ388563.1 GI:10502271
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997). Location/Qualifiers
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                                                                                                                                                                                                                                                                                                     Score 12.2; DB 107; Length 50;
Pred. No. 6.2e+04;
0; Mismatches 3; Indels 0
                                                                                                                                                       sapiens cDNA library"
16 t
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Pred. No. 6.2e+04;
); Mismatches 3; Indels 0
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m c} 15 g 15 t
                                                                             /organism="Homo sapiens"
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/clone="HEP21348"
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ORGANISM

KEYWORDS

REFERENCE AUTHORS

JOURNAL

COMMENT

TITLE

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Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequencing Center
information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 49)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Longarce, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly M., Rose, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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                                                                                                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                        1 (bases 1 to 49)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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100.0%; Pred. No. 7.8e+04;
ive 0; Mismatches 0;
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High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.49
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1737047"
/clone_lib="Soares_testis_NHT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Trace considered overall poor quality
                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
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AI125432
AI125432.1 GI:3593946
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                                                                                                                                                                                                                                                                         Tumor Gene Index
Unpublished (1997)
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Best Local Similarity 100.
Matches 12; Conservative
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TITLE
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//organism="157BLL69"
//db_xref="taxon:10090"
//clone="uuccIM0148F08"
//clone="uuccIM0148F08"
//clone="uuccIM0148F08"
//clone="uuccIM0148F08"
//lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
//lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
//note="vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/60/ (male) was obtained from the Jackson
Laboratory Mouse DNA Resources
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynuclectide kinase. Adaptor oligonuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gil4732114|gb]AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. E. 1 (bases 1 to 43)
E. 1 (bases 1 to 43)
E. 1 (bases 1 to 43)
S. Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Stokes, R., Tingey, A., von Niederhausern, A. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                        Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0148 row: F column: 08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 43.
Location/Qualifiers

    .43
/organism="Mus musculus"

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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddun@geneti
                                                      Mus musculus
                         house mouse.
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Best Local Simi
Matches 15;
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source

FEATURES

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Gaps ;; 0

AI125432/c LOCUS

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RESULT

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DEFINITION

BASE COUNT ORIGIN

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high monar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114(jb)AR123072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Dunn, D., Aoyadi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                              S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                          Mouse whole genome scaffolding with paired end reads from 10kb
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Pred. No. 1.2e+05;
0; Mismatches 4; Indels 0;
                                                                                                                                                                                              Rm. 308, Biomedical Polymers Research Bldg., 20
84112, USA
                                                                                                                                                                                                                                                Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunnegenetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0255 row: E column: 08
Seq primer: CGTGAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
                                                    plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0255E08"
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and Wright, D., Weiss, R.
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Matches 14; Conserv
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AZ663664/C
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//note="Vector: PW042nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end repaired with TA DNA polymerase and T4
polynuclectide kinase. Adaptor oligonuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pW042 (gill #1732114 gpl AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XLIO-Gold (Stratagene) cells
and selected for amplicitin resistance."
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 31)
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Mouse whole genome scaffolding with paired end reads from 10kb
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                       plasmid inserts
Unpublished (2000)
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 30, Biomedical Polymers Research Bldg., 20 S. 2030
84112, USA
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                                                                                                                                                                                                                   Tel: 801 585 5606
Fax: 801 585 7177
Emall: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Seq primer: CACACAGGAAACAGCTATGACC
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/clone="UUGC1M0026K11"
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch oritice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pwAPA2 (gillAlighlARI29072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically competent E. coli XLLO-Gold (Stratagene) cells and selected for ampicillin resistance."
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Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                      Mouse whole genome scaffolding with paired end reads from 10kb
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0485 row: J column: 13
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Seq primer: CGTTGTAAAACGACGGCCAGT
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                                                                                                                                          Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/db_xref="taxon:10090"
/clone="UUGC1M0485J13"
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High quality sequence stop: 35.
Location/Qualifiers
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
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AZ631220
AZ631220.1 GI:11753410
'M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
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                                                      Mouse whole genome scaffolding with paired end reads from 10kb
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/strain="C57BL/6J"
/db.ztrain=10900"
/clone="UGGCIM054320"
/clone=lib="Mouse 10kb plasmid UGGIM library"
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                                                                                                                                                                                                                                                                                                                           Email: ddunnegenetics.utah.edu
Insert Length: 10000 std Error: 0.00
Plate: 0543 row: J column: 20
Seg primer: CGTFGTAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                               Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 34. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA
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77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35 bp
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                                                                                                             Unpublished (2000)
                                                                                                                                                                                                                                                                            Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                plasmid inserts
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Mus musculus
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Matches 14; Conserv
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Gaps

ACCESSION VERSION KEYWORDS SOURCE

AZ631220

RESULT

à g

ORIGIN

REFERENCE AUTHORS us-09-757-100b-18.szlim50.rst

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Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags cenome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                         WARNING: There is evidence that suggests that the 384-well parent plate of this chone contains both human and mouse derived clones. Thus, the origin of this clone is uncertain. This caution should be kept in mind should you use this clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 46)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
'M., Rose, M., Rose, R.,
and Wright, D., Welss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AZ777948 46 bp DNA GSS 16-FEB-2001
2M0012P13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0012P13 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       \rm Rm.~308 , Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 84112, USA
                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28M13 rev2 from Amersham High quality sequence stop: 1.

Location/Qualifiers
                                                                                                                                                          Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 11.6; DB 2;
Pred. No. 1.2e+05;
); Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="GDB:3920910"
/db_xref="taxon:9606"
/clone="IMAGE:531398"
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                        Email: est@watson.wustl.edu
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AZ777948.1 GI:12907079
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ilarity 77.8%;
Conservative (
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                                                                                                                                       Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plasmid inserts
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Best Local Similarity
Matches 14; Conserv
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A2777948/c
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                                                                                                               MEDLINE
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
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Hiller,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,
                                           Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Mortis,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"Organ: lymph node; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; ist strand cDNA was primed with a Not I - oligo(dT) primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                   This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:446242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra MyMouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
A444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Pax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 11.6; DB 4; Length 36;
Pred. No. 1.2e+05;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Soares mouse lymph node NbMLN"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                      Trace considered overall poor quality
Seq primer: -28mil rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="lymph node"
/dev_stage="4 weeks"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism-"Mus musculus"
                                                                                                                                                                                                                                                                                                                                             Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
/clone="IMAGE:720746"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA075907.1 GI:1615777
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Best Local Similarity 77.8
Matches 14; Conservative
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                                                                                                                                    Waterston, R.
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LOCUS
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                     REFERENCE
                                           AUTHORS
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KEYWORDS
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Gaps

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The library was constructed by Wenhong Lu. The library is available from Dr. S.A. Williams, email genome@smith.edu When requesting this clone from Dr. Williams, please reference the Williams lab clone id - SWOVISCAN20F05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Those transcores filatial nematode parasite of humans.

MRNA was prepared from third stage infective larvae of onchocerca volvulus isolated from mosquitoes 10 days after infection and converted to double stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNApol I. The library had 1.8 x 10E5 independent recombinants and average insert size was 900 base pairs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The library was constructed by Wenhong Lu. The library is available from Dr. S.A. Williams, email genome@smith.edu.'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host="XL1-Blue MRF'"
/note="Vector: lambda UniZap XR; Site_1: EcoR I; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA936922 42 bp mRNA EST 17-JUN-1998 om55c08.sl NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1551086 3' similar to gb:M38188 OVARIAN GRANULOSA CELL 13.0 KD PROTEIN HGR74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 42)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
Department of Biological Sciences, Clark Science Center, Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="onch1306"
/clone_lib="Onchocerca volvulus infective larva cDNA
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Pred. No. 1.9e+05;
0; Mismatches 3; Indels (
                                                                                                                                                                                                                                                     Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: T3 ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Onchocerca volvulus"
/strain="Sierra Leone"
/db_xref="taxon:6282"
                             Northampton, MA, 01063, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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AA936922
AA936922.1 GI:3094956
                                                                                                             Email: genome@smith.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56.0%;
81.2%;
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Unpublished (1997)
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                          College, Northan
Tel: 4135853826
Fax: 4135853786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch oritice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWAPA2 (gif4732114 gb]AR129072.1), a copy.number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
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1 (bases 1 to 34)
Williams,S.A., Lizotte-Waniewski,M., Laney,S., Wenhong,L., Hillier
Li., Allen,M., Bowles,L., Gelsel,S., Jost,S., Kucaba,T., Martin,J.,
Steptoe,M., Theising,B., White,Y., Wylie,T., Chappell,J., Person,B.,
Glibbons,M., Harvey,N., Pape,D., Chamberlain,A., Morales,R.,
Molecular Parasitology OvL3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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SWOVL3CANZOROS Onchocerca volvulus infective larva cDNA
(SAW94WL-OVL3) Onchocerca volvulus cDNA clone onch1306 5' similar
to TR:Q25606 Q25606 LARVAL 18 KDA PROTEIN. ;, mRNA sequence.
A1096045
                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="Male"
/lab_nost="E. Coll strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Smith College Department of Biological Sciences
              Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0012 row: P column: 13
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                               /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
/clone="UUGC2M0012P13"
                                                                                                                                                                                          High quality sequence stop: 46.
Location/Qualifiers
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Contact: Steven A. Williams
                                                                                                                                                                                                                                                                                                             /strain="C57BL/6J
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Search completed: October 2, 2001, 15:01:08 Job time: 10837 sec

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Gaps

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Query Match 56.0%; Score 11.2; DB 13; Length 42; Best Local Similarity 81.2%; Pred. No. 1.9e+05; Matches 13; Conservative 0; Mismatches 3; Indels (

Searched:

Run on:

Database

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                            1344157 seqs, 7733874588 residues
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Maximum Match 100%
Listing first 45 summaries

    nucleic search, using sw model

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AX04389 Sequence 41 AX043850 Sequence AX090386 Sequence AX090365 Sequence X70713 M.musculus AX026028 Sequence E28465 Hyaluronate AR095613 Sequence

192389 AX043850 AX090386 AX090365 AMTCRAIC7 AX026028 AX026028 AX05613

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Description

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SUMMARIES

| RESULT 2 AX043850 LOCUS LOCUS LOCUS LOCUS AX043850 LOCUS SOURCE ORGANISM SYNTHETIC CONSTRUCT ORGANISM AX043850 LOCUS AUTHORS SAVIGGE, B., Lassner, M.W., Weiss, J.D. and Post-Beittenmiller, D. AUTHORS AUTHORS SAVIGGE, B., Lassner, M.W., Weiss, J.D. and Post-Beittenmiller, D. AUTHORS AUTHORS SAVIGGE, B., Lassner, M.W., Weiss, J.D. and Post-Beittenmiller, D. AUTHORS AUTHORS AUTHORS AUTHORS LOCUS LOCUS LOCUS LOCUS LOCUS LOCUS LOCUS AUTHORS LOCUS LOCUS LOCUS LOCUS AUTHORS LOCUS LOCUS AUTHORS AUTHORS LOCUS LOCUS AUTHORS AUTHO | Query Match 66.0%; Score 13.2; DB 9; Length 50; Best Local Similarity 83.3%; Pred: No. 4.7e+04; Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0; Qy 1 ccgcgggctcacagtggt 18 | | ORGANISM synthetic construct REFERENCE 1 (bases 1 to 37) ATTHORS Lassner,M. and van Benennaam,A. TITLE Plant sterol acyltransferases JOURNAL Patent: WO 0116308A. 79 08-MAR-2001; MONSANTO COMPANY (US) FEATURES 137 Aorganism="synthetic construct" Ab_xref="taxon:32630" Ab_xref="taxon:32630" Ance="Synthetic oligonucleotide primer" ORIGIN 8 a 12 c 11 g 6 t | Query Match 63.0%; Score 12.6; DB 10; Length 37; Best Local Similarity 78.9%; Pred. No. 1e+05; Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0; Qy 1 ccgcgggctcacagtggtc 19 IIIII Db 5 CCGCGCCCACAATGGGC 23 | RESULT 4 AX090365 LOCUS AX090365 41 bp DNA PAT 21-MAR-2001 DEFINITION Sequence 58 from Patent W00116308. ACCESSION AX090365 GI:13444226 KEYWORDS KEYWORDS |
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| AR095615 Sequence AX043844 Sequence AX043846 Sequence AX043846 Sequence I43055 Sequence I43055 Sequence AR041128 Sequence AR041129 Sequence I31649 Sequence I31472 Sequence I11472 Sequence I117472 Sequence I11952 Sequence I11953 Sequence I11953 Sequence I11953 Sequence I11953 Sequence I19530 Sequence I86210 Sequence I86210 Sequence I86210 Sequence I86250 Sequence I86250 Sequence I86250 Sequence I86250 Sequence I86250 Sequence | 119534 Sequence 11 121731 Sequence 6 186214 Sequence 6 1809374 Sequence AR09535 Sequence AX033429 Sequence AS8773 Sequence AS8773 Sequence 19 AR078873 Sequence 176917 Sequence 25 A65881 Sequence 25 | AX042765 Sequence S45430 V alpha J a AR067323 Sequence AR073339 Sequence | PAT 01-DEC-1998 | ; t DB 10; Length 33; | 3; Indels |
| 9 12.2 61.0 40 9 AR095615 10 12.2 61.0 41 10 AX090361 11 12.2 61.0 44 10 AX090361 12 12.2 61.0 44 10 AX090361 13 11.8 59.0 16 9 AR041128 14 11.8 59.0 22 10 I43055 15 11.8 59.0 29 9 AR041129 17 11.8 59.0 30 9 AR041129 18 11.8 59.0 35 10 I31649 19 11.8 59.0 35 10 I31649 19 11.8 59.0 35 10 I31649 20 11.8 59.0 35 10 I31649 21 11.6 58.0 24 10 I33051 22 11.6 58.0 25 10 I39529 23 11.6 58.0 25 10 I39529 24 10.65209 25 11.6 58.0 25 10 I39529 26 27 11.6 58.0 25 10 I39529 27 11.6 58.0 25 10 I39529 28 11.6 58.0 25 10 I39529 29 11.6 58.0 25 10 I39529 20 11.6 58.0 25 10 I39529 21 11.6 58.0 25 10 I39529 22 11.6 58.0 25 10 I39529 23 11.6 58.0 25 10 I39529 24 10 I39532 25 11.6 58.0 25 10 I39532 26 27 11.6 58.0 25 10 I39532 27 11.6 58.0 25 10 I39532 28 11.6 58.0 25 10 I39532 | 11.6 58.0 26 10 11.6 58.0 26 10 11.6 58.0 30 9 11.6 58.0 30 9 11.6 58.0 30 9 11.4 57.0 18 9 11.4 57.0 25 10 | 11.4 57.0 25 9 11.4 57.0 25 9 11.2 56.0 20 9 11.2 56.0 20 9 | RESULT 1 192389 LOCUS LOCUS SEQUENCE 41 from patent US 5728519. DEFINITION SEQUENCE 41 from patent US 5728519. DEFINITION 192389 VERSION 192389.1 GI:3936859 KEYWORDS SOURCE ONGANISM UNKNOWN. ORGANISM UNKNOWN. ORGANISM LEVERENCE 1 (bases 1 to 33) AUTHORS Levenbook I.S., Chumakov, K.M., Norwoch TITLE ASSAY for virulent revertants of atte | nerelor atent: US 5728519-A 41 17-MAR-1998 Location/Qualifiers 1. 33 /organism="unknown" 6 a 7 c 9 g 11 66.0%; Score 13.2; | Similarity 83.3%; Pred. No. 5.2 5; Conservative 0; Mismatches cgggctcacagtggt 18 |

SOURCE

FEATURES

ORIGIN

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synthetic construct.
synthetic construct
artificial sequence.
1 (bases 1 to 29)
Eshhar, Z., Bolhuis, R. L. and Willemsen, R.A.
Immune cells having predefined biological specificity, comprising chimeric t cell receptor
Patent: WO 0031239-A 9 02-JUN-2000;
ESHHAR ZELIG (IL); YEDA RES & DEV (IL); BOLHUIS REINDER L H (NL);
WILLEMEN RALPH A (NL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YOICHI YAMADA,NAOKI ITANO,KOJI KIMATA
C12N15/09,C12N9/00,C12Q1/68//(C12N15/09,C12R1:91),C12N15/00,
(C12N15/00,C12R1:91)
Strandedness: Single;
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Pred. No. 1.7e+05;
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic DNA"
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Yolchi,Y.N.I.I. and Kimata.
Hyaluronate synthase promoter DNA
Patent: JP 1999196875-A 13 27-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .30
/organism="unidentified"
/db_xref="taxon:32644"
a 11 c 7 g 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  n2040) 30 bp DNA
Hyaluronate synthase promoter DNA.
E28465
                                                                                               Sequence 9 from Patent WO0031239.
AX026028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unidentified
JP 1999196875-A/13
27-JUL-1999
14-JAN-1998 JP 1998006191
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                                                                            DNA
                                                                                                                                AX026028.1 GI:10187483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Topology: Linear;
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                                                                                 29 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82.48;
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 18 CCGCGCGCTCACAG
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AX026028/c
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ACCESSION
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ORIGIN
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E28465/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                               MMTCRAIC7 45 bp mRNA ROD 15-MAR-1993 M.musculus mRNA for T-cell receptor, V-J alpha junction (A3/IIIC7). \chi_7^0 0\overline{1}13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (15-JAN-1993) J. Casanova, INSERM U132, Developpement Submitted (15-JAN-1993) J. Casanova, INSERM U132, Developpement Normal et Pathologique du, Systeme Immunitaire, Necker, Pavillon Kirmisson, 149 rue de Sevres, 75743 Paris Cedex, FRANCE 2 (bases 1 to 45)
Casanova,J.L., Martinon,F., Gournier,H., Barra,C., Pannetier,C., Regnault,A., Kourilsky,P., Cerottini,J.C. and Maryanski,J.L. Tell receptor selection by and recognition of two class I major histocompatibility complex restricted antigenic peptides that J. Exp. Med. 177 (3), 811-820 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
1 (bases 1 to 45)
                                                                                                                                                                                                                                                                                                                 Gaps
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J-alpha gene segment; junction; T-cell receptor; V-alpha gene
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9 c 18 q 12 t
                                                                                                                                            1. 41
/organism="synthetic construct"
/db_xref="taxon:33630"
/note="synthetic oligonucleotide primer"
a 13 c 15 g 8 t
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Pred. No. 9.9e+04;
0; Mismatches 4;
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                           artificial sequence.

1 (bases 1 to 41)
Lassner,M. and van Eenennaam,A.
Plant sterol acyltransferases
MONSANTO COMPANY (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/strain="DBA2"
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/db_xref="taxon:10090"
/haplotype="H2-d"
/tissue_type="T cell"
/cell_type="CTL"
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78.9%;
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synthetic construct
                 synthetic construct
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Mus musculus
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Best Local Similarity
Matches 15; Conserv
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Best Local Similarity
Matches 13; Conserv
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REFERENCE

KEYWORDS

RESULT

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REFERENCE AUTHORS

TITLE

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Gaps

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synthetic construct.
synthetic construct
artificial sequence.
1 (bases 1 to 41)
Savidge,B., Lassner,M.W., Weiss,J.D. and Post-Beittenmiller,D.
Nucleic acid sequences to proteins involved in tocopherol synthesis
Patent: WO 0063391-A 51 26-OCT-2000;
Calgene LLC (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                         Score 12.2; DB 9; Length 41; Pred. No. 1.6e+05; 0; Mismatches 3; Indels
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide primer"
a 11 c 14 g 6 t
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/db_xref="texon:32630"
/note="01jgonuclectide"
13 c 11 g 11 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               synthetic construct.

synthetic construct
artificial sequence.

( bases 1 to 44)
Lassner, M. and van Eenennaam, A.
Plant sterol acyltransferases
Patent: WO 0116308-A 54 08-MAR-2001;
MONSANTO COMPANY (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AKU90361 44 bp DNA
Sequence 54 from Patent WO0116308.
                             AX043844 41 bp DNA
Sequence 51 from Patent WO0063391.
AX043844
AX043844.1 GI:11342429
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Sequence 53 from Patent WO0063391.
AXO43846
AXO43846.1 GI:11342431
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Best Local Similarity 82.4%;
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Best Local Similarity
Matches 14; Conserv
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AX090361
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               AX043844
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Unclassified.

Unclassified.

Lunnen,K.D., Dalton,M.A., Wilson,G.G. and Xu,S.

Method for cloning and producing the Aval restriction endonuclease endonuclease endonuclease endonuclease endonuclease

Patent: US 6004793-A 8 21-DEC-1999;
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Lunnen, K.D., Dalton, M.A., Wilson, G.G. and Xu, S.

Method for cloning and producing the AvaI restriction endonuclease in E. coli and purification of the recombinant AvaI restriction endonuclease and purification of the recombinant and restriction patent: US 6004793-A 10 21-DEC-1999;

Location/Qualifiers
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   Length 30;
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Pred. No. 1.6e+05;
0; Mismatches 3; Indels
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Pred. No. 1.6e+05;
0; Mismatches 3; Indels
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Score 12.2; DB 10;
Pred. No. 1.7e+05;
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                                                                                                                                                           AR095613 40 bp DNA
Sequence 8 from patent US 6004793.
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US (
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AR095615
AR095615.1 GI:10023644
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Best Local Similarity 82.4%;
Matches 14; Conservative (
y Match 61.0%;
Local Similarity 82.4%;
hes 14; Conservative
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Best Local Similarity 82.4%;
Matches 14; Conservative
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18 CGCGTGCTCATGGTGGT 2
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|| CCCGGGCTCAAAGTTG 24
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CCCCGGGCTCAAAGTIG 24
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Unclassified.
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Best Local S:
Matches 14,
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KEYWORDS
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Search completed: October 2, 2001, 15:56:35 Job time: 14159 sec
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1 (bases 1 to 45)
Savidge, B., Lassner, M.W., Weiss, J.D. and Post-Beittenmiller, D.
Nucleic acid sequences to proteins involved in tocopherol synthesis Patent: WO.0063391-A 53 26-OCT-2000;
Calgene LLC (US)
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Nadeau, J.G., Dean, C.H., Schram, J.L., Howard, D.R., Dey, M.S. and
Wright, D.J.
Wright, D.J.
Detection of mycobacteria by multiplex nucleic acid amplification
Patent: US 5811269-A 13 22-SEP-1998;
Location/Qualifiers
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Leckie, G.W., Davis, A.H., Semple-Facey, I.E., Manlove, M.T. and
Solomon, N.A.
Materials and methods for the detection of Mycobacterium
tuberculosis
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Pred. No. 1.5e+05;
0; Mismatches 3; Indels
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/db_xxef="taxon:32630"
/note="Oligonuclectide"
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Best Local Similarity 82.4%;
Matches 14; Conservative (
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Defection of mycobacteria by multiplex nucleic acid amplification Patent: US 5811269-A 3 22-SEP-1998; Location/Qualifiers
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Nadeau,J.G., Dean,C.H., Schram,J.L., Howard,D.R., Dey,M.S. and
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Pred. No. 2.9e+05;
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Pred. No. 2.7e+05;
0; Mismatches 2;
Patent: US 5631130-A 38 20-MAY-1997;
Location/Qualifiers
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Sequence 3 from patent US 5811269.
AR041128 GI:5961624
                                                 /organism="unknown"
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                           10228115 seqs, 4726426750 residues
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Maximum Match 100%
Listing first 45 summaries
                                              OM nucleic - nucleic search, using sw model
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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MRNAs using full-length enriched and 5'-end enriched CDNA libraries Unpublished (2001)
Contact: Yutaka Suzuki
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Bmail: ysuzukiélma.u-tokyo.ac.jp
Suzuki,Y...Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched CDNA library. Gene 200 (1-2), 149-156 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 46)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lery,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.

Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                               AA196905 46 bp mRNA EST 12-MAR-1998 zq09b06.rl Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:629171 5' similar to TR:E36241 E36241 PM5 PROTEIN. ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="SOLR (kanamycin resistant)"
/note="Organ: skeletal muscle; Vector: pBluescript SK-;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Insert Length: 1100 Std Error: 0.00
Insert Length: 1100 Std Error: 0.00
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Pred. No. 4.8e+03;
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/clone_lib="Stratagene muscle 937209"
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High quality sequence stop: 1.
Location/Qualifiers

    .50
    /organism="Homo sapiens"

    .46
    /organism="Homo sapiens"

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/clone_lib="Sugano Homo
12 c 22 g 1
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/db_xref="taxon:9606"
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/dev_stage="adult"
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AU104386 AU104386
AL476427 T. brucei
AZ34556 1M0080114
AI684291 tw97b09.x
AZ812781 ZM0079B17
BG292849 60389872
AU102352 AU102352
AU102356 AU102356
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AZ404438 1M0173116
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AI762402 wh65e10.x
AA845818 ak85f01.s
AZ465895 1M0276F12
AZ834614 2M0117121
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AU106948 AU106948
AL466405 T. brucei
AI735009 as44e04.x
                                                                                                    AU107932 AU107932 AZ453043 IM0254A13
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Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo,K., Suyama,A. and Sugano,S.
Fine Structural analysis of transcription start sites of human
                                                                                    AU106328 AU106328
AA196905 Zq09b06.r
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AU106328 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone KAT00883, mRNA sequence.
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                                                            Description
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                 SUMMARIES
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TA140A04P
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AA466917
AA607492
A1149037
7 AU106912
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AZ591206
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with 74 DNA polymerase and 74 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (qi|4732114 qiplaF129072.1), a copy-number inducible derivative of plasmid Rl. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLLO-Gold (Stratagene) cells and selected for ampicillin resistance."
                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 40)
                                                                              Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                         Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab host="E. Coll strain XL10-Gold, T1-resistant, F-"/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                               Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCIM0254A13"
/clone=lb="Mouse 10kb plasmid UUGCIM library"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                      Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plate: 0254 row: A column: 13
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 40.
Location/Qualifiers
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87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plasmid ends
                                                                                                                                                                                                                                   Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                      Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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Best Local Similarity
Matches 14; Conser
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Butherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 50)

Suzukl,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo,K., Suyama,A. and Sugano,S.
Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ins.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              AU107932 50 bp mRNA EST 05-APR-2001
AU107932 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
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9 t lothers
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                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                         Score 13.6; DB 3;
Pred. No. 1.2e+04;
                                                                                                                                                                                                                                                              Mismatches
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Sugano Homo
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Department of Virology
                                                                                                                                                                                                         68.0%;
80.0%;
                                                                                                                                                                                                                                                                                                      1 ccgcgggctcacagtggtcg 20
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Matches 15; Conservative
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vp30g03.rl Barstead mouse proximal colon MPLRB6 Mus musculus cDNA clone IMAGE:1078228 5' similar to gb:U13705 Mus musculus domesticus C57BL/6J plasma glutathione (MOUSE);, mRNA sequence.
AA822940.1 GI:2892808
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                                                Gaps
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Score 12.8; DB 244; Length 40;
Pred. No. 3e+04;
0; Mismatches 2; Indels 0;
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/note="Organ: Kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: ECO RI; Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and so circles were made in vitro. Pollowing HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pol of 5,000 clones made from the same library (cloneIDs 13223/6-1333911, 1456007-1456775, and 150552-150285). Subtraction by Bento Soares and M. Patima Bonaldo. "
                                                                                                                                                                CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 31)
Hillar,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptco,M., Tan,F., Theising,B.,
Washle,Y., Walle,T., Waterston,R. and Wilson,R.
Unpublished (1997)
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
                                                                                                      Ph.D., Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., I
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                www-bio.llnj.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                              Trace considered overall poor quality Insert Length: 436 Std Error: 0.00 Seq primer: -40UP from Gibco High quality sequence stop: 1. Location/Qualifiers
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/clone_lib="NCI_CGAP_Kid11"

    .25
    /organism="Homo sapiens"
/db_xref="taxon:9606"

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/db_xref="taxon:10090"
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/clone="IMAGE:1078228"
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/clone="IMAGE:1078228"
/clone="IMAGE:1078258"
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/dab
                                                                                                                                                         Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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                                                                Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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1 (bases 1 to 25)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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Pred. No. 3e+04;
); Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                        The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trace considered overall poor quality Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 1. Location/Qualifiers
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Best Local Similarity 87.5%;
Matches 14; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 46)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
M., Rose, M., Rose, R.,
Stokes, R., Tingey, A., von Niederhausern, A.
Mouse whole genome scaffolding with paired end reads from 10kb
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Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. Sb Hommedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality Posstble reversed clone: similarity on wrong strand Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
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                                                                                                                                                                                                                               1. .31
/organism="Homo sapiens"
/db.xref="taxon:9606"
/clone="InAGE:1414681"
/clone_lib="Barstead spleen HPLRB2"
/sex="male"
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0276 cow: F column: 12
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
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/strain="C57BL/6J"
/db_xref="taxon:10090"
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SOURCE
ORGANISM
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AZ465895/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
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                                                                                                                                                                                                      FEATURES
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/Jab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G75BL/67 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil472114) [pl]AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 50)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A2834614 50 bp DNA GSS 20-FEB-2001
2M0117121F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0117121 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
/clone="UUGC1M0276F12"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 12.6; DB 244; Length 46;
Pred. No. 3.8e+04;
0; Mismatches 4; Indels 0
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Insert Length: 10000 Std Error: 0.00
Plate: 0117 row: I column: 21
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 50.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"/strain="C57BL/6J"
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78.9%;
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Best Local Similarity 78.9
Matches 15; Conservative
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Fax: 801 585 7177
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Gaps

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 50)
2 (bases I to 50)
3 (bases I to 50)
4 (bases I to 50)
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8 (bases I to
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AU106948 Sugano Homo sapiens CDNA library Homo sapiens CDNA clone
ACA03735, mRNA sequence.
AU106948. GI:13556469
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T. brucei sheared genomic DNA clone 140a04, forward sequence,
genomic survey sequence.
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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                                                                                                                                                                                                                                                                    Length 44;
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                                                                                                                                                                                                                                                                                                                                      5; Indels
                                                                                                                                                                                                                                                            60.0%; Score 12; DB 258;
75.0%; Pred. No. 7.5e+04;
tive 0; Mismatches 5;
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/db_xref="taxon:9606"
/clone="CAS03735"
                               /db_xref="taxon:5691"
/clone="233a12"
10 c 12 q
                                                                                                            12 g
/strain="TREU927"
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Best Local Similarity 75.0
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                          15; Conservative
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TA140A04P/c
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AU106948/c
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                                                                                                                                                                                                                                                                                (http://www.par.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (qi|4732114|qb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
                                                                                                                                                                               /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                            /lab_host="E. Coli strain XL10-Gold, Tl-resistant,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 44)
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                               /clone="UUGC2M0117121"
/clone_lib="Mouse 10kb plasmid UUGClM library"
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/db_xref="taxon:10090"
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                                                                                                         /sex="Male"
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Matches 15; Conserv
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Sreptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 37)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA466917 37 bp mRNA EST 11-JUN-1997 vf10g04.rl Knowles Solter mouse blastocyst B3 Mus musculus CDNA clone IMAGE:835350 5' similar to SW:RS9_RAT P29314 40S RIBOSOMAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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/clone_lib="Knowles Solter mouse blastocyst B3"
/tissue_type="blastocyst"
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Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                        /clone="IMAGE:2320062"
/clone_lib="Barstead aorta HPLRB6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 11.6; DB 24;
Pred. No. 1.2e+05;
0; Mismatches 4;
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t
                                                                                                                                       /sex="male"
/dev_stage="adult, age 64"
                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
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/db_xref="taxon:10090"
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Location/Qualifiers
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77.8%;
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Matches 14; Conser
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                                                                                                                                                                                                        nhiseanger ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU327/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Miller,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kriaman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., Wahlte,Y., Wylle,T., Waterston,R. and Wilson,R.
         1/pgusozamic.

1 (bases 1 to 22)

Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,

Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,

Melville,S.E., Rajandream,M.A. and Barrell,B.G.

Direct Submission

Submitted (10-DEC-2000) Trypanosoma brucel genome sequencing

project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,

Cambridge CBIO 1SA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
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Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 11.6; DB 258; Length 22;
Pred. No. 1.2e+05;
0; Mismatches 4; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism-"Trypanosoma brucei"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:5691"
/clone="140a04"
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Best Local Similarity 77.8%;
Matches 14; Conservative
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  rypanosoma.
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AI735009/c
                   REFERENCE
AUTHORS
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JOURNAL
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COMMENT
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KEYWORDS
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ò a

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/organism="Mus musculus"
/db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="rakafe:1002771"
/clone=lib="Stratagene mouse Tcell 937311"
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/dev_stage="Mi3 CD4+ cells"
/lab_host="SOLR (kanamycln resistant)"
/note="Organ: blood; Vector: pBluescript SK-; Site_1:
/note="Organ: blood; Vector: pBluescri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vm61h02.rl Stratagene mouse Tcell 937311 Mus musculus cDNA clone IMAGE:1002771 5' similar to SW:RS9_RAT P29314 40S RIBOSOMAL PROTEIN AA607492
                                                                        /note="Organ: embryo; Vector: pSPORT; Site_1: NotI;
Site_2: Sal1: Cloned unidirectionally from mRNA prepared
from 800 blastocysts. Primer: Sal1(dT):
5'-CGGTCGACCGTCGACCGTTTTTTTTTTTTTT-3'. CDNAs were
cloned into the NotI/SalI sites of a pSPORT vector (Life
Technologies). Two different size selections: B1 (larger
inserts) and B1.
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Parkway, Box 8501, St. Louls, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 11.6; DB 7; Length 37;
Pred. No. 1.2e+05;
0; Mismatches -4; Indels
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/dev_stage="embryo (pre-implantation)"
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The WashU-HHMI Mouse EST Project
                                      /lab_host="DH10B
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Best Local Similarity 77.8%;
Matches 14; Conservative (
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Search completed: October 2, 2001, 15:00:45 Job time: 10814 sec

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127712 Sequence 19
183056 Sequence 19
AX094895 Sequence
A09940 oligonucleo
A47740 Sequence 4
AR019411 Sequence
1.32460 Human (clon
AR092516 Sequence
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                             1344157 segs, 7733874588 residues
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Maximum Match 100%
Listing first 45 summaries
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10-JUN-1998

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EUKATYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 21)
Lander, E.S., Gargill, M., Ireland, J.S., Bolk, S., Daley, G.Q. and McCarthy, J.J.
Single nucleotide polymorphisms in genes
Patent: WO 0110350-A 73 15-MAR-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US); Millennium
                                                                                          1 (bases 1 to 21) Wang,C.J. and \mbox{Nu},\mbox{K.} Kits for detecting a target nucleic acid with blocking
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Pred. No. 2.2e+05;
1; Mismatches 2; Indels (
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Patent: US 5712386-A 19 27-JAN-1998;
Location/Qualifiers
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Sequence 73 from Patent W00118250.
AX094895.1 GI:13511098
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/db_xref="taxon:9606"
5 c 4 g 4
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Location/Qualifiers
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          183056 21 bp DNA Sequence 19 from patent US: 183056 183056.1 GI:3211353
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108721 Sequence 9
155881 Sequence 11
AR004362 Sequence
AR097153 Sequence
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AR044492 Sequence
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AR012355 Sequence
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I92341 Sequence 2
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Methods for reducing non-specific priming in DNA detection
Patent: US 5567583-A 19 22-OCT-1996;
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        unclassified.

1 (bases 1 to 22)

Moureau,P., Derclaye,I., Delor,I. and Cornelis,G.

Nucleic acid probes useful for detecting specifically different
bacterial species of the genus Campylobacter
Patent: EP 0350392-A 2 10-JAN-1990;
IRE-MEDGENIX S.A

Location/Qualifiers
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                                                                                                                                                                                    Length 22;
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Pred. No. 2.7e+05;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                               w unidentified unclassified.

1 (bases 1 to 38)
Wood, P.C. and Quirk, A.V.
YEAST STRAINS
PATENT: WO 9533833-A 4 14-DEC-1995;
DELTA BIOTECHNOLOGY LTD (GB)
Other publication AU 2626295 960104.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 38)
Wood,P.Carolyn and Quirk,A.Victor.
Yeast strains
Patent: US 5783423-A 4 21-JUL-1998;
Location/Qualifiers
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/organism="unidentified"
/db_xref="taxon:32644"
a 9 c 13 g 9
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AR019411
AR019411,1 GI:3974525
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/organism="unidentified"
/db_xref="taxon:32644"
                                                                                                                                                                                                                                                                                                     A4/740 38 bp DNA Sequence 4 from Patent W09533833.
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82.4%;
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Matches 14; Conservative
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Matches 14; Conserv
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HUMTCVDIDK 47 bp mRNA pRI 10-FEB-1995
Human (clone: 3cpj20) T-cell receptor delta-chain (V-delta-1) mRNA.
L32460
L32460.
L32460.1 GI:497530
T-cell receptor; delta chain.
Homo sapiens intestine cDNA to mRNA.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Manmalia; Eutheria: Primates; Catarrhini; Hominidae: Homo.
1 (bases 1 to 47)
Chowers; Y., Holtmeier, W., Harwood, J., Morzycka-Wroblewska, E. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 50)
Loosmore, S.M., Yacoob, R.Khayyam, Zealey, G.Ross and Klein, M.Henri.
Expression of gene products from genetically manipulated strains of
bordetella
Patent: US 5998168-A 46 07-DEC-1999;
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82.4%; Pred. No. 2.3e+05;
live 0; Mismatches 3;
                                                                                   Score 12.2; DB 9;
Pred. No. 2.4e+05;
0; Mismatches 3;
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J. Exp. Med. 180 (1), 183-190 (1994)
94275371
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AR092516
AR092516.1 GI:10019270
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/db_xref="taxon:9606"
/tissue_type="intestine"
15 c 9 9 14
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07-SEP-2000

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Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 20)
1 (bases 1 to 20)
1 (bases N.M.P. and David,G.J.
New members of the 91ypican gene family
Patent: WO 9937764-A 49 29-JUL-1999;
VEUGELERS MARK PAUL DITTMAR (BE); VLAAMS INTERUNIV INST BIOTECH
(BE); DAVID GUIDO JOSEPH FRANS (BE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polypeptidic compositions and methods for the treatment of tumors Patent: Wo 0108385-A 58 25-JAN-2001; Genentech, Inc. (US) Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  synthetic construct.
synthetic construct
artificial sequence.
1 (bases 1 to 25)
Botstelin, D., Goddard, A., Gurney, A.L., Hillan, K.J., Roy, M.A. and
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Pred. No. 4.2e+05;
0; Mismatches 2; Indels
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/db_xref="taxon:32630"
/note="Synthetic Oligonucleotide Probe"
1 8 c 5 9 3 t
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Pred. No. 5.1e+05;
0; Mismatches 4;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
a a 3 c 6 g 2
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Sequence 32 from patent US 5817495.
ARO44492
AXU20035 20 bp DNA
Sequence 49 from Patent WO9937764.
AX020035
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Sequence 58 from Patent WO0105836.
AX076946
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Best Local Similarity 86.7%;
Matches 13; Conservative C
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Knappik, A. Pack, P., Ilag, V., Ge, L., Moroney, S. and Plueckthun, A. PROTEIN (POLY) PEPTIDE LIBRARIES
PAGENT. WO 9708320-A 157 06-MAR-1997;
MORPHOSYS PROTEINOPTIMIERUNG (DE)
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      Score 12.2; DB 9;
Pred. No. 2.3e+05;
0; Mismatches 3;
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75.0%; Pred. No. 3.4e+05;
iive 0; Mismatches 5.
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1 (bases 1 to 20)
Wallace,R.Bruce and Ugozzoll,L.
Manchyping of multiple allele systems
Patent: US 5521301-A 4 28-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADU848 48 bp DNA
Sequence 157 from Patent WO9708320.
A60848
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Sequence 4 from patent US 5521301.
121584
121584.1 GI:1601938
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/db_xref="taxon:32644"
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        Ouery Match
Best Local Similarity 82.4%;
Matches 14; Conservative
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Matches 15; Conserv
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RESULT 10 A60848

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RESULT 121584/c LOCUS

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REFERENCE AUTHORS TITLE JOURNAL FEATURES BASE COUNT ORIGIN

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RESULT 11 AX020035

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Score 11.6; DB 9; Length 43; Pred. No. 4.6e+05; 0; Mismatches 4; Indels

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Search completed: October 2, 2001, 15:56:37 Job time: 14161 sec
 /organism="unknown"
                                                               Query Match 58.0%;
Best Local Similarity 77.8%;
Matches 14; Conservative
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1 (bases 1 to 36)
Dahm, M.W.
METHOD OF QUANTIFYING TUMOUR CELLS IN A BODY FLUID AND A SUITABLE
                                  1 (bases 1 to 27)
Pedersen, A. Hjelholt, Vind, J., Svendsen, A., Cherry, J.R., Lamsa, M., Schneider, P. and Jensen, B. Kostgaard.
H. sub. 2 0. sub. 2 - stable peroxidase variants
Patent: US 5817495-A 32 06-OCT-1998;
                                                                                                                                                                                                                           Gaps
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Unknown.
Unclassified.
1 (bases 1 to 43)
11 (bases 1 to 43)
Tal,R., Wong,H.C., Casipit,C., Chavaillaz,P. and Wittman,V.
Methods for peptide synthesis and purification
Patent: US 5763284-A 46 09-JUN-1998;
Location/Qualifiers
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Pred. No. 5e+05;
0; Mismatches 4; Indels
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Pred. No. 4.7e+05;
0; Mismatches 4; Indels
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Location/Qualifiers
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Sequence 46 from patent US 5763284.
AR012355 GI:3970345
                                                                                                                                                                                                                                                                                                                                      36 bp DNA
Sequence 13 from Patent WO9718322.
A93959
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                                                                                                                             /organism="unknown"
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77.8%;
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Best Local Similarity 77.8%;
Matches 14; Conservative
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18 GGCGACGGAATCGATGG 1
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Homo saplens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 50)
Suzuki,Y., Tsunoda,T., Tanaka,T., Makamura,Y., Morishita,S., Hata, K., Suyama, A. and Sugano,S.
Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries of Upublished (2001)
Contact: Yutaka Suzuki
Department of Virology Institute of Medical Science, University of Tokyo
1 Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
5. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library, Gene 200 (1-2), 149-156 (1997).
mRNAs using full-length enriched and 5'-end enriched CDNA libraries Unpublished (2001)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedal, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki.Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched CDNA library. Gene 200 (1-2), 149-156 (1997).
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AU105195 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
AU105195 mRNA sequence.
AU105195 GI:13554716
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CoLF6124"
/clone_lib="Sugano Homo sa
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/db_xref="taxon:9606"
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo,K., Suyama,A. and Sugano,S.
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AU105198 AU105198
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AU103598 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
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AU103598
AU103598.1 GI:13553119
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Mammalla; Euteleostomi;
Mammalla; Euteria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
1 (bases 1 to 50)
2 Suzuki,Y., Tsunoda,T., Tanaka,T., Makamura,Y., Morishita,S., Okubo,Y., Suyama,A. and Sugano,S.
7 H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo,Y., Suyama,A. and Sugano,S.
Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries
L. Unpublished (2001)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ins.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
                                                                                                                                                                                                                                                                                Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo,K., Suyama,A. and Sugano,S., Nakamura,Y., Morishita,S., Okubo Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries Contact: Yutaka Suzuki
Department of Virology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers
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AU105198 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HSIO1637, mRNA sequence.
AU105198.1 GI:13554719
                                         AU105197 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
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Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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4-6-1, Shirokanedal, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
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/clone="HRC08429"
                                                                                       HRC08429, mRNA sequence
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,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers
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2M0085D03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0085D03 R, DNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Dases 1 to 47)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Jalan, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. Mouse whole genome scaffolding with paired end reads from 10kb
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Unpublished (2000)
Contact: Robert B. Weiss
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HSIQ1637"
/clone_lib="Sugano Homo sapiens cDNA library"
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0085 cow: D column: 03
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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80.0%;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 50)
Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo,K., Suyama,A. and Sugano,S.
Fine Structural analysis of transcription start sites of human onpublished (2001)
Contact: Yutaka Suzuki
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Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries Unpublished (2001)
Department of Wirology
Institute of Medical Science, University of Tokyo
Enstitute of Medical Science, University of Tokyo
Email: ysuzuki@ims.u-tokyo.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                                   Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Institute of Medical Science, Tokyo 108-8639, Japan
Email: ysuzukielins.u-tokyo.ac.jp
Suzuki.Y., Yoshitomo-Nakagawa.K., Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched CDNA library. Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers
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AU103768 Sugano Homo sapiens CDNA library Homo sapiens CDNA clone
HEP12651, mRNA sequence.
AU103768
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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0; Mismatches 2;
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/db_xref="taxon:9606"
/clone="HEP12651"
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AU103765.1 GI:13553286
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Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
5-6-1, Shirokaneda, Minatoku, Tokyo 108-8639, Japan
5-8mail: ysuzukiélans.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

Location/Qualifiers
10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMM42 (gil4732114(gb)AF129072.1), a copy-number inducible derivative of plasmid Rl. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampliallin resistance."
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Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries Unpublished (2001)
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AU103765 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HEP11908, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 1.5e+04;
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/db_xref="taxon:9606"
/clone="HEP15178"
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AU105437.1 GI:13554958
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83.3%;
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Best Local Similarity 83.3%;
Matches 15; Conservative
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Best Local Similarity
Matches 15; Conserv
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RESULT 6 AU105437/C LOCUS DEFINITION

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ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

BASE COUNT

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AU103765/c LOCUS DEFINITION

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AU103771/c

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REFERENCE AUTHORS

JOURNAL

COMMENT

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Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata, H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo, K., Suyama,A. and Sugano,S.
Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries uppublished (201)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Bmail: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries Unpublished (2001)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
Fmail: ysuzukielms.u-tokyo.ac.jp
Email: ysuzukielms.u-tokyo.ac.jp
Suzuki;Y. Yoshitomo-Makagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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AU103791 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HED16708, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
/clone="HEP15173"
/clone=lib="Sugano Homo sapiens cDNA library"
1 3 c 11 g 20 t
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Pred. No. 2.4e+04;
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Pred. No. 2.4e+04;
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/db_xref="taxon:9606"
/clone="HEP16708"
/clone=lib="Sugano Homo sap
a 13 c 13 g 18
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Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Suzuki, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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1 (bases 1 to 50)

Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo,K., Suyama,A. and Sugano,S.

Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries Unpublished (2001)
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AU103787. GI:13553308
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 2.4e+04;
0; Mismatches 2; 1
                                                                                                                     Score 12.8; DB 107;
Pred. No. 2.4e+04;
0; Mismatches 2;
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/db_xref="taxon:9606"
/clone="HEP13114"
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l Similarity 87.5%;
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Best Local Similarity 87.5%;
Matches 14; Conservative
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Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Brail: Suzuki@ims.u-tokyo.ac.jp
Suzuki,Y: Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
Institute of Medical Science, University of Tokyo 4-6-1, Shirorkanedal, Minatoku, Tokyo 108-8639, Japan 4-6-1, Shirorkanedal, Minatoku, Tokyo 108-8639, Japan Email: ysuzukieims.u-tokyo.ac.jp Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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Eukaryota, Matazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Eukaryota, Matazoa, Chordates, Catarrhini; Hominidae; Homo.

(bases 1 to 50)
Suzuki, Y., Tsunoda, T., Taira, H., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isoqai, T., Tanaka, T., Nakamura, Y., Morishita, S., Okubo, K., Suyama, A. and Sugano, S.
Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries
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AU103977 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HEP17580, mRNA sequence.
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Pred. No. 2.4e+04;
0; Mismatches 2; Indels
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/db_xref="taxon:9606"
-/clone="HEP10657"
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/organism="Homo sapiens"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 50)
Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Tsunoda,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo,K., Suyama,A. and Sugano,S.

H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo,K., Suyama,A. and Sugano,S.

Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries Oppublished (2001)
Contact: Yutaka Suzuki
Department of Virology
                                                                                                                                                                                                                                                                                                                                                        Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 50)

Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo,K., Suyama,A. and Sugano,S.

Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Smail: Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo. Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
'S. Construction and characterization of a full length-enriched and
's'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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AU103974 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HEP00461, mRNA sequence.
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AU103975 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HER10657, mRNA sequence.
AU103975 GI:13553496
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/clone="HEP00461"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 50)

Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo,K., Suyama,A. and Sugano,S.
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4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y. Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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AU103980 50 bp mRNA EST 05-APR-2001
AU103980 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
KAT01573, mRNA sequence.
AU103980. GI:13553501
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Best Local Similarity 87.5%; Pred. No. 2.4e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0;
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/db_xref="taxon:9606"
/clone="KAT01573"
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68.0
67.0
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                                                          October 2, 2001, 15:56:37 ; Search time 3339.34 Seconds (without alignments) 92.640 Million cell updates/sec
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      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                  1344157 seqs, 7733874588 residues
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Maximum Match 100%
Listing first 45 summaries
                                           OM nucleic - nucleic search, using sw model
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em_htg_inv2:*
em_htg_other:*
em_htg_rod:*
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14-AUG-2000

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 42)
Jorgensen, J.L., Esser, U., de St Groth, B.F., Reay, P.A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              red guenon.
Erythrocebus patas
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 38)
Karanth, P. and Stewart, C.B.
Direct Submission
Submitted (16-OCT-1999) Biological Sciences, State University of
New York, 1400 Washington Avenue, Albany, NY 12222, USA
1.38
                                                                                                                                                                                                                                                                                                                      <1 >>42
/note="This sequence comes from FIG. 4 c; conceptual
translation presented here differs from translation in
publication"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cercopithecinae; Erythrocebus.

1 (bases 1 to 38)
Karanth, P., Stewart, C.B., Holt, R.A., deKoning, J. and Messier, W. Positive Darwinian selection on the lineage leading to humans Unpublished
                                                                                                                                                                                                                       92114961
GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 77087] from the original journal article.
This sequence comes from FIG. 4 c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EPPROTII2 38 bp DNA PRI 23-DEC-2000
Erythrocebus patas protamine P2 gene, exon 2 and complete cds.
ARI95645.1 GI:11990583
                                                                                                                                                                                      Mapping T-cell receptor-peptide contacts by variant peptide immunization of single-chain transgenics Nature 355 (6357), 224-230 (1992)
                                 S77087 42 bp mRNA ROD 14-AUG-20
T-cell receptor beta chain V-J region {CDR3 region} {mice, transgenic, mRNA Partial, 42 nt].
                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
/product."T-cell receptor beta chain V-J region"
/protein_id="AAB20964.2"
/db_xref="G1:9800659"
/translation="CASSAFWGYAEQFF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 13.8; DB 95;
Pred. No. 2.1e+04;
); Mismatches 2;
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/db_xref="taxon:10095"
<1. .>42
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88.2%;
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S77087.1 GI:242717
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Best Local Similarity 88.2
Matches 15; Conservative
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A08101 Synthetic o
A08100 Synthetic o
A62490 Sequence 5
A69043 Sequence 1
L139593 Homo sapien
AR011280 Sequence
117918 Sequence
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AR003624 Sequence
A08096 Synthetic o
I79231 Sequence
AR101074 Sequence
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Chandy,K.G., Kalman,K., Chandy,G. and Gutman,G.A.
Voltage-gated potassium channel gene, KV1.7, vectors and host cells comprising the same, and recombinant methods of making potassium channel proteins
Channel proteins
Patent: US 5559009-A 3 24-SEP-1996;
Location/Qualifiers
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A36503 Sequence 44
AR080136 Sequence
AX097533 Sequence
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179830 Sequence 15
AR052426 Sequence
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I33779 Sequence 49
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191198 Sequence 39
            E04313 PCR primer
A45762 Sequence 19
AR069418 Sequence
                                              143148 Sequence 1
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A46142 Sequence 37
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Pred. No. 2.1e+04;
0; Mismatches 2;
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A62490
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AR003624
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11 c 5 a
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88.2%;
I26640.1 GI:1606510
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Best Local Similarity 88.2
Matches 15; Conservative
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                                                                                                                                                                                                                       Baudu, P., Riviere, M., Audonnet, J. and Bouchardon, A. ELINE POLYNCLEOTIDE VACCINE FORMULA PACH. FOLINE FORMULA PACH. WO 9803660-A 25 29-JAN-1998; BAUDU PHILIPPE (FR) Other publication FR 2751223 19980123.
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Pred. No. 3.4e+04;
0; Mismatches 1;
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Dillon, P.J. and Vockley, J.G.
Arginase II
Patent: US 5780286-A 12 14-JUL-1998;
    Mismatches
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AR018055
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Sequence 25 from Patent WO9803660.
A69037
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/organism="unidentified"
/db_xref="taxon:32644"
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10 c 8 g
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93.3%;
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Best Local Similarity 93.3%;
Matches 14; Conservative
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9
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Best Local Similarity 93.3
Matches 14; Conservative
 16; Conservative
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AR018055/c
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AR071945/c
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                       /product="protamine 2"
/protein_id="AAG42202.1"
/da_xref="G1:119905800"
/translation="WMYRMRSLSERPHEWHGQOVYGGEGGCHNGGEEGGLSPEHVEVY
ERTHQGYSHHRRRRCSRRRLYRIHRRRHRSCRRRRRRSCRHRRRRRRGCRTRRRRCRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Semnopithecus entellus.
Semnopithecus entellus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 38)

Raranth,P. and Stewart,C.B.

Direct Submission
Submitted (16-OCT-1999) Biological Sciences, State University of
New York, 1400 Washington Avenue, Albany, NY 12222, USA
                                                                                                                                                                                                                                                                                                                                                                                                 SEPROTII2 38 bp DNA PRI 23-DEC-2000 SEPROTIILL SAGMODILIA PRI 23-DEC-2000 AF195643 GI:11990579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Colobinae; Semnopithecus.

1 (bases 1 to 38)
Karanth, P., Stewart, C.B., Holt, R.A., deKoning, J. and Messier, W. Posttive Darwinian selection on the lineage leading to humans Unpublished
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Pred. No. 2.7e+04;
0; Mismatches 4; Indels
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/organism="Semnopithecus entellus"
/db_xref="Leaxon:88029"
/note="Common name:Hanuman langur"
join(AF195642.1:<1. .274,1. .>38)
/product="protamine 2"
join(AF195642.1:1. .274,1. .38)
/organism="Erythrocebus patas"
/db_xref="taxon:9538"
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80.0%;
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Best Local Similarity 80.0%;
Matches 16; Conservative (
                                                                                                                                                                                                                                                                                                       1 gaaactgcagaaggcactga 20
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C12N9/22,C12N1/21,C12N15/55,(C12N9/22,C12R1:19),(C12N1/21, PC
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                                                                                                                                                                                                                                                                                                                                                                                       66.0%; Score 13.2; DB 10; Length 27; 83.3%; Pred. No. 4.4e+04; tive 0; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 65.0%; Score 13; DB 10; Length 44; Best Local Similarity 100.0%; Pred. No. 5.4e+04; Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                                                      1 (bases 1 to 27)
Cimino,G.D. and Lin,L.
Quality control assay for platelet decontamination
Patent: US 5565320-A 13 15-OCT-1996;
Location/Qualifiers
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E04313.1 GI:2172516
JP 1993038286-A/3.
synthetic construct.
M synthetic construct.
artificial squence.
1 (bases 1 to 44)
Kimuta.S.
VARIANT TYPE ESCHERICHIA COLI RIBONUCLEASE H
PATENT. JP 1993038286-A 3 19-FEB-1993;
TANPAKU KOGAKU KENKYUSHO:KK
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/db_xref="taxon:32630"
10 c 12 g 7 t
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Artificial sequence; Genes.
JP 1993038286-A/3
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07-AUG-1991 JP 1991197703
                                                                                                                                                                                                                                                              /organism="unknown"
1 c 6 q
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topology: Linear;
hypothetical: No;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              anti-sense: No;
I27338.1 GI:1818114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 AACTGCAGAAGGCTAGGA 19
                                                                                                                                                                                                                                                                                                                                                                                         Query Match 66.0 Best Local Similarity 83.3 Matches 15; Conservative
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Synthetic construct.

SM synthetic construct.

SM synthetic construct.

artificial sequence.

E 1 (bases 1 to 44)

S Kimura,S., Ishikawa, H. and Nakamura, H. .

KHILISTANG PROFEIN MOLECULE

L Patent: JP 1993308963-A 3 22-NOV-1993;

TANPARU KOGAKU KENKYUSHO: KK

OS Artificial gene

OC Artificial sequence; Genes.

PN JP 1993308963-A/3

PD 22-NOV-1993

PD 22-NOV-1993

PD 22-NOV-1993

PP 08-NAY-1992 JP 1992115877

PI KIMURA SHIGENOBU, ISHIKAWA HIROKI, NAKAMURA HARUKI PC

C112N-/22, COTKA/308, C12N15/55, C12P21/00;

CC strandedness: Single;

CC topology: Linear;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    67.0%; Score 13.4; DB 9; Length 43; 93.3%; Pred. No. 3.4e+04; 1ve 0; Mismatches 1; Indels
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/db_xref="taxon:32630"
9 c 11 g 7 t
                                                                                                                      Unknown.
Unclassified.
1 (bases 1 to 43)
Vockley,J.G and Dillon,P.J.
Arghase II
Patent: US 5912159-A 12 15-JUN-1999;
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Sequence 13 from patent US 5565320.
127338
Sequence 12 from patent US 5912159.
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10 c 8 g
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                                               AR071945.1 GI:7222833
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Serine protease inhibitor proteins, medicaments containing them, DNA sequences coding for these proteins and methods for producing Phase proteins, medicaments and DNA sequences Patent: EP 0373335-A 19 20-JUN-1990; Gruenenthal GmbH
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synthetic construct
artificial sequence.
1 (bases 1 to 28)
Heinzel-Wieland, R., Anmann, J., Steffens, G.J. and Flohe, L.
Serine protease inhibitor proteins, medicaments containing them,
DNA sequences coding for these proteins and methods for producing
                                      1 (bases 1 to 22)
Martin,M.T., Smith,R.G., Darsley,M.J., Simpson,D.M. and
Backburn,G.F.
Beaction-based selection for expression of and concentration of
catalytic moieties
Patent: US 5631137-A 1 20-MAY-1997;
                                                                                                                                                                                                                                                   Gaps
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1 (bases 1 to 28)
Heinzel-Wieland, R., Ammann, J., Steffens, G.J. and Flohe, L.
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Pred. No. 7.1e+04;
0; Mismatches 2;
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Pred. No. 7.1e+04;
0; Mismatches 2;
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                                                                                                                                                  /organism="unknown"
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Synthetic oligonucleotide M2.
A08097.1 GI:413338
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Cecutti, M., Chabli, H., Devauchelle, G., Gauthier, L., Kaczorek, M., Lefranc, M. and Poul, M.
RECOMBINANT BACULOVIRUS AND USE THEREOF IN THE PRODUCTION OF MONOCLONAL ANTIBODIES
PATENT: WO 9520672-A 19 03-AUG-1995,
PROTEINE PERFORMANCE (FR)
Other publication AU 1582495 950815
Other publication FR 2715664 950804.
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  07-MAR-1997
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Martin,M.T., Smith,R.G., Darsley,M.J., Simpson,D.M. and
Blackburn,G.F.
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Pred. No. 7.1e+04;
4; Mismatches 1; Indels
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Pred. No. 7.1e+04;
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Patent: US 5891648-A 1 06-APR-1999;
         Sequence 19 from Patent W09520672.
A45762
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Sequence 1 from patent US 5631137.
143148.1 GI:2468392
                                                                                                                                                                                                                                                            /organism="unidentified"
/db_xref="taxon:32644"
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87.5%;
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68.8%;
 22 bp
                                       A45762.1 GI:2300149
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Best Local Similarity 68.8
Matches 11; Conservative
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Matches 14; Conservative
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these proteins, medicaments and DNA sequences
Patent: EP 0373335-A 23 20-JUN-1990;
Gruenenthal GmbH
Location/Qualifiers
1. 28
//organism="synthetic construct"
//db_xref="taxon:32630"
5 a 9 c 9 g 5 t
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                    JOURNAL
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BASE COUNT ORIGIN

; 0 Gaps ö Query Match

64.0%; Score 12.8; DB 9; Length 28; Best Local Similarity 87.5%; Pred. No. 7.1e+04; Matches 14; Conservative 0; Mismatches 2; Indels

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Search completed: October 2, 2001, 15:56:39 Job time: 14163 sec

| 13.4 67.0 43 18 AAV00587 13.4 67.0 43 20 AAX7316 13.4 67.0 43 21 AAA08070 13.4 67.0 44 14 AAQ40649 13.4 67.0 44 15 AAQ5496 13.4 67.0 44 15 AAQ5275 13.2 66.0 27 14 AAQ47315 13.2 66.0 27 17 AAT47908 13.2 66.0 27 17 AAT47908 | 13 65.0 44 14 AAQ38711 MUE 13 65.0 44 14 AAQ38711 MUE 13 65.0 44 14 AAQ38711 MUE 2.8 64.0 21 16 AAQ95581 PPTH 2.8 64.0 35 19 AAV9413 PPTH 2.8 64.0 35 22 AAX56735 2.8 64.0 36 21 AAC9404 FPU 2.8 64.0 36 21 AAC95237 RAC 2.6 63.0 21 14 AAQ35338 PCR 2.6 63.0 21 14 AAQ35338 PCR 2.6 63.0 25 16 AAX9564 PCR 2.6 63.0 21 14 AAQ35338 PCR 2.6 63.0 25 16 AAX9564 PCR 2.6 63.0 22 16 AAX9564 PCR 2.6 63.0 25 16 AAX9564 PCR 2.6 63.0 25 16 AAX9564 PCR 2.6 63.0 26 AAX964 PCR 2.6 63.0 26 AAX964 PCR 2.6 63.0 AAX | 12.6 63.0 26 18 12.6 63.0 26 18 12.6 63.0 26 19 12.6 63.0 36 20 12.6 63.0 36 21 12.6 63.0 39 21 12.4 62.0 25 18 12.4 62.0 28 21 12.4 62.0 28 21 12.4 62.0 28 21 12.4 62.0 30 21 | RESULT 1 AAC65538 ID AAC65538 standard; DNA; 20 BP. XX ACA AAC65538; XX ACA AAC65538; XX XX ACA AAC65538; XX XX XX XX XX XX XX XX XX | AXX XXX XXX XXX XXX Homo saplens. XX US6133031-A. XX 17-0CT-2000. XX |
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| | | | ZZHXXZZZXŽŽ | \$333\$ |
| 4.5 Compugen Ltd. ; Search time 876.95 Seconds (without alignments) | . 854978 | eneseqn/NA1980.DAT:* eneseqn/NA1981.DAT:* eneseqn/NA1982.DAT:* eneseqn/NA1983.DAT:* eneseqn/NA1984.DAT:* | geneseqn/Na1986.DaT:* geneseqn/Na1986.DaT:* geneseqn/Na1981.DaT:* geneseqn/Na1989.DaT:* /geneseqn/Na1991.DaT:* /geneseqn/Na1991.DaT:* /geneseqn/Na1991.DaT:* /geneseqn/Na1992.DaT:* /geneseqn/Na1992.DaT:* /geneseqn/Na1992.DaT:* /geneseqn/Na1995.DaT:* /geneseqn/Na1995.DaT:* /geneseqn/Na1996.DaT:* /geneseqn/Na1996.DaT:* /geneseqn/Na1996.DaT:* /geneseqn/Na1996.DaT:* /geneseqn/Na1996.DaT:* /geneseqn/Na1996.DaT:* /geneseqn/Na1996.DaT:* /geneseqn/Na1996.DaT:* /geneseqn/Na1996.DaT:* | dicted by chance to have a re of the result being printed, 1 score distribution. S Description Human focal adhesi Human focal adhesi Dystrophin gene sp Neisseria species Splice site for mo Soluble mouse Fas HIV Vpr C terminal HIV-1 fragment PCR PCR Primer used to Primer AB067 for F PCR Primer SR used |
| GenCore version Copyright (c) 1993 - 2000 nucleic search, using sw model October 2, 2001, 16:18:35; | ' 0 H G 6 | length: 0 length: 50 length: 50 I Minimum Match 00% Listing first 45 summaries N_Geneseq_0601:* SIDS8/gcgdata/geneseq/geneseqn/NA1980.DAT:* SIDS8/gcgdata/geneseq/geneseqn/NA1981.DAT:* SIDS8/gcgdata/geneseq/geneseqn/NA1981.DAT:* SIDS8/gcgdata/geneseq/geneseqn/NA1983.DAT:* SIDS8/gcgdata/geneseq/geneseqn/NA1983.DAT:* SIDS8/gcgdata/geneseq/geneseqn/NA1984.DAT:* SIDS8/gcgdata/geneseq/geneseqn/NA1984.DAT:* SIDS8/gcgdata/geneseq/geneseqn/NA1984.DAT:* SIDS8/gcgdata/geneseq/geneseqn/NA1984.DAT:* SIDS8/gcgdata/geneseq/geneseqn/NA1984.DAT:* SIDS8/gcgdata/geneseq/geneseqn/NA1984.DAT:* SIDS8/gcgdata/geneseq/geneseqn/NA1984.DAT:* SIDS8/gcgdata/geneseq/geneseqn/NA1984.DAT:* SIDS8/gcgdata/geneseqn/geneseqn/NA1984.DAT:* | 7: /SIDSB/gcgdata/geneseq//geneseqn/NA1986.DAT:* 8: /SIDSB/gcgdata/geneseq//geneseqn/NA1986.DAT:* 9: /SIDSB/gcgdata/geneseq//geneseqn/NA1987.DAT:* 10: /SIDSB/gcgdata/geneseq//geneseqn/NA1999.DAT:* 11: /SIDSB/gcgdata/geneseq//geneseqn/NA1999.DAT: 12: /SIDSB/gcgdata/geneseq//geneseqn/NA1991.DAT:* 14: /SIDSB/gcgdata/geneseq//geneseqn/NA1991.DAT:* 15: /SIDSB/gcgdata/geneseq//geneseqn/NA1991.DAT:* 16: /SIDSB/gcgdata/geneseq//geneseqn/NA1993.DAT:* 17: /SIDSB/gcgdata/geneseq//geneseqn/NA1994.DAT:* 18: /SIDSB/gcgdata/geneseq//geneseqn/NA1996.DAT:* 18: /SIDSB/gcgdata/geneseq//geneseqn/NA1996.DAT:* 18: /SIDSB/gcgdata/geneseq//geneseqn/NA1996.DAT:* 18: /SIDSB/gcgdata/geneseq//geneseqn/NA1999.DAT:* 20: /SIDSB/gcgdata/geneseq//geneseqn/NA1999.DAT:* 21: /SIDSB/gcgdata/geneseq//geneseqn/NA1999.DAT:* 22: /SIDSB/gcgdata/geneseq//geneseqn/NA2000.DAT:* 22: /SIDSB/gcgdata/geneseq//geneseqn/NA2000.DAT:* 23: /SIDSB/gcgdata/geneseq//geneseqn/NA2000.DAT:* 23: /SIDSB/gcgdata/geneseq//geneseqn/NA2000.DAT:* 23: /SIDSB/gcgdata/geneseq//geneseqn/NA2000.DAT:* 23: /SIDSB/gcgdata/geneseq//geneseqn/NA2000.DAT:* 24: /SIDSB/gcgdata/geneseq//geneseqn/NA2000.DAT:* 25: /SIDSB/gcgdata/geneseq//geneseqn/NA2000.DAT:* 25: /SIDSB/gcgdata/geneseq//geneseqn/NA2000.DAT:* 25: /SIDSB/gcgdata/geneseq//geneseqn/NA2000.DAT:* 25: /SIDSB/gcgdata/geneseq//geneseqn/NA2000.DAT:* 25: //SIDSB/gcgdata/geneseq//geneseqn/NA2000.DAT:* 26: //SIDSB/gcgdata/geneseq//geneseqn/NA2000.DAT:* 27: //SIDSB/gcgdata/geneseq//geneseqn/NA2000.DAT:* 27: //SIDSB/gcgdata/geneseq//geneseqn/NA2000.DAT:* 27: //SIDSB/gcgdata/geneseq//geneseqn/NA2000.DAT:* 27: //SIDSB/gcgdata/geneseq//geneseqn/NA2000.DAT:* 27: //SIDSB/gcgdata/geneseq//geneseqn/NA2000.DAT:* 28: //////////////////////////////////// | Profit than or equal to the score of the derived by analysis of the total score discreted by a current and the score of the match Length DB ID 20 100.0 22 AAC6558 14 70.0 33 21 AAZ4655 18 69.0 40 21 AAZ4655 18 69.0 40 22 AAZ4675 18 69.0 42 21 AAZ86558 18 69.0 42 21 AAZ86558 18 67.0 36 19 AAZ4625 18 67.0 36 19 AAZ4625 18 67.0 36 19 AAZ4625 |
| OM nucleic - nucl Run on: | ore: | Ub seq DB seq Ocessing : | | Result C Score great and 1s deri and 1s de |

adeno-associated virus; AAV;

98JP-0142134. 98JP-0142134

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A gene encoding a shortened dystrophin - useful for the treatment of
                                                                                                                                                                                                                                                                                                                                                                     (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
(KOKU-) KOKURITSU SEISHIN SHINKEI CENT SOCHO
                                                                                                                                                                                                  Muscular dystrophy; rod domain; adeno-assodystrophin gene; truncated; PCR primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 10; 44pp; Japanese.
                                                                                                                                                                        Dystrophin gene specific primer R5.
                                                                               582/c
AAZ48582 standard; DNA; 40 BP
                                                                                                                                              31-MAR-2000 (first entry)
               3 aactgcagaaggcac 17
                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-100771/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    muscular dystrophy
                                                                                                                                                                                                                                                                 JP11318467-A.
                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                             08-MAY-1998;
                                                                                                                                                                                                                                                                                          24 - NOV - 1999
                                                                                                                    AAZ48582;
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ID AAZ48
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                       The present invention describes a number of phosphorothioate antisense sequences to the human focal adhesion kinase (FAK) protein. This protein is involved in integrin-mediated signal transduction, and is implicated
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                                                             in cancer, particularly colon, breast and oral tumours, embryonic development disorders, anglogenic disorders and wound healing. The antisense sequences, including the one shown here, can be used in the treatment of all of these.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in cancer, particularly colon, breast and oral tumours, embryonic development disorders, angiogenic disorders and wound healing. The antisense sequences, including the one shown here, can be used in the treatment of all of these.
                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antisense compounds for inhibiting focal adhesion kinase expression, especially useful for inhibiting retinal neovascularization, or for diagnosing and treating e.g. colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                       Human; focal adhesion kinase; FAK; signal transduction; cancer;
embryonic development disorder; angiogenic disorder; wound healing;
antisense; phosphorothioate; ss.
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                                                                                                                                                                        22; Length 20;
                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                               Human focal adhesion kinase antisense sequence #24.
                                                                                                                                                                        Score 20; DB 2
Pred. No. 1.7;
                                                                                                                                Sequence 20 BP; 8 A; 4 C; 6 G; 2 T; 0 other;
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                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Column 25; 30pp; English
Claim 3; Column 23; 30pp; English
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                                                                                                                                                                       100.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaarde WA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-006141/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-AUG-1999;
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The invention provides a gene for the treatment of muscular dystrophy having at least one rod repeat structure of hinge 1, hinge 4 and rod domain of dystrophin gene and having a base sequence of 4.5 kb. The gene and a gene-introducing medium consisting of an adeno-associated virus (AAV) vector or lentivirus vector containing the rod shortened dystrophin genes can be used for the genetic treatment of muscular dystrophy of low immune reaction. Sequences AAZ48572-584 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia; antibacterial; gene therapy; PCR primer; ss.
                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                 Length 40;
                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                               21;
                                                                                                                                                                                                                                                             Score 14.8; DB 21;
Pred. No. 4.6e+02;
0; Mismatches 2;
                                                                                                                                                                                                Sequence 40 BP; 4 A; 13 C; 12 G; 11 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neisseria species ORF cloning PCR primer #60.
                                                                                                                                                      dystrophin gene specific primers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP.
                                                                                                                                                                                                                                                             74.0%;
88.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                         21 AGACTGCAGAAGGCCCTG 4
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Best Local Similarity
Matches 16; Conserv
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Gaps

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Length 15;

75.0%; Score 15; DB 22; Length 15 ilarity 100.0%; Pred. No. 3.3e+02; Conservative 0; Mismatches 0; Indels

Query Match Best Local Similarity Matches 15; Conserv

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Cenomic sequences AAT04954-55 of mouse Kv1.7 voltage-gated potassium channel (see AAT04953) show the splice donor and acceptor sites which form the boundaries of the single intervening sequence (see Fig 1A). These sequences are compared with that of mouse (mKv1.7 and hamster (haKv1.7) cDNAs. The potassium channel may be used in drug screening for identification of therapeutics which modulate the channel and, therefore, modulate insulin secretion. Selective antagonists increase insulin release and thereby reduce hyperglycemia associated with non-insulin-dependent diabetes
                                                                                                                                                                                                                                                                                                                                                                    New voltage-gated potassium channel gene - used to identify material(s) which can increase insulin release e.g. for treating non-insulin dependent diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fas ligand; transplant rejection; autoimmune disease; diabetes; inflammation; graft rejection; rheumatoid arthritis; allergy; cystic fibrosis; multiple sclerosis; polymerase chain reaction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 13.8; DB 16; Length 25;
Pred. No. 1.3e+03;
0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 25 BP; 2 A; 11 C; 5 G; 7 T; 0 other;
                                                                                                                                                                                                                                                                                             Gutman GA, Kalman K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Soluble mouse Fas ligand gene 5' DNA primer.
                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 20; 38pp; English.
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88.2%;
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                                                                                                                                                                                                     94US-0288405.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 gaaactgcagaaggcac 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 69.0
Best Local Similarity 88.2
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 GGAACTGCAGAAGGGAC 1
                                                                                                                                                                                                                                                         (REGC ) UNIV CALIFORNIA.
                                      14..25
/*tag=
                                                                                                                                                                                                                                                                                             Chandy KG,
                                                                                                                                                                                                                                                                                                                                WPI; 1995-320573/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCR; DNA primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9532627-A1
                                                                                          WO9523858-A1
                                                                                                                                                                                                     10-AUG-1994;
                                                                                                                                                                                                                        04-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-JAN-1995;
                                                                                                                                                                 23-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-0CT-1996
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                                                                                                                            08-SEP-1995
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                                                                                                                                                                                                                                                                                             Chandy G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT09688;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                   Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT09688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         represent novel Neisseria menigitis and N. gonorrheae polynucleotides and polypeptides. AAZ5457 to AAZ54576 and AAZ54616 to AAZ55473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention
                                                                                                                                                                                                                                                                                                                                                                                      Masignani V, Mora M;
Scalato E, Scarselli M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse Kv1.7 voltage-gated potassium channel splice site;
insulin antagonist drug screening; insulin agonist drug screening;
non-insulin-dependent diabetes mellitus; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel Neisserial polypeptides predicted to be useful antigens for vaccines and diagnostics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Splice site for mouse Kv1.7 voltage-gated potassium channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70.0%; Score 14; DB 21; Length 33; 100.0%; Pred. No. 1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                      Hickey E,
Ratti G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 33 BP; 14 A; 5 C; 9 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  be used in gene therapy protocols.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 16; Page 141; 1453pp; English.
                                                                                                                                                                                                                                                                                                                                                                                      Galeotti C, Grandi G,
, Pizza M, Rappuoli R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAT04955 standard; DNA; 25 BP
                                                                                                                                                           98US-0083758.
98US-0098894.
98US-0099094.
98US-0103749.
98US-0103794.
98US-0103796.
                                                                                                                          99WO-US09346
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                                                                                                                                                                                                                                                                                                                                                 (GENO-) INST GENOMIC RES.
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                                                                                                                                                                                                                                                                                                                                                                                                                          Venter JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 aaactgcagaaggc 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Petersen J, Pizza M,
Tettelin H, Venter J(
                                                                                                                                                                                                                                                                                                                              (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-062150/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 14; Conserv
                 Neisseria sp.
                                                                                                                                                                                                                                                     09-OCT-1998;
09-OCT-1998;
25-FEB-1999;
                                                   WO9957280-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
                                                                                                                          30-APR-1999;
                                                                                                                                                                                                   02-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-APR-1996
                                                                                        11-NOV-1999
                                                                                                                                                                                                                     02-SEP-1998
                                                                                                                                                                                                                                        09-OCT-1998
Synthetic
                                                                                                                                                                                                                                                                                                                                                                                  Fraser C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAT04955;
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RESULT 5

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Gaps

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20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0086635
                                                                                                                                                                                                                                                                                                                                                  AAZ56558/c
ID AAZ56558 standard; DNA; 42
                                                                                                                                                                                                                                                                                                                                                                                                                                21-MAR-2000 (first entry)
                                                                                                                                                                                                                                                                        42 GAAAGAGCAGAAGACAGTGA
                                                                                                                                                                                                                                                       1 gaaactgcagaaggcactga
                                                                                                                                                                                       Query Match
Best Local Similarity 80.0°
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYFL ) UNIV FLORIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e.g. in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-072617/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lentiviral vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09961598-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                  AAZ56558;
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                                                                                                                                                                                                                                                                                                                                       RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a packaging vector (PV) comprising a nucleotide sequence encoding Gag and Pol proteins of a reference lentivius that differes from the reference lentivius at least in that:

(a) its major splice donor site is either deleted or is sufficiently different from the reference lentivirus so that it is not a potential site for homologous recombination; and (b) it lacks a functional major packaging signal so that the introduced vector causes the host cell to produce packaging vector particles comprising functional Gag and Pol proteins. The vectors are useful for transforming (eukaryotic) cells to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             packaging vector comprising a nucleotide sequence encoding Gag and proteins of a reference lentivirus useful for the delivery of
                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lentiviral vector; packaging; gag; pol; gene therapy; infection; gene expression; PCR primer; ss.
                                                                                                                                                                                                         the full-length
                                                                                                                        Use of Fas ligand - for suppressing lymphocyte-mediated immune responses, e.g. transplant rejection or auto-immune conditions
                                                                                                                                                                                                  This 5' DNA primer is used for the synthesis of the full-lengt. soluble mouse Fas ligand gene. It is used in conjunction with the 3' DNA primer (AAT07687).
                                                                                                                                                                                                                                                                                                                                                  ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HIV Vpr C-terminal and Tat N-terminal PCR primer SEQ ID NO:15.
                                                                                                                                                                                                                                                                                                                    Length 40;
                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                 69.0%; Score 13.8; DB 17; 88.2%; Pred. No. 1.3e+03;
                                                                                                                                                                                                                                                                   Sequence 40 BP; 9 A; 13 C; 11 G; 7 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              non-lentiviral genes to target cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 148; 311pp; English.
                                                                                                                                                                        Disclosure; Page 32; 51pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ88079 standard; DNA; 42 BP
94US-0250478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US11516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                 3 aactgcagaaggcactg 19
                                                                                                                                                                                                                                                                                                                                                                                                               22 acctgcagaaggaactg 38
                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 88.2
Matches 15; Conservative
                                                                                                                      Use of Fas ligand - for
                             (COLS ) UNIV COLORADO
                                                             Duke RC;
                                                                                          WPI; 1996-030252/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-137067/12.
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27-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-APR-2000
                                                             Bellgrau D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAZ88079;
                                                                                                                                                                                                                                                                                                                    Query Match
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express specific genes at high levels, e.g. for gene therapy. The improved vectors are safer, yet permit increased efficiency of packaging the recombinant viral genome and increased long-term gene expression. These properties are required for gene therapy as a means of treating infectious and non-infectious diseases. Unlike other retroviruses, the lentiviruses are able to infect non-dividing cells. The present sequence represents an HIV VPR C-terminal and Tat N-terminal PCR primer which is used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vector system provides increased long-term gene expression compared with other viral vectors (e.g. could remain transduced for at least 120 days), so it may be possible for the vector to remain transduced for the necessary time course of a particular treatment. AAZ5638 to AAZ54578 represent nucleotide sequences used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New gene amplification system, useful to express a target gene in cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene amplification system; gene therapy; packaging;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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Pred. No. 1.6e+03;
); Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 42 BP; 4 A; 15 C; 5 G; 18 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; Page 98; 197pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68.08;
80.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HÎV-1 fragment PCR primer #2.
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BP.

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Multivalent vaccine; cat; pathogen; respiratory disease; FeLV; FPV; FCV digestive disease; feline leukaemia virus; feline palleukopaenia virus; feline calcivirus; feline immunodeficiency virus; FTV; rabies virus; vector; envelope glycoprotein; primer; PCR; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Multi-valent polynucleotide vaccines against feline pathogens consist of at least 3 plasmids able to express protective antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 17; Page 16; 42pp; French.
                                                                                                                                                              for FIV env gene.
                                                                                                                                                                                                                                                                     Feline immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                     96FR-0009337.
                                                                                                                                                                                                                                                                                                                                                                               96FR-0009337.
                                                                                 AAV49285 standard; DNA; 36
                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                          (INMR ) RHONE MERIEUX SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Baudu P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from specified viruses
    19 ACTGCAGAATGCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-112823/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                     Audonnet JCF,
                                                                                                                                                              Primer AB067
                                                                                                                                                                                                                                                                                              FR2751223-A1.
                                                                                                                                                                                                                                                                                                                                                     19-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                               19-JUL-1996;
                                                                                                                                   28-OCT-1998
                                                                                                                                                                                                                                                                                                                          23-JAN-1998
                                                                                                                                                                                                                                                         Synthetic.
                                                                                                          AAV49285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                      10
                                                                   AAV49285
                                                        RESULT
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                                                                                                                                                                                                                                                                                                                                     paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis; nongonococcal uretritis; epidymitis; cervicitis; salpingitis; PCR primer; bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCR primers AAZ01426-206209 were used to amplify open reading frames (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs encode polypeptides (see AAX36754-Y37949) which can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye
                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diseases such as conventional trachom, nonendemic trachom, paratrachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal uretritis, epidymitis, cervicitis, salpingitis, perihepatitis, bartholinitis; pneumopathy in breast feeding infants; and veneraal lymphogranulomatosis. The polypeptides of the invention may be of use in treating these diseases.
                                                                                                                                                                                                                                                                                                                       eye disease; conventional trachoma; nonendemic trachoma;
                                                                                              ö
                                                                    Length 42;
                                                                                                                                                                                                                                                                                              PCR primer used to amplify an ORF of Chlamydia trachomatis.
                                                                                              Indels
                                                                 DB 21;
                                                                 68.0%; Score 13.6; DB 21
80.0%; Pred. No. 1.6e+03;
ive 0; Mismatches 4.
                          Sequence 42 BP; 4 A; 15 C; 5 G; 18 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome sequence of Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 1720; 1755pp; English.
                                                                                                                                                                                                                  BP.
                                                                                                                     1 gaaactgcagaaggcactga 20
                                                                                                                                     97FR-0015041,
97FR-0016034,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0107077
                                                                                                                                                                                                                 AAZ04825 standard; DNA; 20
                                                                                                                                                                                                                                                                   07-OCT-1999 (first entry)
                                                                 Query Match 68.0°
Best Local Similarity 80.0°
Matches 16; Conservative
the present invention
                                                                                                                                                                                                                                                                                                                                                                                                       Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-371125/31.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  W09928475-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Griffais R;
                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                           AAZ04825;
                                                                                                                                                                                                                                                                                                                          Vaccine;
                                                                                                                                                                                                    AAZ04825/c
                                                                                                                                                                                      RESULT
SXC
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Riviere MEA;

Bouchardon A,

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The invention relates to a multivalent vaccine for protecting cats against several pathogens, especially pathogens associated with respiratory and digestive diseases. The pathogens are especially selected from feline leukaemia virus (FeLV), feline panleukopaenia virus (FPV), feline calcivirus (FCV), feline immunodeficiency virus (FIV), or rabies virus. The vaccines are preferably composed of polynucleotide sequences encoding 3 antigens, all as part of vectors. Primers AAV49285-V49286 were used to PCR amplify the feline immunodeficiency virus (FIV) petaluma strain gene encoding the envelope glycoprotein. The sequence sub-cloned into the plasmid pVR1012 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  67.0%; Score 13.4; DB 19;
93.3%; Pred. No. 2e+03;
ive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                          generate plasmid pAB030 for use in the vaccine.
                                                                                                                                                                                                                                                                                                                                                  Sequence 36 BP; 14 A; 6 C; 11 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAT84971 standard; DNA; 43 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-APR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 aaactgcagaaggca 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT84971;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
AAT84971/0
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Gaps

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Indels

Length 20;

Score 13.4; DB 20; Pred. No. 1.9e+03; 0; Mismatches 1;

67.0%; 93.3%;

Query Match 67.0 Best Local Similarity 93.3 Matches 14; Conservative

4 actgcagaaggcact 18

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(first entry)

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Arginase II; proline production; glutamate production; hyperarginaemia; nitric oxide biosynthesis; arginase activity; urea cycle disease; hypertension; hypotension; hyperammonaemia; prostate disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid encoding human arginase II - useful for treating, diagnosing and monitoring e.g. urea cycle disorders, hypotension, nitric oxide-mediated immune and nervous diseases, etc
                                                                                   PCR primer 5R used to amplify arginase II from a cDNA library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC. (SMIK ) SMITHKLINE BEECHAM CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-470868/43.
                                                                                                                                                                                                                                    PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                               WO9733986-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-MAR-1996;
                          25-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                          18-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dillon PJ,
                                                                                                                                                                                                                                                                                         Synthetic.
Turkat cell line CDNA library. The CDNA sequence of Arginase I was used as a probe sequence for a computer search of CDNA databases. Several expressed sequence for a computer search of CDNA databases. Several expressed sequence for a computer sequence homology were identified. These were combined to give a 1075 bp sequence. The above PCR primers were designed to the extreme 3' and 5' ends of the consensus sequence, and used to isolate arginase II. In addition to a hypothetical role in the production of proline and glutamate, it is postulated that arginase II may play an important role in nitric oxide biosynthesis through the production of confithine as a precursor of glutamate. Arginase II, or its agonists, and fragments, are used to treat conditions associated with lack of arginase activity. Compounds that inhibit activation of the protein are used to treat conditions that can be treated are diseases of the protein are used to creat conditions sasociated with excess arginase activity. Typical conditions that can be treated are diseases of the urea cycle, hypertension, hypothension sportated and related spaticity, prostate disease (e.g. cancer, hyperarginaemia and related spaticity, prostate or kidney damage, also nitric oxide associated immune and nervous system diseases. The arginase II cDNA is used to produce recombinant protein and for chromosome in the related are used to produce recombinant protein and for chromosome in the state of arginase in the state of produce recombinant protein and for chromosome arginate arginase in the state of arginase in the state of produce recombinant protein and for chromosome arginate arginase in the state of arginate are used (as primers and probes) to addition, while its fragments are used (as primers and probes) to a determine and nervous system diseases.
                                                                                Arginase II; proline production; glutamate production; hyperarginaemia; nitric oxide biosynthesis; arginase activity; urea cycle disease; hypertension; hypotension; hyperammonaemia; prostate disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           identification, while its fragments are used (as primers and probes) to detect arginase II-encoding sequences and to diagnose the above
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            primers AAT84962-74 were used to amplify human arginase II from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polynucleotide encoding human arginase II - useful to treat, diagnose and monitor, e.g. urea cycle disorders, prostatic disease, hypotension and nitric oxide mediated immune and nervous diseases
                          PCR primer 5R used to amplify arginase II from a cDNA library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 43 BP; 8 A; 10 C; 8 G; 17 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Fig 3; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dillon PJ, Vockley JG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-470867/43.
                                                                                                                                                                      PCR primer; ss
                                                                                                                                                                                                                                                                                      WO9733985-A1
                                                                                                                                                                                                                                                                                                                                                                                                       14-MAR-1996;
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                                                                                                                                                                                                                              Synthetic.
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96WO-US13455. 96WO-US03561.

Vockley JG;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treated are diseases of the urea cycle, hypertension, hypotension (caused by sepsis or cytokines), episodic hyperammonaemia, defective synthesis of proline, glutamate, nitric oxide or ornithine, prostatitis and benign hypertrophy), prostate disease (e.g. cancer, prostatitis and benign hypertrophy), prostate or kidney damage, also nitric oxide associated immune and nervous system diseases. The arginase II CDNA is used to produce recombinant protein and for chromosome identification, while its fragments are used (as primers and probes) to detect arginase II-encoding sequences and to diagnose the above
                                                                                                                                                                                                                                                                                                                                           through the production of ornithine as a precursor of glutamate.
Arginase II, or its agonists, antagonists and fragments, are used to treat conditions associated with lack of arginase activity. Compounds that inhibit activation of the protein are used to treat conditions associated with excess arginase activity. Typical conditions that can be
PCR primers AAV00578-90 were used to amplify human arginase II from a Jurkat cell line cDNA library. The cDNA sequence of Arginase I was used as a probe sequence for a computer search of cDNA databases. Several expressed sequence tags with 50-60% sequence homology were identified. These were combined to give a 1075 bp sequence. The above PCR primers were designed to the extreme 3' and 5' ends of the consensus sequence, and used to isolate arginase II. In addition to a hypothetical role in the production of proline and glutamate, it is postulated that arginase II may play an important role in nitric oxide biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 13.4; DB 18;
Pred. No. 2e+03;
); Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 43 BP; 8 A; 10 C; 8 G; 17 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
AAV17634/c
ID AAV17634 standard; DNA; 43 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67.0%;
93.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 actgcagaaggcact 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 ACTGCAGAAGGCAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diseases
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Matches
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Gaps

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Length 43; Indels

Score 13.4; DB 18; Pred. No. 2e+03;); Mismatches 1;

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67.0%; 93.3%;

Query Match 67.0 Best Local Similarity 93.3 Matches 14; Conservative

4 actgcagaaggcact 18

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16 ACTGCAGAAGGCAAT

AAV00587 standard; cDNA; 43 BP.

RESULT 12 AAV00587/c AAV00587;

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The invention relates to a polypeptide with Arginase II activity. The Arginase II polypeptides may be used in gene therapy for the treatment of type I arginase disorders resulting in hyperargininemia. The polypeptide sequences may also be used as immunogens to produce antibodies, these antibodies may then be used to treat numerous diseases e.g. urea disorders, hypertension, hypotension, prostate cancer, benign prostatic hyperplasia. Sequences AAXY7307-319 represent PCR primers used for cloning the Arginase II cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           uropathic; cytostatic; neuroprotective; gene therapy; hypertension; nitric oxide biosynthesis modulator; urea cycle disease; hypotension; episodic hyperammonaemia; hyperargininaemia; spasticity; prostatitis; growth retardation; progressive mental impairment; prostate disease; prostate cancer; benign prostatic hyperplasia; hypertrophy; prostate damage; kidney disease; kidney damage; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  arginase II; arginase I; diagnosis; hypotensive; hypertensive;
                                                                                                                                                                                                                                                                                                                                                                                                            Polypeptides with Arginase activity, useful for treating type arginase and disorders resulting in hyperargininemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20; Length 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 43 BP; 8 A; 10 C; 8 G; 17 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 13.4; DB 7
Pred. No. 2e+03;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human arginase II PCR primer SEQ ID NO:12.
                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC. (SMIK) SMITHKLINE BEECHAM CORP.
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97US-0914981.
96US-0700186.
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93.3%;
                                                    97US-0914981.
                                                                                                                                           96US-0700186
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                                                                                                                  97US-0914981
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 67.0
Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 actgcagaaggcact 18
                                                                                                                                                                                                                                                                                            Vockley JG;
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20-AUG-1997;
20-AUG-1996;
                                                       20-AUG-1997;
                                                                                                                                              20-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUN-2000
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                                                                                                                  20-AUG-1997;
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15-JUN-1999
                                                                                                                                                                                                                                                                                         Dillon PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA08070;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence is that of a PCR primer (5R) which was synthesised based on a potential arginase II EST consensus sequence. It was used in the amplification and cloning of the human arginase II gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human arginase II protein – useful for treating, e.g. diseases associated with defect in arginase II gene such as episodic
                                                                                                                                                                                                                           diagnosis; susceptibility; urea cycle; hypertension; hypotension; episodic; proline; biosynthesis; defect; glutamate; nitric oxide; ornithine; hyperargininaemia; spasticity; growth retardation; mental impairment; prostate; cancer; prostatis; benign prostatic; hyperplasia; hypertrophy; damage; kidhey; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arginase II; gene therapy; hyperargininemia; immunogen; human; urea cycle disorder; hypertension; hypotension; prostate cancer; benign prostatic hyperplasia; PCR primer; ss.
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                                                                                                                                                                                                   human; arginase II; disease; gene defect; hyperammonaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 13.4; DB 19;
Pred. No. 2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 43 BP; 8 A; 10 C; 8 G; 17 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                           Homo sapiens arginase II gene PCR primer.
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                                                                                   (first entry)
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Matches 14; Conservative
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Gaps

Dillon PJ, Vockley JG;

WPI; 2000-328355/28

Novel human arginase II polypeptides useful for treating urea cycle diseases, hypertension, hypotension, episodic hyperammonemia, to control nitric oxide formation and kidney damage -

Example 1; Fig 3; 37pp; English

The present invention describes human arginase II. Arginase II has
hypotensive, hypertensive, uropathic, cytostatic and neuroprotective
activities, and can be used in gene therapy and as a nitric oxide
biosynthesis modulator. Human arginase II proteins can be used to treat
diseases associated with or caused by a defect in the arginase II gene
or arginase II gene expression, such as, for e.g. urea cycle diseases,
hypertension, hypotension, episodic hyperammonaemia, defects in
biosynthesis of proline, quitamete, nitric oxide and ornithine, as well
as hyperargininaemia and its related spasticity, growth retardation,
and progressive mental impairment, and prostatic disease, particularly
prostate cancer, prostatic damage, kidney disease and kidney
constate cancer, prostate damage, kidney disease and kidney
damage. It is also used to control nitric oxide formation in an
individual Arginase II or its fragments, variants or derivatives can be
used as diagnostic reagents for diagnosing arginase II deficiency in an
individual having or suspected of having a defect in the nitric oxide pathway and the urea cycle. The genes encoding arginase II are used in gene therapy techniques to treat the above mentioned disorders. It is also used to deplete systemic arginine levels in an individual. AAA08061 to AAA08073 represent PCR primers used in the cloning of human arginase

Sequence 43 BP; 8 A; 10 C; 8 G; 17 T; 0 other;

Gaps ; 0 67.0%; Score 13.4; DB 21; Length 43; 93.3%; Pred. No. 2e+03; 1.1ve 0; Mismatches 1; Indels (Query Match 67.0 Best Local Similarity 93.3 Matches 14; Conservative

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Search completed: October 2, 2001, 16:18:36 Job time: 15480 sec

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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts JOURNAL Unpublished (2000) COMMENT Contact: Robert B. Weiss University of Utah Genome Center | ## 1306 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 8112, USA 7177 ## 120 1985 5606 | Oy 5 ctgcagaaggcactga 20 | RESULT 2 AZ758899 34 bp DNA GSS 16-FEB-2001 LOCUS DEFINITION 1M0553A10F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0553A10 F, DNA sequence. AZCESSION AZ759899 GI:12867159 KEYWORDS GSS. SOURCE Muss musculus CRGANISM Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1; Marmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus. REFERENCE 1 (Dases 1 to 34) AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Tingey, A., von Niederhausern, A. |
|---|--|------------------------------|--|
| SUMMARIES Query Match Length DB ID Description | 64.0 33 250 AZ809697 AZ809697 ZA0073M14 64.0 37 249 AZ759899 AA519828 TAGESTZ35 AG 63.0 46 129 AZ759899 AA519828 TAGESTZ35 AG 63.0 47 244 AZ46547 AA013218 NA0673 YA79211.71 63.0 49 107 AU102228 AU102238 AU102238 AU102328 AU102308 AU10230 | ALIGNMENTS | A2809697 33 bp DNA GSS 20-FEB-2001 2M0073M14R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0073M14 R, DNA sequence. A2809697 A2809697 GSS. house mouse. Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mus musculus Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Musinamalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musina. 1 (bases 1 to 33) Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. |
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                                                                                                                                                        Rm.\ 308 , Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112 , USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab host="E. Coli strain XLIO-Gold, Tl-resistant, F-"/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
         Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
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Toxoplasma gondii.
Eukaryota, Alveolata; Apicomplexa; Coccidia; Eimeriida;
Sarcocystidae; Toxoplasma.
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                                                                                                                                                                                            Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunfgenerics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0553 row: A column: 10
Seq primer: CGTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 34.
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/clone="UUGC1M0553A10"
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and Wright, D., Weiss, R.
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Matches 14; Conserv
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Allen, M., Bowles, L., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, N., Jost, S., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, Freising, B., Bowers, Y., Wylie, T., Ajioka, J.A., Aslett, M.A., Wan, K.L., Wilson, R., Waterston, R. and Boothroyd J.C.
Wash U. Stanford-PAMF-NIH Toxoplasma EST project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="ME49"
//db_xref="taxon:5811"
//clone="tgzz35906.r1"
//clone_lib="tgzz35906.r1"
//clone_lib="tgzz35906.r1"
//clone_lib="tgzz35906.r1"
//clone_lib="tgzz35906.r1"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BE739126 33 bp mRNA EST 15-SEP-2000 601556265F1 NIH_MGC_58 Homo sapiens CDNA clone IMAGE:3826072 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 33)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                              Email: toxo@watson.wustl.edu
Contact John Boothroyd (jboothr@eland.Stanford.EDU) for
information on clone and library availability.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                  Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Pred. No. 6.6e+04;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .37
/organism="Toxoplasma gondii"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
;
                                                                                                                 Unpublished (1997)
Contact: Marra M
WashU-Merck EST Project
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Best Local Similarity 87.5%;
Matches 14; Conservative (
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BE739126
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Far: 801 585 566
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (base; 1 to 47)

Dunn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly and Wright, D., Weiss, R., Stokes, R., Tingey, A., von Niederhausern, A. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1M0274A02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0274A02 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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/clone_lib="Mouse 10kb plasmid UUGCIM library"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63.0%; Score 12.6; DB 159; Length 46; 78.9%; Pred. No. 8.4e+04; ive 0; Mismatches 4; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0274 row: A column: 02
Seq primer: GGTrGTAAAACGACGCCAGT
    1. .46
/organism="Homo sapiens"
/db_xref="GDB:3888014"
/db_xref="taxon:9606"
/clone="IMAGE:258404"
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/strain="C57BL/6J"
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                                                                                                                                                                              /usale="Homo sapiens"
/db_xref="taxon.9606"
/clone="IMAGE:3826072"
/clone="IMAGE:3826072"
/clone="IMAGE:3826072"
/clone="IMAGE:3816072"
/tissue_type="hypernephroma"
/lab_bbst="Plat108 (Ti phage-resistant)"
/note="Organ: kidney: Vector: pDNR-LIB (Clontech); Site_1: Sfil (ggcgcctcggcc); Site_2: Sfil (ggcattatggcc);
Sfil (ggcgcctcggcc); Site_2: Sfil (ggcattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTACAGCCCAGCGCGCGCATCATG-4T(30)BNS: 5'
(where B = A, C, or G and N = A, C, G, or T).
(where B = A, C, or G and N = A, C, G, or T).
/insert size 1.35 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 46)

4 Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hullman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.

The Washur Merck Esy Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       yw78q11.rl Soares_placenta_8to9weeks_2NbHP8to9w Homo sapiens cDNA clone IMAGE:258404 5' similar to gb:J00117 CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: estewatson.wustl.edu
High quality sequence starts: 1
High quality sequence storts: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: T7
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.a column: 17
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                                                                                                                   High quality sequence stop: 33.
Location/Qualifiers
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N40673.1 GI:1164270
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/tissue_type="placenta"
/dev_stage="adult"
/dev_stage="adult"
/lab_host="DHIOB"
/note="Organ: placenta; Vector: pT/T3D-Pac (Pharmacia)
with a modified polylinker; Site_1: Not 1; Site_2: Eco RI;
lst strand cDNA was primed with a Not I - oligo(dT) primer
                                                                                                                                                                                                                                                                                                        1 (bases 1 to 50).
Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo,K., Suyama,A. and Sugano,S.
Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries
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Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Suzuki, Wohiromo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
Suzuki, Y., Yoshiromo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
S. Construction and characterization of a full length-enriched and
a S.-end-enriched CDNA library. Gene 200 (1-2), 149-156 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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      /clone_lib="Soares mouse placenta 4NbMP13.5 14.5"
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15 t
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Pred. No. 8.5e+04;
); Mismatches 4; Indels
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/db_xref="taxon:9606"
/clone="KAT06002"
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AU102328 Sugano Homo sapi
KAT06002, mRNA sequence.
AU102328
AU102328.1 GI:13551848
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78.9%;
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Best Local Similarity 78.9
Matches 15; Conservative
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Best Local Similarity
Matches 15; Conserv
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                                                                                          (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (qil4732114 qplAR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptce,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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mh10d05.rl Soares mouse placenta 4NbMP13.5 14.5 Mus musculus cDNA
clone IMAGE:442089 5' similar to WP:F35G12.9 CE00978 ;, mRNA
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
/note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
WashU-HMI Wa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 12.6; DB 244; Length 47;
Pred. No. 8.4e+04;
0; Mismatches 4; Indels 0;
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Possible reversed clone: similarity on wrong strand
Seq primer: ETPrimer
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/organism="Mus musculus"
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/db_xref="taxon:10090"
/clone="IMAGE:442089"
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78.9%;
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19 AGTGCAGAAGGCAC 32
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1. (bases 1 to 50)

Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata, H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo, K., Suyama,A. and Sugano,S.

Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries Unpublished (2001)

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Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries Unpublished (2001)
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4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzukiéims.u-tokyo.ec.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and
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                                           AU102796 50 bp mRNA EST 05-APR-2001
AU102796 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
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/db_xref="taxon:9606"
/clone="CAS11037"
/clone=lib="Sugano Homo sapiens cDNA library"
/ 5 c 21 g 5 t
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AU102800.1 GI:13552321
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AU102796.1 GI:13552317
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Department of Virology
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92.9%;
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Best Local Similarity 92.9
Matches 13; Conservative
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AUTHORS
RESULT 9
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SOURCE
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel
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2M0016K13F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0016K13 F, DNA sequence.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997). Location/Qualifiers
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/db_xref="taxon:10090"
/clone="UGGC2M0016K13"
/sex="Male"
                                                                                                                                                                   sapiens cDNA library"
6 t
                                                                                                                                                                                                                                                                                                               Length 50;
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84112, USA
                                                                                                                                                                                                                                                                                                               Score 12.4; DB 107;
Pred. No. 1.1e+05;
0; Mismatches 1;
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Insert Length: 10000 Std Error: 0.00
Plate: 0016 row: K column: 13
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                  1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CAS11356"
/clone_lib="Sugano Homo se
a B c 16 g 6
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/organism="Mus musculus"
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                            62.0%;
92.9%;
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Fax: 801 585 7177
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/organism="Homo sapiens"
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/clone="IMAGE:1583634"
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Best Local Similarity 82.4%;
Matches 14; Conservative 0
                                                                                                                                                                                                                                                                                                              61.0%;
                                                                                                                                                                                                                                                                                                                                  82.48;
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Unpublished (1997)
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Matches 14; Conser
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electrophoresis. Vector DNA was prepared from a derivative of pWD42 (qil4732114)gb/RF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymorleoctide kinase. Adaptor oligonucleoctides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
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1M0219A01F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0219A01 F, DNA sequence.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., 181am, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Welss, R.
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                                                                                                                                                                                                                                                                                 Score 12.2; DB 249; Length 31; Pred. No. 1.2e+05; 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20
84112, USA
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0219 row: A column: 01
Seg primer: CGTr@TAAACGACGCCAGT
Class: plasmid ends
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0219A01"
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                                                                                                                                                                                                                                                                                      61.0%;
82.4%;
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Another—"Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCBI) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Spares and M. Fatima Bonaldo. "
10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil/4732114/gb)A21.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 43)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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This clone is a vailable royalty-free through LLNL; contact the
This clone is a vailable royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 429 Std Error: 0.00
Seq primer: -40m13 Fwd. Er from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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0955c10.s1 Soares_NFL_T_GBG_S1 Homo sapiens CDNA clone
IMAGE:1583634 3' similar to SW:PWPZ_HUMAN Q15269 PERIODIC
TRYPTOPHAN PROTEIN 2 HOWOLOG:;, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 12.2; DB 243; Length 38;
Pred. No. 1.3e+05;
0; Mismatches 3; Indels 0;
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Pred. No. 1.3e+05;
0; Mismatches 3; Indels (
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/lab_host="DH10B"
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8 c 12 g 15 t
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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

ACCESSION

TITLE JOURNAL COMMENT

DEFINITION

RESULT 14 AI048043

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chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
AZ826678 32 bp DNA GSS 20-FEB-2001
2M0102P06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGGC2M0102P06"
/clone_lib="Mouse 10kb plasmid UGGLM library"
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100.0%; Pred. No. 1.6e+05;
ive 0; Mismatches 0;
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                                      clone UUGC2M0102P06 R, DNA sequence.
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/organism="Mus musculus"
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0102 row: P column: 06
                                                                           AZ826678.1 GI:12996586
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Best Local Similarity 100.
Matches 12; Conservative
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                                                                                                              house mouse.
Mus musculus
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DEFINITION
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                                                                                                                                                                                                                                                                                                               Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 43)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: embryo; Vector: pSPORT; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally from mRNA prepared
from 800 blastcoysts. Primer: SalI(dT):
5'-CGGTCGACCGTCGACCGTTTTTTTTTTTTTTTTTT.3'. CDNAs were
cloned into the NotI/SalI sites of a pSPORT vector (Life
Technologies). Two different size selections: B1 (larger
inserts) and B1
5 c 16 g 9 t
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                                                                                                                                               AIO48043 43 bp mRNA EST 08-JUL-1998 v021f12.r1 Knowles Solter mouse blastcoyst B1 Mus musculus cDNA clone IMAGE:1021871 5' similar to WE:T13H5.2 CE03653 RETINAL-BINDING LIKE PROTEIN; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/strain="B6D2 F1/J"
/db_xref="taxon:10090"
/clone="IMAGE:101871"
/clone="IMAGE:101871"
/tlssue_type="blastocyst"
/dev_stage="embryo (pre-implantation)"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1996)
Contact: Marra M/Mouse EST project
Washb-HHMI Mouse EST project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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Possible reversed clone: similarity on wrong strand
Seq primer: -40RP
High quality sequence stop: 1.
Location/Qualifiers
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Pred. No. 1.3e+05;
0; Mismatches 3;
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AI048043.1 GI:3296330
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82.4%;
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Best Local Similarity 82.4°
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                                                 house mouse.
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FEATURES

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Gaps

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RESULT 15 AZ826678

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BASE COUNT

Search completed: October 2, 2001, 15:00:48 Job time: 10817 sec

Searched:

Run on:

Database

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                        gb_sts1:*
gb_sts2:*
gb_sts3:*
gb_sy:*
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                                                                            October 2, 2001, 15:56:39 ; Search time 3339.34 Seconds (without alignments) 92.640 Million cell updates/sec
        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                    1344157 seqs, 7733874588 residues
                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
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Maximum Match 1008
Listing first 45 summaries
                                                        - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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em_htg_other:*
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Maximum DB seq length: 50
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Perfect score:
Sequence:
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AX060862 Sequence AR109090 Sequence A81012 Sequence 64 A95391 Sequence AR004745 Sequence AR008231 Sequence 177015 Sequence 75 IR1010 Sequence 75

AX060862 AR109090 A81012 A95391 AR004745 AR008231 177015

00000001

33355

Description

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DB

SUMMARIES

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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 20)
Kahn, A. and Chelly, J.
A gene called XLIS and the XLIS gene product, called doublecortin and their applications
Patent: EP 0918091-A 64 26-MAY-1999;
INST NAT SANTE RECH MED (FR)
                      Gaps
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Score 13.8; DB 9;
Pred. No. 1.2e+04;
                                                                                                                                                                                          Unclassified.

1 (bases 1 to 41)

1 (bases 2 to 41)

1 (bases 3 to 41)

Branieux, Bradry, B.S. and Sapolsky, R.J.

Brassica polymorphisms

Patent: US 6114116-A 49 05-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 12.6; DB 9;
Pred. No. 4.9e+04;
); Mismatches 4;
                                                                                                                                                                                                                                                                                                                       Score 13.8; DB 9;
Pred. No. 1.2e+04;
1; Mismatches 3;
           Pred. No. 1.2e
0; Mismatches
                                                                                                                  AR109090 41 bp DNA
Sequence 49 from patent US 6114116.
AR109090
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/organism="Homo sapiens"
/db_xref="taxon:9606"
a 7 c 0 g 12
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Sequence 64 from Patent EP0918091.
A81012
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78.9%; Pred
0; 1
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69.0%;
88.2%;
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Best Local Similarity
Matches 15; Conserv
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A04979 Artificial
A04980 Artificial
AR036378 Sequence
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AR104422 Sequence
A46553 Sequence 9
A18117 Oilgonucleo
A82690 Sequence 35
A82705 Sequence 50
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I51986 Sequence 20
AR039578 Sequence
AR089681 Sequence
AR030029 Sequence
                                                                                                         116209 Sequence 35
166695 Sequence 35
                                                                                                                                                                       I72126 Sequence 41
                                                                                                                                                                                             I15938 Sequence 39
                                        AX043897 Sequence
AX059414 Sequence
AX043901 Sequence
AR3876 Sequence 11
AR061353 Sequence
AR108252 Sequence
                                                                         Sequence 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         synthetic construct
artificial sequence.

I (bases I to 33)
Huse, W.D. and Wu.H.
Anti-_g(a) v?_g(b)3? recombinant human antibodies, nucleic acids encoding same and methods of use
Patent: WO 0078815-A 83 28-DEC-2000;
Applied Molecular Evolution (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                       AR022302 Sequence
AR066394 Sequence
AR084122 Sequence
                                                                                                                                                                                                                                                                                                                                    A64833 Sequence 9
                                                                                                                                                                                                                                                                                                                                                                                        AX011523 Sequence
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    .33
    /organism="synthetic construct"
/db_xref="taxon:32630"

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/protein_id="CAC24917.1"
/db_xref="G1:12406241"
/translation="LIRYSSOSIS"
13 c 2 9 14 t
                                                                                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
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Sequence 83 from Patent WO0078815.
AX060862
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AR061353
AR061353
AR06252
116209
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A04980
AR036378
172126
AX080565
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AR104422
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AR039578
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                                                   synthetic construct.
DEFINITION
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VERSION
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JOURNAL

FEATURES

CDS

REFERENCE AUTHORS

TITLE

KEYWORDS

RESULT AX060862

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1 (bases 1 to 30)
Schlück, W.H., Goldgar, D.E., Miki, Y., Swenson, J., Kamb, A.,
Harshman, K. D., Shattuck-Eidens, D.M., Tavtigian, S.V., Wiseman, R.W.
and Futreal, P. Andrew.
170-linked breast and ovarian cancer susceptibility gene
Patent: US 5753441-A 75 19-MAY-1998;
Location/Qualifiers
                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                     03-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shattuck-Eidens, D.N., Simard, J., Durocher, F., Emi, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 30)
Shattuck-Eidens, D.M., Simard, J., Durocher, F., Emi, M. and
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Linked breast and ovarian cancer susceptibility gene
Patent: US 5693473-A 75 02-DEC-1997;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Linked breast and ovarian cancer susceptibility gene
Patent: US 5709999-A 75 20-JAN-1998;
Location/Qualifiers
1.30
                                                                                                                                                                                                                            9; Length 30;
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Pred. No. 5e+04;
0; Mismatches 4;
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Pred. No. 5e+04;
0; Mismatches
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Sequence 75 from patent US 5693473.
177015
177015.1 GI:3013169
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US 5709999.
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14 c 2 g
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Sequence 75 from patent
IB1010
IB1010.1 GI:3209300
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78.9%;
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Best Local Similarity 78.9%;
Matches 15; Conservative
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              Unknown.
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                                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 20)
Francis,F. and Kahn,A.
A GENE CALLED XLIS AND THE XLIS GENE PRODUCT, CALLED DOUBLECORTIN
AND THEIR PREPARATIONS
Patent: WO 9927089-A 64 03-JUN-1999;
INST NAT SANTE RECH MED (FR); FRANCIS FIONA (FR)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 30)
Skolnick,M.H., Goldgar,D.E., Miki,Y., Swenson,J., Kamb,A.,
Skolnick,M.H., Goldgar,D.E., Miki,Y., Swenson,J., Kamb,A.,
Harshman,K.D., Shattuck-Eidens,D.M., Tavtigian,S.V., Wiseman,R.W.
and Futreal,P.Andrew.
170-linked breast and ovarian cancer susceptibility gene
Patent: US 5747282-A 75 05-MAY-1998;
Location/Qualifiers
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Pred. No. 5e+04;
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Pred. No. 4.9e+04;
0; Mismatches 4.
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Sequence 75 from patent US 5753441.
AR008231 GI:3967340
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Sequence 75 from patent US 5747282.
AR004745.1 GI:3965624
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                 A93391 20 bp DNA
Sequence 64 from Patent W09927089.
A95391
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/db_xref="taxon:9606"
7 c 0 q 12
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Best Local Similarity 78.9
Matches 15; Conservative
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Pred. No. 7.9e+04;
0; Mismatches 3;
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Pred. No. 7.8e+04;
0; Mismatches 3;
                                                                                                                                                              Unclassified.

1 (bases 1 to 22)

North,M., Nishina,P. and Naggert,J.

Genes associated with retinal dystrophies

Patent: US 5686598-A 4 11-Nov-1997;

Location/Qualifiers
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Inouye,M. and Nakamra,K.
Plasmid cloning vehicles
Patent: EP 0055942-A2 11 14-JUL-1982,
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103808
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                                                                  173726 22 bp DNA
Sequence 4 from patent US 5686598.
173726.1 GI:3009867
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82.4%;
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Best Local Similarity 82.4
Matches 14; Conservative
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Unclassified.
I (bases 1 to 30)
Skolnick, M. H., Goldgar, D. E., Miki, Y., Swenson, J., Kamb, A.,
Harshman, K. D., Shattuck-Eidens, D. M., Tavtigian, S. V., Wiseman, R. W.
and Futreal, P. Andrew.
17q-linked breast and ovarian cancer susceptibility gene
Patent: US 5710001-A 75 20-JAN-1998;
Location/Qualifiers
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Pred. No. 5e+04;
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North, M., Nishina, P., Naggert, J. and Noben-Trauth, K. Gene family associated with neurosensory defects
Patent: 185 6114502-A 38 05-SEP-2000;
Location/Qualifiers
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61.0%; Score 12.2; DB 9; Length 22;
Best Local Similarity 82.4%; Pred. No. 7.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels
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Pred. No. 5e+04;
0; Mismatches 4;
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Sequence 38 from patent US 6114502.
AR110286.1 GI:12826562
/organism="unknown"
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78.9%;
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Best Local Similarity 78.9%;
Matches 15; Conservative
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Best Local Similarity 78.9
Matches 15; Conservative
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Unclassified.
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Bugnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 26)
Preuss, D., Copenhaver, G. and Keith, K.
Plant chromosome compositions and methods
Patent: WO 0055325-A 147 21.5EP-2000;
The University of Chicago (US)
Location/Qualifiers
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1 (bases 1 to 26)
Graham,F.L., Ng,P., Parks,R., Bacchetti,S. and Anglana,M.
A system for production of helper dependent adenovirus vectors bas ed on use of endoncleases
Patent: WO 0049166-A 10 24-AUG-2000;
Merck & Co., Inc. (US)
Location/Qualifiers
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artificial sequence.
1 (bases 1 to 27)
Graham,F.L., Ng,P., Parks,R., Bacchetti,S. and Anglana,M.
A system for production of helper dependent adenovirus vectors bas ed on use of endonuclasses
Patent: WO 0049166-A 14 24-AUG-2000;
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/organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
1 c 10 g 2 t
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="cDNA"
a 5 c 3 g 1 t
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Sequence 147 from Patent WO0055325.
AXO59414
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AX043901
AX043901.1 GI:11342484
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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em_gss_fun:* em_gss_hum1:* em_gss_hum2:*

gb_est110:*
gb_est111:*

em_gss_hum3:*

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117; gp_est48:*
118: gp_est49:*
119: gp_est50:*
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em_gss_other:* gb_gss33:* gb_gss34:* em_gss_inv4:* em_gss_pro:* em_gss_rod1:* em_gss_rod2:* em_gss_rod3:* em_gss_vrt2:* em_gss_vrt3:* gb_gss1:* em_gss_pln1:* em_gss_pln2:* em_gss_hum4:* em_gss_hum5:* em_gss_hum7:* em_gss_hum8:* em_gss_inv2:* em_gss_inv3:* em_gss_rod5:* em_gss_vrtl:* em_gss_hum9:* em_gss_invl:* em_gss_rod4:* em_gss_rod8:* gb_gss35:* gb_gss36:* gb_gss37:* gb_gss23:* gb_gss24:* gb_gss25:* em_gss_rod6 96-9812:*
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96-98810:* gb_gss10:* gb_gss11:* gb_gss4:* gb_gss5:* 952-9556:* 95-9557:* 95-9558:* gb_gss2:* gb_gss3:* gb_gss29 gb_gss9:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| | | | Trypanosoma brucei (TRE09274 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is | described in detail in Smith, H. and Vener, J.C. (Marking Small insert libraries for whole genome Shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. | Barrell, Oxford University Press, 1999). Email: nelsayed@tigr.org Details of # brings someoring at the Sanger Centre are available | at http://www.sanger.ac.uk/Projects/T_bruce1/ Location/Qualifiers | source 135 /organism="Trypanosoma brucei" | /strain="TREU927" /db_xref="taxon:5691" | /clone="124f02" COUNT 14 a 2 c 11 q 8 t | | Ouery Match 71.0%; Score 14.2; DB 258; Length 35; Best Local Similarity 84.2%; Pred. No. 7 1e+03: | 0 | 2 tetecettecgttattett 20 | 28 TCTCCCTCTGTTATTATT 10 | | 36 2 | AZ810736 49 bp ZM0076B05R Mouse 10kb | AZ810736 | | house mouse. Mus musculus | Eukaryota, Mammalia; | | <pre>1Slam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly , M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.</pre> | | plasmid inserts AL Unpublished (2000) | <pre>l Contact: Robert B. Weiss University of Utah Genome Center</pre> | University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112 HEA | Tel. 801 585 5606 | Email: ddunn@genetics.utah.edu Tneart ranch, 10000 etd Brant, 0 00 | 0 4 | Class: plasmid ends | | source 1a.; /organism="Mus musculus" /strain="C57BL/6J" | /db_xref="taxon:10090" |
|-----------|--|------------------------|--|--|--|--|--|--|--|--|--|--|--|--|---------------------|--|---|--|---------------------|--|--|--|---|-------|---------------------------------------|--|--|--------------------|---|-----|-------------------------|---|--|-------------------------|
| JOURNAL | ENGRADO | COMMEN | | | | FEATURES | S | | BASE C | | Quer | Matc | QY | qq | | RESULT AZ810736 | LOCUS | ACCESSION | KEYWORDS | SOURCE | | REFERENCE | | TITLE | JOURNAL | COMMENT | | | | | | FEATURES | n | |
| | Dogod to the state of the state | Describrion | AL463359 T. brucei AZ810736 2M0076B05 AA500031 v196ell.r | | AZ357911 IMO099L13 T49694 ya789L1.s1 A7247655 N1940A | A2385263 IM0143109 A1355496 qu15c07.x | AZ850974 2M0153109 A1551509 vo54h02.x | AZ357613 1M0099K18 AZ829796 2M0107H11 | AI125022 ao10c10.s AZ483277 1M0308P15 | AI419045 tf53c09.x AZ466785 IM0315c23 AII07265 AII107306 | A2785697 2M029A20 A2785697 2M029A20 A2482018 1M3306116 | AA739457 vv54a03.r AA815634 vt03d02.r | A2806493 2M0068M06 A2467429 1M0278M13 | AZ400227 1M0350A24 AZ40026 m buncoi | X88437 H.sapiens D | AZ795977 2M0051C03 AI583566 ts15906.x | AA828900 od75h11.s TG1777 Y893006.r1 | AL/35103 ZNOWOELZ AL/35103 ZNOWOELZ AL/37272 140002173 | A2837415 2M0132K08 | AIS3918/ tp/8hU/.x AZ809250 2M0073J08 | AI748505 SD53h08.y AI130467 SWOVL3CAN | AL45/9/3 T. Druce1 AA226145 nc09f09.r | A1442931 SA29aU/.X A2452742 1M0252G17 | | ··· | | GSS 13-DEC-2000 |) ; | | | tida; Trypanosomatidae; | - + + + + + + + + + + + + + + + + + + + | Dogger, El-Sayed, N., Hou, L., Barrell, B.G. | |
| SUMMARIES | Result Query No Score Match Length DR ID | score march belight be | 4.2 71.0 35 258 3.6 68.0 49 250 2.8 64.0 37 8 | 5 12.6 63.0 50 249 6 12.2 61.0 37 243 | 12.2 61.0 39 242 12.2 61.0 46 189 12.2 61.0 49 24 | 12 60.0 29 242 12 60.0 31 19 | 12 12 60.0 32 250 13 12 60.0 34 21 | 12 60.0 34 242 12 60.0 35 250 | 16 12 60.0 37 16 17 12 60.0 43 244 | 12 60.0 12 60.0 | 21 12 60.0 50 249 22 11.8 59.0 27 244 | 11.8 59.0 40 11 11.8 59.0 43 12 | 11.6 58.0 22 249 | 27 11.6 58.0 29 245 28 11 6 58.0 34 258 | 29 11.6 58.0 37 258 | 11.6 58.0 39 249 | 32 11.6 58.0 46 12 33 11.6 58.0 47 189 | 11.6 58.0 48 113 | 37 11.4 57.0 45 250 | 11.2 56.0 25 21 | 40 11.2 56.0 28 24 41 11.2 56.0 34 16 | 42 11.2 56.0 38 258 43 11.2 56.0 40 4 | 11.2 56.0 45 24 AZ4 | | ALIGNMENT | RESULT 1 | TAL24FUZU/C LOCUS TAL24FUZQ 35 bp DNA GSS DEFINITION T. hrunel sheared cenomic DNA clone 124f02 | genomic survey sec | VERSION AL463359.1 GI:11833869 KEYWORDS GSS | | Eukaryota; E | REFERENCE 1 (bases 1 co. 35) | Chillingworth, C., Ormond,D., Harris,B., El-Sayed,N., Hou, Melville,S.E., Rajandream,M.A. and Barrell,B.G. | TITLE Direct Submission |

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/organism="Mus musculus"
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                                                                /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/60 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynuclectide kinase. Adaptor oligonuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gal
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114|gb|AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
Eukaryota, Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Matazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 37)
Marra M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Marra M., Hillier, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA500031 37 bp mRNA EST 01-JUL-1997 v196e11.rl Barstead mouse pooled organs MPLRB4 Mus musculus CDNA clone IMAGE:920108 5' similar to SW:COXI_RAT P05503 CYTOCHROME C OXIDASE POLYPEPTIDE I; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@lmage.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                          /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68.0%; Score 13.6; DB 250; Length 49; 80.0%; Pred. No. 1.4e+04; 1ve 0; Mismatches 4; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Waterston, R.
The WashU-HHMI Mouse EST Project
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/clone="UUGC2M0076B05"
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AA500031.1 GI:2234998
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Fax: 314 286 1810
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Dunn, D., Aoyai, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. Mouse whole genome scaffolding with paired end reads from 10kb
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-
/note="Vector: PWD42nv; Purified genomic DNA from M.
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="inMdE:920108"
/clone=lib="Barstead mouse pooled organs MPLRB4"
/sex="mixed"
/tissue_type="pooled organs"
/dev.stage="7 day"
/lab_host="DH108"
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/clone="UUGCIM0244J07"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 12.8; DB 8; Length 37; Pred. No. 3.3e+04; 0; Mismatches 2; Indels
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Insert Length: 10000 Std Error: 0.00
Plate: 0244 row: J column: 07
Seq primer: CGTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 30.
Location/Qualifiers
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87.5%;
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Unpublished (2000)
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Fax: 801 585 7177
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil4732114) plant29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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1 (bases 2 to 37)
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                                     musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
   /note="Vector: PWD42nv; Purified genomic DNA from M.
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030
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Live 0; Mismatches 4; Indels 0;
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Insert Length: 10000 Std Error: 0.00
Plate: 0173 row: D column: 10
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Class: plasmid ends
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/clone="UUGC1M0173D10"
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A2404740.1 GI:10528753
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Fax: 801 585 7177
Email: ddunn@genet
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                                                        (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gelectrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114)pblARI29072.1), a copyrnumber inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10.Gold (Stratagene) cells and selected for ampicillin resistance."
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2M0010A23F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0010A23 F, DNA sequence.
AZ776590
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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musculus C57BL/6J (male) was obtained from the Jackson
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                                     Laboratory Mouse DNA Resource
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Insert Length: 10000 Std Error: 0.00
Plate: 0010 row: A column: 23
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Fax: 801 585 7177
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Best Local Similarity
Matches 15; Conserv
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us-09-757-100b-7.szlim50.rst

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Seg primer: -21m13
High quality sequence stop: 1.
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Contact: Wilson RK
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    /sex="Male"
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 39)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
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/lab_host-"E. Coli strain XLIO-Gold, T1-resistant, F-"
/note-"Vector: PWD42nv: Purified genomic DNA from M.
musculus C57BL/67 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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/strain="c57BL/6J"
/db_xref="taxon:10000"
/clone="UGGCIM0099L13"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 12.2; DB 243; Length 37;
Pred. No. 6.3e+04;
0; Mismatches 3; Indels 0;
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Insert Length: 10000 Std Error: 0.00
Plate: 0099 row: L column: 13
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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High quality sequence stop: 39.
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Fax: 801 585 7177
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (qil4732114) (pblAR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for amploillin resistance."
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Hillier, L., Lennon, G., Becker, M., Bonaldo, M. F., Chiapelli, B., Chisoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Le, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags
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                                    /note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Pred. No. 6.4e+04;
0; Mismatches 3; Indels 0;
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Insert Size: 711
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Plasmid inserts
Unpublished (2000)
Contract: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
double-stranded cDNA was ligated to a DraIII adaptor [CTGTCGCTARCTG5], digsted and cloned into distinct DraIII sites of the pME185-FL3 vector [5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments cl.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). CUTCTGCTCTRAAAGCTGCG and 3' end primer CTGCTGCAGCACACA."
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Dunn,D., Aoyal,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly and Wright,D., Weiss,R., Tingey,A., von Niederhausern,A. Mouse whole genome scaffolding with paired end reads from 10kb
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/sex="Male"
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Pred. No. 6.6e+04;
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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0143109"
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Location/Qualifiers
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Insert Length: 10000 Std Erro
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Fax: 801 585 7177
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Best Local Similarity
Matches 14; Conserv
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AZ385263/c
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                                                                             Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

1 (bases 1 to 49)
Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Marra, M., Hallier, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R.,
F., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
Materston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ul19d03.x1 Sugano mouse embryo mewa Mus musculus cDNA clone
IMAGE:2088005 3' similar to TR:089050 089050 MUSKELIN. ;, mRNA
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
T=1: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                      61.0%; Score 12.2; DB 189; Length 46; 73.7%; Pred. No. 6.5e+04; ive 0; Mismatches 5; Indels 0
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Possible reversed clone: similarity on wrong strand
Seq primer: custom primer used
High quality sequence stop: 1.
Location/Qualifiers
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                                        /organism="Homo sapiens"
/db_xref="GDB:489509"

    .49
    /organism="Mus musculus"

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AI747625.1 GI:5125827
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Best Local Similarity
Matches 14; Conserv
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ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel. electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chanically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
MA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
ound through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A1355496 31 bp mRNA EST 15-FEB-1999 qu15c07.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:1964844 3' similar to TR:Q60501 Q60501 P7 PREINSERTION DNA.; contains element
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 31)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Email: Gapabs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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/clone_lib="NoT_CGAP_Ov23"
/tissue_type="tumor, 5 pooled (see description)"
/lab_host="DH108"
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                                                                                                                                                                                                                                                                                                                                                     Score 12; DB 242; Length 29; Pred. No. 7.6e+04;
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AI355496
AI355496.1 GI:4095649
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27 TCCTCCCTCCTTCTT 8
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Unpublished (1997)
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Best Local Similarity
watches 15; Conserv
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//doce="Vector: PWASING: Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114) (pilahah29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the linsert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli xL10-Gold (Stratagene) cells and selected for amplial in resistance."
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                                                                                                                                                                                                                                                                                                                                         2M0153109F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0153109 F, DNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 32)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Slam, M., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
Contact: Robert B. Weiss
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse whole genome scaffolding with paired end reads from 10kb
                                                           Gaps
                                                                                                                                                                                                                                                                                                                 21-FEB-2001
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  Length 31;
                                                        Indels
Score 12; DB 19; I
Pred. No. 7.6e+04;
); Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0153 row: I column: 09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: CGTTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 32.
Location/Qualifiers
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/db_xref="taxon:10090"
/clone="UUGC2M0153I09"
                                                                                                                                                                                                                                                                                                                       DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                   AZ850974.1 GI:13036700
60.0%;
75.0%;
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                                                                                                           Conservative
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Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plasmid inserts
Query Match
Best Local Similarity
Matches 15; Conserv
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Mus musculus
                                                                                                                                                                                                                                                                  house mouse.
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Best Local Similarity
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                                                                                                              RESULT 14
AZ357613/c
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Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Onderwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., The Washungton Nouse EST Project 1999

Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AI551509 34 bp mRNA EST 23-MAR-1999 vo54h02.x1 Barstead mouse irradiated colon MPLRB7 Mus musculus cDNA clone IMAGE:1053747 3' similar to TR:Q33559 Q33559 NH2 TERMINUS UNCERFAIN ;, mRNA sequence.
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Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mousest@wick.
This clone is available royalty.free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                             Gaps
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/organism="Mus musculus"
/strain="FVBAN"
/db_xref="taxon:10090"
/clone="IMAGE:1053747"
/clone_lib-"Barstead mouse irradiated colon MPLRB7"
/dev_stage="8 weeks"
/lab_host="DH10B"
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Pred. No. 7.7e+04;
0; Mismatches 5; Indels
                                          Score 12; DB 250; Length 3:
Pred. No. 7.7e+04;
n. Mismatches 5; Indels
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Best Local Similarity 75.0°
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil4732114) gblaFT23072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bidg., 20 S. 2030 E., SLC, UT
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance." 1\ c 15\ g 0 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinee; Mus. L bases 1 to 34)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                        A2357613 34 bp DNA GSS 02-OCT-2000
1M0099K18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
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/clone_lib="Mouse 10kb plasmid UUGCIM library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0099 row: K column: 18
                                                                                                                                                                                                                                                                                                            clone UUGC1M0099K18 F, DNA sequence.

    . 34
    /organism="Mus musculus"
    /strain="C57BL/6J"

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Class: plasmid ends
High quality sequence stop: 34.
Location/Qualifiers
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1 ttctcccttccgttattctt 20
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                                   2 TTTTCTCTTTATTCT
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Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
Contact: Robert B. Welss
University of Utah Genome Center
University of Utah
Wan 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Criurognathi; Muridae; Murinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Lo 35)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Stalm, J., Longacre, S., Mahmoud, M., Meenen, E., Padesen, T., Reilly, M., Rose, M., Rose, M., Stokes, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Welss, R., Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                    AZ829796 35 bp DNA GSS 20-FEB-2001
ZMO107HIIR MOUSE 10kb plasmid UUGCIM library Mus musculus genomic
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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/strain="c57bL/6J"
/db_xref="taxon:10000"
/clone="UGGC2M0107H11"
/clone=lib="Mouse 10kb plasmid UGGIM library"
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0107 row: H column: 11
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
  Mismatches
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AUTHORS
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60.0%; Score 12; DB 250; Length 35;

Query Match

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75.0%; Pred. No. 7.8e+04;
tive 0; Mismatches 5;
 Best Local Similarity 75.09
Matches 15; Conservative
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32 TCTCCCTTCTCTCTT 13

2, 2001, 15:00:51 Search completed: October Job time: 10820 sec

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APPLICANT: Monia, Brett P.
APPLICANT: Monia, Brett P.
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
FILE REPRENCE: ISPH-0389
CURRENT APPLICATION NUMBER: US/09/377,310B
CURRENT APPLICATION NUMBER: US/09/377,310B
SOFTWARE: PATENTIN VOTE: 2.0
SEQ ID NO 7
LENGTH: 20
                    Sequence
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US-08-758-306-426

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US-08-975-138-18

US-08-975-4178-1

US-08-972-4178-1

US-08-972-4178-1

US-08-972-4178-1

US-08-972-119-9

US-08-472-719-9

US-08-472-719-9

US-08-472-719-9

US-08-472-719-9

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US-08-171-389-98

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APPLICANT: Monia, Brett P.
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: Antisense Modulation of Foc;
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0389;
CURRENT APPLICATION NUMBER: US/09/377,310B;
CURRENT APPLICATION NUMBER: US/09/377,310B;
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
SED ID NO 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 20; DE 100.0%; Pred. No. 0.3; ive 0; Mismatches
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; Patent No. 6133031
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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US-08-481-02-75
US-08-483-5548-75
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US-08-880-727-75
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                                                                         APPLICANT: Swenson, Jeff
APPLICANT: Kamb, Alexander
APPLICANT: Harshman, Keith D.
APPLICANT: Harshman, Keith D.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Wiseman, Roger W.
APPLICANT: Wiseman, Roger W.
APPLICANT: Witceal, P. Andrew
TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,784
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 12.6; DB 1;
Pred. No. 8.5e+02;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109347
TELECOMNUNICATION INFORMATION:
TELEPHONE: 202-962-4810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIETCATION: 435
CLASSIETCATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNDRER: US 08/409,305
FILING DATE: 24-YAR-1995
PRIOR APPLICATION UNBER: US 08/346,824
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,104
FILING DATE: 16-SEP-1994
PRIOR APPLICATION NUMBER: US 08/300,266
FILING DATE: 02-SEP-1994
PRIOR APPLICATION NUMBER: US 08/300,266
FILING DATE: 02-SEP-1994
PRIOR APPLICATION NUMBER: US 08/300,266
FILING DATE: 12-ABC-1994
APPLICATION NUMBER: US 08/299,221
FILING DATE: 12-AGC-1994
ATTORNEY AGENT INFORMATION:
                  Skolnick, Mark H.
Goldgar, David E.
Miki, Yoshio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.0%;
ilarity 78.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 30 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                            STREET: 120-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                    20002
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ORGANISM:
US-08-480-784-75
                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -g
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                                                                                                                                         Gaps
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                                                                                                DB 3; Length 15;
61;
                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Lemieux, Bertrand
APPLICANT: Lemieux, Benoit S.
APPLICANT: Lemieux, Benoit S.
APPLICANT: Sapolsky, Ronald J.
TITLE OF INVENTION: Brassica Polymorphisms
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STRETT: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 13.8; DB 3;
Pred. No. 2.4e+02;
1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: u.o.,
ZIP: 9411-3834
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERTING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION WINBER: US/08/813,507
FILING DATE: U7-AAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            018547-030100US
                                                                                              75.0%; Score 15; DB 100.0%; Pred. No. 61; Live 0; Mismatches
                ; OTHER INFORMATION: antisense sequence US-09-377-310-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/032,069
FILING DATE: 02-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                   Sequence 49, Application US/08813507 Patent No. 6114116 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 75, Application US/08480784 Patent No. 5693473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 0185
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415 576-0200
TELEFAX: 415 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 49
SEQUENCE CHARACTERISTICS:
LENGTH: 41 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ttctcccttccgttattct 19
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                                                                                              Query Match 75.0
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 69.0
Best Local Similarity 78.9
Matches 15; Conservative
                                                                                                                                                                             3 ctcccttccgttatt 17
                                                                                                                                                                                                  STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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US-08-813-507-49
                                                                                                                                                                                                                                                                                                  US-08-813-507-49
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FEATURE:
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Gaps
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                                                                                                                                                                                                                       APPLICANT: Shattuck-Eidens, Donna M.
APPLICANT: Simard, Jacques
APPLICANT: Bin, Mitsuru
APPLICANT: Bai, Mitsuru
APPLICANT: Durocher, Francine
APPLICANT: Durocher, Francine
TITLE OF INVENTION: 179-Linked Breast and Ovarian Cancer
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP STREET: 1201 New York Avenue, N.W., Suite 1000 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24884-109347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,305
FILING DATE: 24-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,266
FILING DATE: 16-SEP-1994
PRIOR APPLICATION NUMBER: US 08/300,266
FILING DATE: 02-SEP-1994
PRIOR APPLICATION NUMBER: US 08/300,266
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: 110-NUMBER: 28/957
REFERENCE/DOCKET NUMBER: 28/957
REFERENCE/DOCKET NUMBER: 24/884-10934
TELECHORE: 202-962-4810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                          Sequence 75, Application US/08487002
Patent No. 5710001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM:
US-08-487-002-75
                                                                                                              RESULT 6
US-08-487-002-75
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                                                                                                                                                                      APPLICANT: Swenson, Jeff
APPLICANT: Kamb, Alexander
APPLICANT: Kamb, Alexander
APPLICANT: Harshman, Keith D.
APPLICANT: Shattuck-Eidens, Donna M.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Futreal, P. Andrew
TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63.0%; Score 12.6; DB 1; Length 30; 78.9%; Pred. No. 8.5e+02; Live 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP STREET: 1201 New York Avenue, N.W., Suite 1000 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24884-109347
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CLASSIETCATION AND ATERIA COLONDOLOGY
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,305
FILING DATE: 24-MAR-1995
FILING DATE: 29-NOV-1994
FILING DATE: 29-NOV-1994
FILING DATE: 10-SEP-1994
FILING DATE: 10-SEP-1994
FILING DATE: 10-SEP-1994
FILING DATE: 10-SEP-1994
FILING DATE: 12-MAC:
APPLICATION NUMBER: US 08/200,266
FILING DATE: 12-MG-1994
FILING DATE: 12-MG-1994
ATORNEY AGENT INFORMATION:
NAME: Inhen, Jeffrey L:
REGISTRATION NUMBER: 28,957
REGISTRATION NUMBER: 28,957
REGISTRATION NUMBER: 28,957
REGISTRATION NUMBER: 28,957
REJECOMMUNICATION INFORMATION:
TELEBHONE: 202-967-4810
                                     Sequence 75, Application US/08483553 Patent No. 5709999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                         Skolnick, Mark H.
Goldgar, David E.
Miki, Yoshio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 78.9°
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                    GENERAL INFORMATION:
APPLICANT: Skolni
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: "CZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL:
RESULT 5
US-08-483-553-75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM:
US-08-483-553-75
                                                                                                                                 APPLICANT:
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Skolnick, Mark H.
APPLICANT: Goldgar, David E.
APPLICANT: Miki, Yoshio
APPLICANT: Miki, Yoshio
APPLICANT: Swenson, Jeff
APPLICANT: Swenson, Jeff
APPLICANT: Harshman, Keith D.
APPLICANT: Tavigian, Keith D.
APPLICANT: Tavigian, Sean V.
APPLICANT: Tavigian, Roger W.
APPLICANT: Futreal, P. Andrew
TITLE OF INVENTION: 179-Linked Breast and Ovarian Cancer
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP STREET: 1201 New York Avenue, N.W., Suite 1000 CITY: Washington STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA

ZIP: 20005
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,554B
FILING DATE: 07-JUN 1995
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: US/08/483,554B
FILING DATE: 24-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,305
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION DAMBER: US 08/348,824
FILING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION DAMBER: US 08/300,266
FILING DATE: 07-SEP-1994
PRIOR APPLICATION DATA:
APPLI
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APPLICATION NUMBER: US 08/289,221
FILING DATE: 12-A0C-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-10934
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                     Sequence 75, Application US/08483554B
Patent No. 5747282
GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
2 totocottocottattott 20
                                          8 TCTCTTCCTCTTCTT 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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; ORGANISM: Hom
US-08-483-554B-75
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Length 30;
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APPLICANT: Shattuck Eidens, Donna M.
APPLICANT: Tavitgian, Sean V.
APPLICANT: Wiseman, Foger W.
APPLICANT: Futreal, P. Andrew
TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 85
                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OURENTING SYSTEM:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,011B
FILING DATE: 07-JUN-1995
CLASSITCATION: 435
PRIOR APPLICATION NUMBER: US 08/409,305
FILING DATE: 24-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824
FILING DATE: 25-MOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,104
FILING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,266
FILING DATE: 16-SEP-1994
PRIOR APPLICATION NUMBER: US 08/300,266
FILING DATE: 02-SEP-1994
PRIOR APPLICATION NUMBER: US 08/300,266
FILING DATE: US 08/300,266
FILING DATE: US 08/300,200
APPLICATION NUMBER: US 08/200,200
APPLICATION NUMBER: US 08/289,221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Venable, Baetjer, Howard & Civiletti, STREET: 1201 New York Avenue, N.W., Suite 1000
Score 12.6; DB 1;
Pred. No. 8.5e+02;
); Mismatches 4;
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                                                                                                                                                                                                                                                     Sequence 75, Application US/08488011B Patent No. 5753441 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey
REGISTRATION NUMBER: 28,957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE DOCKET NUMBER: 24
TELECOMMUNICATION:
TELEPHONE: 202-962-4810
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Goldgar, David E.
Miki, Yoshio
  63.0%;
78.9%;
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Kamb, Alexander
                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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  Query Match
Best Local Similarity
Matches 15; Conserv
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT: Shattuck-Eidens, Donna M.
APPLICANT: Shattuck Jacques
APPLICANT: Nakamura, Yusuk
APPLICANT: Nakamura, Yusuk
APPLICANT: Durocher, Francine
TITLE OF INVENTION: In Vivo Mutations and Polymorphisms
TITLE OF INVENTION: in the 1/q-Linked Breast and Ovarian Cancer
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADRESS:
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                                                                                                                                                                                                                                                63.0%; Score 12.6; DB 4; Length 30; 78.9%; Pred. No. 8.5e+02; ive 0; Mismatches 4; Indels
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FILLING DATE: PCT/US95/10202 FILLING DATE:
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COUNTY: USA
ZIP: ZOODS
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
"""UTTER: IBM PC compatible
""""FR: PC DOS/MS-DOS
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FILING DATE: 24 MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824
FILING DATE: 29-NOV-1994
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FILING DATE: 02-SEP-1994
FILON PEPLICATION DATA: 0S 08/289,221
APPLICATION NUMBER: US 08/289,221
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REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 241
TELECOMMUNICATION INFORMATION:
                                                                                                    MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
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                                                                                                                                                                   Homo sapiens
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Best Local Similarity 78.9
Matches 15; Conservative
  SEQUENCE CHARACTERISTICS:
                                  nucleic acid
EDNESS: single
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                                                                                     linear
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                                       TYPE: nucleic
STRANDEDNESS:
TOPOLOGY: line
                                                                                                                                             ORIGINAL SOURCE:
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PCT-US95-10202-75
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STATE: DC
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US-08-850-727-75
                     LENGTH:
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                                                                                                                                       63.0%; Score 12.6; DB 1; Length 30; llarity 78.9%; Pred. No. 8.5e+02; Conservative 0; Mismatches 4; Indels
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APPLICANT: Futreal, P. Andrew
TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
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1201 New York Avenue, N.W., Suite 1000
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
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Kamb, Alexander
Harshwan, Keith D.
Shattuck Eidens, Donna M.
Tavtigian, Sean V.
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FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,104
FILING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/483,554
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824
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APPLICATION NUMBER: US/08/850,72
                                                                                                                                                                                                                                                                                                                                                US-08-850-727-75
; Sequence 75, Application US/08850727
; Patent No. 6162897
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Skolnick, Mark H.
Goldgar, David E.
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 12-AUG-1994 ATTORNEY/AGENT INFORMATION:
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TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO:
                                                             Homo sapiens
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                                                                                                                                         Query Match
Best Local Similarity
Matches 15; Conserv
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               HYPOTHETICAL: NC
CRIGINAL SOURCE:
CREANISM: HOMC
US-08-488-011B-75
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APPLICANT:
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APPLICANT:
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Futreal, P. Andrew
NVENTION: Method for Diagnosing a
NVENTION: Predisposition for Breast and Ovarian Cancer
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STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10220
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APPLICATION NUMBER: US
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,305
FILING DATE: 24-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824
FILING DATE: 29-NOV-1994
   US 08/289, 221
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Kamb, Alexander
Harshman, Keith D.
Shattuck Eidens, Donna M
Tavtigian, Sean V.
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GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Goldgar, David E.
APPLICANT: Miki, Yoshio
                                                                                                                                          REFERENCE/DOCKET NUMBER: 2488
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ. ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                        NAME: Ihnen, Jeffrey L. REGISTRATION NUMBER: 28,957
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                               FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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Matches 15; Conservative
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   APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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PCT-US95-10220-75
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT: Wiseman, Roger W.
APPLICANT: Putreal, P. Andrew
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 85
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Venable, Baetjer, Howard & Civiletti, LLP
1201 New York Avenue, N.W., Suite 1000
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APPLICATION NUMBER: PCT/US95/10203
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APPLICATION NUMBER: US
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,305
FILING DATE: 24-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824
FILING DATE: 29-WOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,104
FILING DATE: 16-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Swenson, Jeff
Kamb, Alexander
Harshman, Keith D.
Shattuck-Eidens, Donna M.
Tavttglan, Sean V.
Wiseman, Roger W.
Futreal, P. Andrew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
PREDICATION NUMBER: US 08/300,266
FILING DATE: 02.SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 75, Application PC/TUS9510203 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                          ; MOLECULE TYPE: DNA (genomic); HYPOTHETICAL: NO ; ORIGINAL SOURCE: CREATER SO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Skolnick, Mark H.
Goldgar, David E.
Miki, Yoshio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 tetecettecgttattett 20
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202-962-4810
            TELEFAN. 202-962-8300
TELEFAN 202-962-8300
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 63.0
Best Local Similarity 78.9
Matches 15, Conservative
                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 02-SEP-
PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Washi
STATE: DC
COUNTRY: US
ZIP: 20005
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TELEPHONE:
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                     Length 22;
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                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: No. 6114502th, Michael
APPLICANT: No. 6114502th, Michael
APPLICANT: No. 6114502th, Design
APPLICANT: No. 6114502en'Trauth, Konrad
APPLICANT: No. 6114502en'Trauth, Konrad
TITLE OF INVENTION: GENE FAMILY ASSOCIATED WITH
TITLE OF INVENTION: NEUROSENSORY DEFECTS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61.0%; Score 12.2; DB 3;
82.4%; Pred. No. 1.3e+03;
tive 0; Mismatches 3;
                                                                                                                                                                                                                                  Score 12.2; DB 1;
Pred. No. 1.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Discrete
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
PILLICATION NUMBER: US/09/032,365A
FILLIG DATE:
                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Bozicevic & Reed, LLP
STREET: 285 Hamilton Avenue, Suite 200
                                                                                                                            MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primers"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 38, Application US/09032365A Patent No. 6114502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36,677
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-327-3400
TELEFAX: 650 327-3231
                                                                                                                                                                                                                                     61.0%;
82.4%;
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ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                     Query Match 61.0
Best Local Similarity 82.4
Matches 14; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 61.0
Best Local Similarity 82.4
Matches 14; Conservative
                                            LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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                                                                                                            linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE:
US-09-032-365A-38
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                                                                                                          TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert STREET: 4 Embarcadero Center, Suite 3400 STRIY: San Francisco STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08701380
Patent No. 5686598
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
NISHINA, Patsy
APPLICANT:
ITLE OF INVENTION:
GENES ASSOCIATED WITH RETINAL
TITLE OF INVENTION:
UNMBER OF SEQUENCES:
UNMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 054111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/701,380
FILING DATE:
             PRIOR APPLICATION UNMBER: US 08-308,104
FILING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,266
FILING DATE: 02-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,221
FILING DATE: 12-AUG-1994
ATTORNEY/ACBNT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
FELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: SHERWOOD, Pamela J.
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: A-63565/PJS
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-494-8701
TELEFAX: 415-494-8771
                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 tctcccttccgttattctt 20
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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Best Local Similarity 78.99
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 30 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCT-US95-10220-75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM:
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60.0%; Score 12; DB 1; Length 30;
Best Local Similarity 75.0%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                        RESULT 15
US-07-931-473B-35/C

Sequence 35, Application US/07931473B
Sequence 35, Application US/07931473B
Sequence 35, Application US/07931473B
Sequence 35, Application US/07931473B
Sequence 35, Application US/07043
SEQUENCE INVENTION:
MPDICANT: Larry Gold
APPLICANT: Craig Tuerk
TITLE OF INVENTION: Nucleic Acid Ligands
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Beaton & Swanson, P.C.
STRET: 4582 South UIster Street Parkway, #403
CITY: Denver
STRET: 4582 South UIster Street Parkway, #403
CONFUTR: USA
STRET: 4582 South UISter Street Parkway, #403
CONFUTR: IBM compatible
COMPUTR: IBM compatible
COMPUTR: IBM compatible
COMPUTR: WordPerfect 5.1
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Search completed: October 2, 2001, 16:03:47 Job time: 14591 sec οy a

Searched:

Run on:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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gb_htg22:*
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Match Length DB
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gb_htg8:*
gb_htg9:*
gb_htg10:*
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gb_htg2:*
gb_htg3:*
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gb_sts2:*
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gb_un:*
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67.0
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63.0
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                                                                                          (without alignments) 92.640 Million cell updates/sec
                                                                            October 2, 2001, 15:56:41; Search time 3339.34 Seconds
         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                            1344157 segs, 7733874588 residues
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                                                                                                                                                                                                                                                                                                                     Listing first 45 summaries
                                                       OM nucleic - nucleic search, using sw model
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Maximum Match 100%
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em_htg_huml: *
em_htg_hum2: *
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em_htgo_inv:*
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em_htg_hum6:*
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20
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gb_ba2: *
gb_ba2: *
gb_ba2: *
gb_in1: *
gb_in3: *
gb_om: *
gb_pat1: *
gb_ph: *
gb_pl1: *
gb_pl1: *
gb_pl1: *
gb_pl3: *
gb_pl3: *
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em_in:*
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em_fun:*
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                                                                                                                                                                                                                                                          Minimum DB seq length: 0 Maximum DB seq length: 50
                                                                                                                            Title:
Perfect score:
Sequence:
                                                                                                                                                                          Scoring table:
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AR079693 Sequence A63162 Sequence A63164 Sequence AR061344 Sequence AR062804 Sequence AR087882 Sequence AR09782 Sequence

AR037524 AR062804 AR087882 AR091352

AR079693 AR081223 A63162 AR001344

Description

SUMMARIES

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                                                                                            (bases I to 43)
Pavlakis,G.N. and Felber,B.K.
Pavlakis,G.N. and Felber,B.K.
Nucleic acid constructs containing HIV genes with mutated inhibitory/Anstability regions and methods of using same Patent: US 5972596-A 17 26-OCT-1999;
Location/Qualifiers
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Pred. No. 9.7e+03;
0; Mismatches 2; Indels
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             PAT
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Pred. No. 4.4e+03;
0; Mismatches 1;
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FAS LIGAND FUSION PROTEIN
PAGENT: WO 9718307-A 5 22-MAY-1997;
SANDOZ LTD (CH)
Other publication AU 7684896 19970605.
    аки81223 43 bp DNA
Sequence 17 from patent US 5972596.
AR081223
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/db_xref="taxon:32644"
5 c 9 g 7
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A63162
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93.38;
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Best Local Similarity 87.5%;
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A39180 Sequence 23
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A46304 Sequence 2
A80185 Sequence 2
AA232757 Mus muscu
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AR069436 Sequence
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I41178 Seguence 34
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AR030753 Sequence
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AX060907 Sequence
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Pavlakis,G.v. and Felber,B.K.
Method of eliminating inhibitory/instability regions of mRNA
Patent: US 5965726-A 17 12-OCT-1999;
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AR053115
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AR012082
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AR079693
AR079693.1 GI:10006434
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Skolnick,M.H., Cannon-Albright,L.A. and Kamb,A.
Methods for detecting predisposition to cancer at the MTS gene
Patent: US 5989815-A 34 23-NOV-1999;
Location/Qualifiers
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1 (bases 1 to 21)
1 (kamb, A.
MTS2 gene
Patent: US 5994095-A 34 30-NOV-1999;
                                                                                                          AR087882 21 bp DNA
Sequence 34 from patent US 5989815.
AR087882.1 GI:10014645
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AR091352
AR091352.1 GI:10018107
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Sequence 34 from patent US 5624819.
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Kamb, A.
Probes for MTS1 gene and polynucleotides encoding mutant MTS1 genes
Patent: US 5801226-A 34 01-SEP-1998;
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Pred. No. 1.3e+04;
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Pred. No. 1.3e+04;
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Pred. No. 1.3e+04;
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E. 1 (bases 1 to 21)

S. Stone, S., Jiang, P. and Kamb, A.

Mouse WTSI gene

Mouse WTSI gene

Location/Qualifiers

Location/Qualifiers

''nnown"
      Kamb, A.
MTS1E1.beta. gene
Patent: US 5739027-A 34 14-APR-1998;
Location/Qualifiers
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US 5801236.
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Sequence 34 from patent US 5843756.
AR062804 GI:5990495
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1 (bases 1 to 21)
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Best Local Similarity 78.9
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Patent: US 5763190-A 7 09-JUN-1998;
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Weiner, D.B. and Refaell, Y.
Methods for the identification of compounds capable of inducing the nuclear translocation of a receptor complex comprising the glucocoticoid receptor type II and viral protein R interacting
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                     Unchassified.

Unclassified.

(bases to 21)

Skolluck, M.H., Cannon-Albright, L.A. and Kamb, A.
Germline mutations in the MTS gene
Patent: US 5624819-A 34 29-APR-1997;
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Pred. No. 1.3e+04;
0; Mismatches 4;
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Patent: US 5763190-A 6 09-JUN-1998;
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Sequence 6 from patent US 5763190.
AR012082
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Best Local Similarity 78.9
Matches 15; Conservative
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Unclassified.
1 (bases 1 to 35)
Terman, B. Israel and Carrion, M. Eduardo.
Recombinant kinase insert domain containing receptor and gene encoding same
encoding same
Patent: US 5861301-A 2 19-JAN-1999;
Location/Qualifiers
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Pred. No. 1.3e+04;
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65.0%; Pred. No. 1.7e+04;
tive 3; Mismatches 4;
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Jiao, S., Habben, J.E. and Niu.X.
Seed-preferred promoter from maize
Patent: WO 0121783-A 5 29-MAR-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
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Sequence 2 from patent US 5861301.
AR030753
AR030753.1 GI:5943967
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Best Local Similarity 65.0°
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Search completed: October 2, 2001, 15:56:42 Job time: 14166 sec
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1 (bases 1 to 44)
WOLF.D., Tomlinson,J.E., Fretto,L.J., Giese,N.A., Escobedo,J.A. and Williams,L.Thomas.
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                                                                                                                                                                                                                                     Unknow...
Unclassified.
1 (bases 1 to 42)
1 (bases 1 to 42)
Capon,D. and Petropoulos,C.J.
Capon,D. and methods for determining anti-viral drug susceptibility and resistance and anti-viral drug screening Patent: US 583746.A 2 17-NOV-1998;
Location/Qualifiers
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Score 12.4; DB 10; Length 37; Pred. No. 1.7e+04; 0; Mismatches 1; Indels
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Location/Qualifiers
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Sequence 10 from patent US 5872218.
AR036477 GI:5953145
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Sequence 2 from patent US 5837464.
AR054989.1 GI:5980566
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts JOURNAL Unpublished (2000) COMMENT Contact: Robert B. Weiss University of Utah Genome Center | ### 1308 Biological Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA FAX: 801 585 7177 FAX: 801 587 8176 FAX: 802 817 817 817 FAX: 802 81 FAX: 802 817 FAX: 802 817 FAX: 802 817 FAX: 802 817 FAX: 8 | Qy | RESULT 2 A1545803 A1545803 DEFINITION F65512.y1 Zebrafish WashU MPING EST Danio rerio cDNA 5' similar to recession A1545803 TR:Q31365 Q31365 UBA*O1 CLASS I MHC MRNA.; mRNA sequence. ACCESSION A1545803 VERSION A1545803 ACTIONOPERIORIS BURBARORE ORGANISM ACTIONOPERIORII, Neopterygii; Teleostei; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Danio. Cypriniformes; Cyprinidae; Rasborinae; Danio. Cypriniformes; Cyprinidae; Rasborinae; Danio. AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS ALIllier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood |
|---|--|------------|--|
| SUMMARIES Result Ouery No. Score Match Length DB ID Description | 12.8 64.0 49 251 AZ568456 AZ668456 20001610111 2 12.2 64.0 49 12 AZ77125 | ALIGNMENTS | AZ868456 LOCUS AZ868456 AZ868456 AZ868456 AZ868456 AZ868456 AZCESSION AZ868456 AZ86866 AZ868666 AZ868666 AZ868666 AZ868666 AZ8686666 AZ8686666 AZ8686666 AZ8686666 AZ8686666 AZ8686666 AZ86866666 AZ86866666 AZ868666666 AZ86866666 AZ8686666666 AZ868666666 AZ8686666666666 |

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                                                                          REFERENCE
                                                                                          AUTHORS
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                                                                                                                                     4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrafish@watson.wustl.edu
CDNA Library Preparation: Matthew Clark. CDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
Info@egenomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@esegen.com) and
RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA797125 49 bp mRNA EST 10-FEB-1998 vn43e06.rl Stratagene mouse skin (#937313) Mus musculus cDNA clone IMAGE:1023970 5' similar to SW:TRHY_RABIT P37709 TRICHOHYALIN. [1]
,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B.,
Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E.,
Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="26 somite embryos, adult livers, shield
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Possible reversed clone: similarity on wrong strand
Seq primer: T3 ET from Amersham
High quality Sequence stop: 1.
Location/Oualifiers
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/organism="Danio rerio"
/db_xref="taxon:7955"
/clone_lib="zebrafish WashU MPIMG EST"
/sex="mixed"
                                                                  Washu Zebrafish EST Project 1998
Unpublished (1998)
Contact: Stephen L. Johnson
Washington University School of Medicine
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AA797125
AA797125.1 GI:2860080
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19 GCTGCTAGTTTTCTGTC 35
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Matches 14; Conservative
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                                                     and Wilson, R.
                                                                                                                                                                                                                                                                                                                                             www.rzpd.de)
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Marra M., Hillier'L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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/dev_stage="11 weeks old"
/dev_stage="11 weeks old"
/dev_stage="11 weeks old"
/dev_stage="11 weeks old"
/note="Organ: skin; Vector: pBluescript SK-; Site_1: Eco
: Site_2: XhoI; Cloned unidirectionally. Primer: Oligo
dT. Whole skin from 11 week old G57BL/6 female mice.
Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5'
adaptor sequence: 5' GAATTCGCACAGA 3' -3' adaptor
sequence: 5' CTCGAGTTTTTTTTTTTTTTTTT 3'"
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                                                                                                                                                                                                                                                                                                                                  Contact: Marra MyMouse EST Project
Washi-HHMI Mouse EST Project
Washi-HHMI Mouse EST Project
Washi-HHMI Mouse EST Project
Washi-HHMI Mouse EST Project
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 44)
NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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/db_xref="taxon:10090"
/clone="TMAGE:1023970"
/clone_lib="Stratagene mouse skin (#937313)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGI:574746
Possible reversed clone: similarity on wrong strand Possible reversed clone: similarity on wrong strand Seq primer: -28ml3 rev1 ET from Amersham High quality sequence stop: 1.
Location/Qualifiers
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    .49
    /organism="Mus musculus"

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                                                                   1 (bases 1 to 49)
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High quality sequence stop: 50.
Location/Qualifiers
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/db_xref="taxon:9606"
Location/Qualifiers
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                                            /ordanism="Homo
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Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    13; Conservative
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                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="InAGE:3956864"
/clone=lib="NHH_MGC_21"
/tissue_type="choriocarcinoma"
/lab_host="ball08 (pinge=resistant)"
/note="Organ: placenta; Vector: pOTB7; Site_1: XhOI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhOI sites using the Directionally cloned into EcoRI/XhOI sites using the following 5' adaptor: GGACGAGGG): Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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1 (bases 1 to 49)

Hilliar,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,Fr., Thierry-Meg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M. Generation and analysis of 280,000 human expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4444 Porest Park Parkway, Box 8501, St. Louis, MO 63108
4444 Porest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
Finail: est@watson.wustl.edu
Insert Size: 446
Figh qality sequence starts: 1 High qality sequence stops: 1
Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL, contact the IMAGE Consortium (info@image.llnl.gov)
for further information. Trace considered overall poor quality
Insert Length: 446 Std Error: 0.00
Seq primer: M13RP1
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                CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM833 row: k column: 09.
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86.7%;
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Best Local Similarity 86.75
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                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I, Chases I to 50)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly and Wright,D.,Weiss,R., Stokes,R., Tingey,A., von Niederhausern,A. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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                                                                                                                                                                                                                                                                                                                                                                                                                 Length 49;
                                                                                                                                                /lab_host="SOLR cells (kanamycin resistant)"
                                                            /clone="IMAGE:6940""
/clone_lib="Stratagene placenta (#937225)"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                               Score 11.8; DB 189; Length
Pred. No. 5.6e+04;
); Mismatches 3; Indels
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Seq primer: CGTTGTAAAACGACGGCCAGT
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University of Utah
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/db_xref="taxon:10090"
/clone="UUGC1M0203P22"
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o.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligomicleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114(gblAF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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was hydrodynamically sheared by repeated passage through a
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 40)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NAILONAl Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Unpublished (1997)
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
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/db_xref="taxon:9606"
/db_xref="ImAGE:217852"
/clone_limaGE:217852"
/tlssue_type="moderately-differentiated endometrial
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Pred. No. 5.6e+04;
0; Mismatches 2; Indels 0;
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86.7%;
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Best Local Similarity 86.7
Matches 13; Conservative
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//note="Vector: PWAZIVY; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (qil4732114|qblAR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampleillin resistance."
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                                                                                                                                                                                                                                                                               AZ471345 41 bp DNA GSS 04-OCT-2000
1M0285119R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC1M0285119 R, DNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Slam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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/sex="Male"
  Length 40;
                                                     Indels
Score 11.6; DB 21;
Pred. No. 6.9e+04;
); Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Class: plasmid ends
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/db_xref="taxon:10090"
/clone="UUGC1M0285119"
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58.0%;
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                                                     Conservative
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Fax: 801 585 7177
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Query Match
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Contact: Yutaka Suzuki
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ins.u-tokyo.ac.jp
Suzuki.Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched con library. Gene 200 (1-2), 149-156 (1997).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 50)
2 (bases I to 50)
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4 (bases I to 50)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata
                                                                                                                                                                                                                                                                                                                                                                                                                                            AU102832 50 bp mRNA EST 05-APR-2001
AU102832 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
CAS01996, mRNA sequence.
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AU102838 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
CASO9268, mRNA sequence.
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                                                                                                                     Length 45;
                                                                                                                                                                               Indels
                                                                                                                     DB 250;
                                                                                                              Score 11.6; DB 250;
Pred. No. 7e+04;
0; Mismatches 4;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CAS01996"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 45)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
                                                                                                                                                                                                                                                                                                                                                                                                             AZ827171 45 bp DNA GSS 20-FEB-2001
2M0103P19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0103p19"
/clone=llb="Mouse 10kb plasmid UUGCIM library"
/sex="Male"
                                                                                   DB 244; Length 41;
                                                                                                                                             Indels
                                                                                                                                             4;
                                                                                Score 11.6; DB 244
Pred. No. 6.9e+04;
0; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               clone UUGC2M0103P19 F, DNA sequence. AZ827171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0
Plate: 0103 row: P column: 19
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 45. Location/Qualifiers
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                                                                                58.0%;
77.8%;
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                                                                                                                                                                                                                                          41 AGATGCCAGTTTTCTGCC 24
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Best Local Similarity 77.8
Matches 14; Conservative
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TITLE

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05-APR-2001

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FEATURES

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L. Codes, T. Tsunoda, T., Taira, H., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Tsunoda, T., Tanaka, T., Nakamura, Y., Morishita, S., Okubo, K., Suyama, A. and Sugano, S.
Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries Unpublished (2001)
Contact: Yutaka Suzuki
Department of Virology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuskiteims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-dayaqawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA275379 36 bp mRNA EST 31-MAR-1997 vc10d01.rl Barstead MPLRB1 Mus musculus cDNA clone IMAGE:766081 5' similar to 9b:L33878 Mus musculus renal sodium phosphate (MOUSE);,
                                                                                                                                                                                   AU102844 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone CAS11168, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CASILIG6"
/clone_lib="Sugano Homo sapiens cDNA library"
/l clone_lib="Sugano Homo sapiens cDNA library"
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The WashU-HMI Mouse EST Project Unpublished (1996)
Contact: Marra M/Mouse EST Project
                                                                                                                                                                 mRNA
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3 agatgctaggtatctgtc 20
                        48 AGAGGTTTGGTATCTGCC 31
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              K., Suyama, A. and Sugano, S.
Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries Unpublished (2001)

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Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki; Y., Yoshiromo-akakagawa, K., Maruyama, K., Suyama, A. and Sugano
Suzuki; Y., Yoshiromo-akakagawa, K., Maruyama, K., Suyama, A. and Sugano
S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo...

1 (bases 1 to 50)

Suzuki, Y., Tsunoda, T., Taira, H., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Nakamura, Y., Morishita, S., Okubo, K., Suyama, A. and Sugano, S., Nakamura, Y., Morishita, S., Okubo mRNAs using full-length enriched and 5'-end enriched cDNA libraries Unpublished (2001)

Department of Virology
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4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ins.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
Ota, T., Isogai, T., Tanaka, T., Nakamura, Y., Morishita, S., Okubo
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AU102843 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
CAS11158, mRNA sequence.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/dlone="Acasilis8"
/clone=lib="Sugano Homo sapiens cDNA library"
^ 11 c 11 g 7 t
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Pred. No. 7.2e+04;
); Mismatches 4; Indels 0
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                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CAS09268"
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6

FEATURES

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EMEATYOLS: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammaliai; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

E 1 (bases 1 to 39)

S Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longarce, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3']; double-stranded cDNA was ligated to Eco RI adaptors [CARGGATTCGGTACC], digested with Not I and cloned into the Not I and Eco. RI sites of the modified pT7T3 vector. Library constructed by Bob Barstead."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington University School of Medicinep
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fal: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:467001
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 31.
Location/Qualifiers
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/sex="mixed"

    .36
    /organism="Mus musculus"

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/db_xref="taxon:10090"
/clone="IMAGE:766081"
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Insert Length: 10000 Std Erro
Plate: 0202 row: H column: 18
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/dev_stage="6 weeks"
/lab_host="DH10B"
WashU-HHMI Mouse EST Project
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92.3%;
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Matches 12; Conservative
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Fax: 801 585 7177
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(http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was putified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (qiiq732114 qib]ART29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-" /note="Weetcr: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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/sex="Male"
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Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 39.
Location/Qualifiers
                                                                                                                                                                                     /organism="Mus musculus"
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/clone="UUGC1M0202H18"
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APPLICANT: Gaarde, William A.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0389
CURRENT APPLICATION NUMBER: US/09/377,310B
CURRENT APPLICATION NUMBER: US/09/377,310B
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 20
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APPLICANT: Monia, Brett P.
APPLICANT: Monia, Brett P.
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0389
CURRENT APPLICATION NUMBER: US/09/377,310B
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SSFTWARE: Patentin Ver. 2.0
SEQ ID NO 28
LENGTH: 15
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             US-08-460-490-10
PCT-US92-00730-10
PCT-US92-00730-10
PCT-US92-00730-10
US-09-377-310-29
US-08-277-803B-21
US-08-271-880A-172
US-08-271-880A-189
US-08-210-408-189
US-08-910-408-189
US-08-910-408-189
US-09-249-215-189
US-07-832-905B-69
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ilarity 100.0%; Pred. No. 0.049;
Conservative 0; Mismatches 0
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US-08-464-531-59
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i. Sequence 8, Application US/09377310B

i. Patent No. 6133031

i. GENERAL INFORMATION:
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 Query Match
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                                                                                                                            Search time 417.38 Seconds
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-377-310-9
US-08-850-049-17
US-08-86-7478-17
US-08-47-47-15-17
US-08-47-47-15-17
US-08-47-17-34
US-08-48-810-34
US-08-88-25-34
US-08-88-60-73-34
US-08-98-01-34
US-08-115-25-34
US-08-115-252-34
US-09-115-252-34
US-09-120-130-34
US-09-115-252-34
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-07-930-548A-2
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US-08-168-917-10
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                                                                                                                            October 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0 Maximum DB seq length: 50
                                                                                                                                                                                                                      Perfect score:
                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    score gand is
                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Database
                                                                                                                            on
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No.
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Gaps

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Score 13.4; DB 2; Length 43; Pred. No. 1.5e+02;
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TITLE OF INVENTION: INHIBITORY/INSTABLLITY REGIONS OF MRNA
NUMBER OF SEQUENCES: 130
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: MORRY, MARY J.
REGISTRATION NUMBER: 34,398
REFERENCE/DOCKET NUMBER: 2026-4006US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)758-4800
INFORMATION FOR SEO ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 BASE PAIRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/02908
FILING DATE: 29-MAR-1993
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/858,747
FILING DATE: 27-MAR-1992
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 10154
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,478
FILING DATE: 26-OCT-1994
CLASSIFICATION DATA:
APPLICATION DATA:
RPICTATION NUMBER: PCT/US93/02908
FILING DATE: 29-MAR-1993
CLASSIFICATION: 435
FILING DATE: 29-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 27-MAR-1992
CLASSIFICATION: 435
                     US 08/050,478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 17, Application US/08050478; Patent No. 5972596; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67.0%;
93.3%;
                                     26-OCT-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14; Conservative
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 GAAGCTAGGTATCTG 5
                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: NUCLEIC ACID
                   APPLICATION NUMBER: FILING DATE: 26-OC CLASSIFICATION: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                    LINEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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NEW YORK
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                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-050-478-17/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT
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                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Monia, Brett P.
APPLICANT: Monia, Brett P.
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0389
CURRENT APPLICATION NUMBER: US/09/377,310B
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver: 2.0
ENGTH: 20
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                                                                                   DB 3; Length 15; 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 20;
                                                                                                                                0; Indels
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100.0%; Pred. No. 20;
tive 0; Mismatches
                                                                                         Score 15; DB 3; Pred. No. 20; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: METHOD OF ELIMIN
TITLE OF INVENTION: INHIBITORY/INSTA
NUMBER OF SEQUENCES: 130
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER: USA
ZIP: 10154
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SUSTINGER: MORDERFECT 5.1
       ; OTHER INFORMATION: antisense sequence US-09-377-310-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTHER INFORMATION: antisense sequence US-09-377-310-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/850,049
FILING DATE: 02-MAY-1997
CLASSIFICATION: 435
                                                                             75.0%; Scur.
100.0%; Pre
0; }
                                                                                                                                                                                                                                                                                                  Sequence 9, Application US/09377310B Patent No. 6133031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 17, Application US/08850049 Patent No. 5965726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
                                                                                         Query Match 75.0
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15; Conservative
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 0: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-850-049-17/C
                                                                                                                                                                                                                                                               RESULT 3
US-09-377-310-9
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FEATURE:
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Gaps

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; OTHER INFORMATION: 3392-3434 OF C-FOS, HUMCFOT, ACC #V01512
US-07-858-747B-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 12.8; DB 4; Length 39;
Pred. No. 3e+02;
0; Mismatches 2; Indels
                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GERMLINE MUTATIONS IN THE MTS GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP STREET: 1201 New York Avenue, Suite 1000 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Wong, Alexander K.C.
APPLICANT: Tavtigian. Sean V.
APPLICANT: Tavtigian. Sean V.
APPLICANT: Tavtigian. Sean V.
APPLICANT: Tavtigian. David H.-F.
ITLE OF INFORTION: TWRRS2 is a Tumor Suppressor
ITLE REFERENCE: 2318-20.
CURRENT APPLICATION NUMBER: US/09/342,749
CURRENT FILING DATE: 1999-06-29
EARLIER APPLICATION NUMBER: US 60/091,044
EARLIER APPLICATION NUMBER: US 60/091,044
EARLIER APPLICATION NUMBER: US 60/091,044
SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NOS: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
OPERATINES: TSTEMS: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                 Score 13.4; DB 4;
Pred. No. 1.5e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Skolnick, Mark H.
APPLICANT: Cannon-Albright, Lisa A.
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: GERMLINE MUTATIC
WUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/474,177
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                  ; Sequence 15, Application US/09342749
; Patent No. 6166194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 34, Application US/08474177
Patent No. 5624819
GENERAL INFORMATION:
                                                                                                 67.0%;
93.3%;
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ilarity 87.5%;
Conservative
                                                                                            Ouery Match 67.0
Best Local Similarity 93.3
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 ATGATAGGTATCCGTC 15
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                           19 GAAGCTAGGTATCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                          US-09-342-749-15/c
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APPLICANT: K.
TITLE OF INVENTION: METHOD OF ELIMINATING
TITLE OF INVENTION: INHIBITORY/INSTABILITY REGIONS OF MRNA
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                  Length 43;
                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: OLIGONUCLECTIDE FOR MUTATING NT
                                                                                                                                                                                                                                                                                                                                Score 13.4; DB 2;
Pred. No. 1.5e+02;
        NAME: MOKKI, FALLEL STATEM TO NUMBER: 34,398
REGISTRATION NUMBER: 2026-4006US1
RELECOMMUNICATION INFORMATION:
TELEPHONE: (212)758-4800
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 BASE PAIRS
TYPE: NUCLEIC ACID
STYPE: NUCLEIC ACID
STYPE: SINGLE
                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O7/858,747B
FILING DATE: 19920327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: MARY J. MORRY
REGISTRATION NUMBER: 34,398
REFERENCE/DOCKET NUMBER: 2026-4006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)758-4800
INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17, Application US/07858747B Patent No. 6174666 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                             67.0%;
93.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                             Query Match 67.0
Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                4 gatgctaggtatctg 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                   19 GAAGCTAGGTATCTG 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: UNKNOWN MOLECULE TYPE: OTHE HYPOTHETICAL: YES FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-07-858-747B-17/C
                                                                                                                                                                                                                                             ; TOPOLOGY:
US-08-050-478-17
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MOLECULE TYPE: CDNA HYPOTHETICAL: NO
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STATE: DC
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ANTI-SENSE:
US-08-487-033-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-480-810-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
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Pred. No. 3.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTTLE OF INVENTION: MISIEL-Beta GENE
TTTLE OF INVENTION: MISIEL-Beta GENE
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ptoppy disk
COMPUTER: Ptoppy disk
COMPUTER: Ptoppy disk
COMPUTER: Ptoppy disk
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/487,033
FILING DATE: 0.7-JUN 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Indels
                                                                                  FILING DATE: 01-JUN-1294

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087

FILING DATE: 18 WAR-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086

FILING DATE: 18 WAR-1994

PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369

FILING DATE: 18 WAR-1994

ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957

REGISTRATION NUMBER: 28,957

RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: 202-962-4810

TELEFAX: 202-962-8300

INFORMATION FOR SED ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
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APPLICATION NUMBER: PCT/US95/03537
FILING DATE: 17-MAR-1995
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APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
                                                                 us 08/251,938
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Patent No. 5739027
GENERAL INFORMATION:
                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US OF FILING DATE: 01-JUN-1994
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Best Local Similarity 78.9°
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
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US-08-474-177-34
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Gaps
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Pred. No. 3.7e+02;
0; Mismatches 4; Indels
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Patent No. 5801236
GENERAL INFORMATION:
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTSI GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSED: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,810
FILING DATE: 07.JUN-1995
CLASSIFICATION: 435
PROFE APPLICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                   24884-109348-C
PRILING DATE: 01-UNN-1994
PRILOR APPLICATION NUMBER: 05 09/231,936
APPLICATION NUMBER: 05 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 05 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: 05 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION NUMBER: 05 08/217,589
FILING DATE: 14-APR-1994
PRILOR APPLICATION NUMBER: 08 08/214,582
APPLICATION NUMBER: 08 08/214,582
ATTORNEY AGENT: 18-PARR-1994
FILING DATE: 18-PARR-1994
ATTORNEY AGENT: 18-PARR-1108:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 17-MAR.1995/03316
FILING DATE: 17-MAR.1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/751 0.0
FILING DATE:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                               NAME: Theen, Jeffrey L. REGISTRATION NUMBER: 28,957 REFERENCE/DOCKET NUMBER: 24, TELECOMMUNICATION INFORMATION: TELEPHONE: 202-962-4810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 202-962-8300 INFORMATION FOR SEQ ID NO: 34:
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3 CTAGAGGCGAATTATCTGT 21
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Best Local Similarity 78.99
Matches 15, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
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APPLICATION NUMBER: F
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STRANDEDNESS: single
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TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE AND TITLE OF INVENTION: METHOD FOR DETECTING PREDISPOSITION TO CANCER AT THE MTS TITLE OF INVENTION: GENE NUMBER OF SEQUENCES: 36 CORRESPONDENCE ADDRESS: ADDRESSE: Venable, Baetjer, Howard & Civiletti, LLP STREET: 1201 New York Avenue, Suite 1000
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Pred. No. 3.7e+02;
0; Mismatches 4; Indels
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ZIP: 20005

COUNTY. USA

ZIP: 20005

COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/848,251

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION NUMBER: US 08/474,083

FILING DATE: 07-JUN-1995

APPLICATION NUMBER: PCT/US95/03537

FILING DATE: 17-MR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/251,938
  28,957
ER: 24884-109348
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FILING DATE: 01-UN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-WAR-1994
PRIOR APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-WAR-1994
PRIOR APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Skolnick, Mark H.
APPLICANT: Cannon-Albright, Lisa A.
APPLICANT: Kamb, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 34, Application US/08848251
Patent No. 5989815
GENERAL INFORMATION:
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4448
TELEPAX: 202-962-8300
                                                                                                                                                                                                                                                                                                                                                                                              63.0%;
78.9%;
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3 CTAGAGGCGAATTATCTGT 21
                                                                                          TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                         Query Match 63.0
Best Local Similarity 78.9
Matches 15, Conservative
                                                                                                                                                             LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                  Linear
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US-08-508-735-34
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US-08-848-251-34
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APPLICANT: Jiang, Ping
APPLICANT: Jiang, Ping
APPLICANT: Mamb; Alexander
TILLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
"ADDRESSE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
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APPLICATION NUMBER: US/08/508,735
           PRIOR APPLICATION NOMER: 05 00/215,007
PRIOR APPLICATION DATA:
APPLICATION NOMER: 05 00/215,006
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NOMER: 05 08/227,369
FILING DATE: 14-AR-1994
PRIOR APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 20,957
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
SCOLOROGONESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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RICOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US to be assigned
FILING DATE: 07-JUN-1995
APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-508-735-34
; Sequence 34, Application US/08508735
; Patent No. 5843756
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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78.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 78.9°
Matches 15; Conservative
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US-08-480-810-34
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24884-109348-B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 34, Application US/09120130 Patent No. 6037462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/480,810
                      REFERENCE/DOCKET NUMBER: 2488
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTS1 GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
      28,957
                                                                                                                                                                                                                                                                                                                                                                                63.0%;
78.9%;
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                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 78.9
Matches 15; Conservative
                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA: APPLICATION NUMBER: (
      REGISTRATION NUMBER:
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
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                                                                                                                                                                                                                                               MOLECULE TYPE:
HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE
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                                                                                                                                                                                                                                                                                            ; ANTI-SENSE:
US-08-486-047-34
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US-09-120-130-34
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Patent No. 5994095
GENERAL INFORMATION:
Alexander
TITLE OF INVENTION: WTS2 GENE
NUMBER OF SEQUENCES: 36
CORRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MCDION TYPE: Filopy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTHARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,047
FILING DATE: 07-JUN 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-MAR-1994
PRIOR APPLICATION NUMBER: US 08/227,369
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APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-ARR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Inhen, Jeffrey L.
                                                                                    REFERENCE/DOCKET NUMBER: 2486
TELECOMMUNICATION INFORMATION:
TELEPRIONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ctagatgctaggtatctgt 19
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                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDRES: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
TYPOTHETICAL: NO
ANTI-SENSE: YES
US-08-848-251-34
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 78.99
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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COUNTRY: US,
ZIP: 20005
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US-08-486-047-34
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Gaps
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0
Length 21;
                                                   4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
Score 12.6; DB 2;
Pred. No. 3.7e+02;
); Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24884-109348
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APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/227,369 FILING DATE: 14-APR-1994
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FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Ihnen, Jeffrey L. REGISTRATION NUMBER: 28,957 REFERENCE/DOCKET NUMBER: 241 TELECOMMUNICATION INFORMATION:
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Gaps

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Score 12.6; DB 3; Length 21;
Pred. No. 3.7e+02;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: October 2, 2001, 16:03:47 Job time: 14591 sec
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78.9%;
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3 CTAGAGGCGAATTATCTGT 21
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                            Query Match 63.0
Best Local Similarity 78.9
Matches 15; Conservative
                                                                     LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-09-115-252-34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 34, Application US/09115252
Patent No. 6060301
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTSI GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Sulte 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/115,252
FLING DATE: 07-JUN-1995
APPLICATION NUMBER: US/08/480,810
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 01-JUN-1994
PRIOR APPLICATION NUMBER: US/08/251,938
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US/08/215,086
FILING DATE: 14-APR-1994
PRIOR APPLICATION NUMBER: US/08/217,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/217,369
FILING DATE: US/08/217,369
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FILING DATE: 18-WAR-1994
ATORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
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                   TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANUEDNESS: single
TOPOLLGY: linear
MOLECULE TYPE: CDNA
  202-962-4810
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Best Local Similarity 78.9°
Matches 15; Conservative
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  TELEPHONE:
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US-09-115-252-34
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Run on:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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A25775
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AR050806
AR053811
AR091592
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Match Length DB
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gb_htg12: *
gb_htg13: *
gb_htg18: *
gb_htg16: *
gb_htg18: *
gb_htg19: *
gb_htg20: *
gb_htg20: *
gb_htg21: *
gb_htg21: *
gb_htg22: *
gb_htg22: *
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gb_sts1:*
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gb_ro1:*
gb_ro2:*
gb_ln4:*
gb_pr10:*
em_ba3:*
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gb_vi2:*
gb_htg1:*
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gb_htg2:*
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gb_sts3:*
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em_ro:*
em_sts:*
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gb_htg6:'
gb_htg7:'
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gb_pr5:
em_ov:*
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                                                                            October 2, 2001, 15:56:42; search time 3339.34 Seconds (without alignments) 92.640 Million cell updates/sec
          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                   1344157 seqs, 7733874588 residues
                                                                                                                                                                                                                                         Fotal number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                         OM nucleic - nucleic search, using sw model
                                                                                                                                                      1 ttttgctagatgctaggtat 20
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                                                                                                                                 Title:
Perfect score:
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124252 Sequence 39 AX100491 Sequence A25775 antisense o AR034285 Sequence AR035391 Sequence AR053810 Sequence AR053811 Sequence AR053812 Sequence

Description

10-APR-2001

PAT

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 12.2; DB 9;
Pred. No. 6.1e+04;
); Mismatches 3;
                                                                                                 1 (bases 1 to 37)
Jiao, S., Habben, J.E. and Niu, X.
Seed-preferred promoter from maize
Patent: WO 0121783-A 5 29-MAR-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
                                                                                                                                                                                                                   Score 12.4; DB 10
Pred. No. 4.8e+04;
); Mismatches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="synthetic construct"
/db_xref="taxon:32630"
8 c 7 g 12 t
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Patent: WO 9304586-A 8 18-MAR-1993;
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          AX100491 37 bp DNA
Sequence 5 from Patent W00121783.
AX100491 GI:13619505
                                                                                                                                                                                                                                                                                                                      antisense oligonucleotide OWB22.
A25775
                                                                                                                                                              /organism="Zea mays"
/db_xref="taxon:4577"
10 c 7 g
                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                   62.0%;
92.9%;
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82.4%;
                                                                                                                                                                                                                                                                                                                   38 bp
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1 (bases 1 to 38)
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Matches 13; Conservative
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Best Local Similarity 82.4
Matches 14; Conservative
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 AX100491/c
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DEFINITION
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                           ACCESSION
VERSION
KEYWORDS
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JOURNAL
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                                                                                                  REFERENCE
                                                                                                           AUTHORS
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A25775/c
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KEYWORDS
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AR034285
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KEYWORDS
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A17446 oligonucleo
AR014421 Sequence
I11864 Sequence 30
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                                                                      A69048 Sequence 6
A71632 Sequence 65
A43390 Sequence 34
AR054989 Sequence
A19662 Nucleotide
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E60316 Identificat
                                            187238 Sequence 64
190213 Sequence 39
                                                               M60145 Human/HIV 3
                                                                                                                                                                       I30679 Sequence 11
I46138 Sequence 11
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876309 PTPH1=cytos
                                                                                                                  AX097685 Sequence
AR040802 Sequence
A98431 Sequence 15
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AX097355 Sequence
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A22305 oligonucleo
AR053115 Sequence
  Sequence 18
                                    Sequence 64
                                                                                                                                                                                                                                                                                        210 PCR primer
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         AX019713 Sequence
AR030753 Sequence
AR075961 Sequence
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A17046 vligonucleo
A17446 oligonucleo
                                                                                                                                               032 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 31)
Gold,L. and Tasset,D.
DNA ligands of thrombin
Patent: US 5542393-A 39 06-AUG-1996;
Location/Qualifiers
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AX097355
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AX043430
E60316
A87635
AR029080
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AR040802
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AX019713
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AX021032
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I11864
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E21659
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3 c 11 q
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A17446
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124252
124252.1 GI:1604122
 ttttgctagatgctaggtat 20
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Best Local Similarity 80.09
Matches 16; Conservative
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Unclassified.
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source
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VERSION

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Gaps

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Indels

Length 37;

DB 10;

22-MAR-1995

PAT

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Gaps

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Indels

Length 38;

29-SEP-1999

PAT

Unknown.

RESULT

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Gaps

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Unclassified.
Unclassified.
1 (bases 1 to 41)
Crabtree,G.R., Schreiber,S.L., Spencer,D.M., Wandless,T.J. and
                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 41)
Crabtree, G.R., Schreiber, S.L., Spencer, D.M., Wandless, T.J. and
                                                                                                                                                                                                                 29-SEP-1999
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                                                                Score 12.2; DB 9; Length 41;
Pred. No. 6.1e+04;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cch 61.0%; Score 12.2; DB 9; Length 41; al Similarity 82.4%; Pred. No. 6.1e+04; 14; Conservative 0; Mismatches 3; Indels
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Belblaw, P.
Regulated apoptosis
Regulated apoptosis
Patent: US 5994313-A 8 30-NOV-1999;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                               Regulated apoptosis
Patent: US 5834266-A 8 10-NOV-1998;
Location/Qualifiers
               12
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Sequence 8 from patent US 5834266.
AR053811 GI:5978673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AR091592 41 bp DNA
Sequence 8 from patent US 5994313.
AR091592.1 GI:10018347
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13 c 9 g
/organism="unknown"
13 c 9 g
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Best Local Similarity 82.4%;
Matches 14; Conservative
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Matches 14; Conservative
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            1 (bases 1 to 41)
Crabtree, G.R., Schreiber, S.L., Spencer, D.M., Wandless, T.J. and
                                       Belshaw,\dot{\mathbf{p}}. Regulated transcription of targeted genes and other biological events
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Crabtree, G.R., Schreiber, S.L., Spencer, D.M., Wandless, T.J.,
Belshaw, P. and Ho, S.
Regulated transcription of targeted genes and other biological
events
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Crabtree, G.R., Schreiber, S.L., Spencer, D.M., Wandless, T.J. and
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Patent: US 5830462-A 8 03-NOV-1998;
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Sequence 8 from patent US 5830462.
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AR050806.1 GI:5974170
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Sequence 8 from patent US 5871753.
AR035391
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                                                                           Patent: US 5869337-A
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Matches 14; Conservative
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(pases 1 to 35)
Thastrup,O., Tullin,S.slashed.ren, Poulsen,L.Kongsbak and Bj.o slashed.rn,S.Petersen.
Method of detecting biologically active substances by using green
                                                                         Unclassified.
1 (bases 1 to 35)
Terman, B.Esrael and Carrion, M.Eduardo.
Recombinant kinase insert domain containing receptor and gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-AUG-2000
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
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Patent: US 5958713-A 22 28-SEP-1999;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                             3; Mismatches
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Sequence 22 from patent US 5958713.
AR075961
                                                                                                                                         encoding same
Patent: US 5861301-A 2 19-JAN-1999;
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64 from Patent W09503412.
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Mabilat,C. and Christen,R.
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               GI:5943967
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Best Local Similarity 63.2%;
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                                                                                                                                                                          unclassified.

1 (bases 1 to 26)
Goebel, W. and Demuth, A.
USE OR A SECRETION VECTOR FOR FERTILITY CONTROL BY ORAL VACCINATION USEDLE WO 985067-A.18 12-NOV-1998;
GOEBEL WERNER (DE): SCHERING AG (DE)
Location/Qualifiers
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synthetic construct
artificial sequence.
1 (bases 1 to 33)
Hentze,M.W. and Paraskeva,E.
Method of isolation of rna-binding compounds
Patent: WO 9937807-A 2 29-JUL-1999;
EUROP MOLECULAR BIOLOGY LAB (DE); HENTZE MATTHIAS W (DE); PARASKEVA
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/db_xref="taxon:32630"
/note="Primer for amplification
4 c 4 q 18 t
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100.0%; Pred. No. 8e+
ive 0; Mismatches
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                                                                          A83432 26 bp DNA
Sequence 18 from Patent W09850067.
A83432 GI:6732770
                                                                                                                                                                                                                                                                                                        /organism="unidentified"
/db_xref="taxon:32644"
5 c 7 g 8
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Sequence 2 from Patent WO9937807.
AX019713
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13 TCTGCTACTTGCTAGGT 29
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NUCLEOTIDE FRAGMENT OF MYCOBACTERIAL RIBOSOMAL RNA 23S, PROBES AND PRIMERS DERIVED THEREFROM, REAGENT AND METHOD FOR DETECTING SAID FRAGMENT PRAGMENT: W0 9503412-A 64 02-FEB-1995; BIO MERIEUX (FR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unividualitied.

1 (bases 1 to 39)

Mabliat,C. and Christen,R.

Nucleotide fragment of the 23S ribosomal RNA of mycobacteria, derived probes and primers, reagent and detection method Patent: US 5703217-A 64 30-DEC-1997;

Location/Qualifiers
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                                                                                                                            /organism="Mycobacterium fortuitum"
/strain="CIP 140 410 001"
/db_xref="taxon:1766" 7 t
11 9 9 7 t
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Thompson, G.A. and Knauf, V.C.
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Patent: US 5723595-A 39 03-MAR-1998;
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                                                                    Other publication CA 2145172 950202
Other publication FR 2709310 950303.
Location/Qualifiers
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Sequence 39 from patent US 5723595.
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Sequence 64 from patent US 5703217.
1187238
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts JOURNAL Unpublished (2000) COMMENT Contact: Robert B. Weiss University of Utah Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddun@qenetics.utah.edu | Insert Length: 10000 Std Error: 0.00 Plate: 0066 row: G 'column: 07 Seq primer: CGTGTAAACGACGCCAGT Class: plasmid ends High quality sequence stop: 23. Location/Qualifiers 1. 23 Source /organism="Mus musculus" / Strain="C57BL/6J" / Ab_Arref="taxon:10090" / Clone="UUGCIMO06G07" / Clone="UUGCIMO06G07" / Clone="UugCIMO06G07" / Aba_Male" / Jab_host="E. Coll strain XLIO-Gold, T1-resistant, F-" / And-Most="C57BL/6J" / Rector: PWD42Dv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson | (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gelectrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil4732114[gb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells | and selected for ampicillin resistance." BASE COUNT 6 a 6 c 4 g 7 t ORIGIN Query Match 64.0%; Score 12.8; DB 241; Length 23; Best Local Similarity 87.5%; Pred. No. 1.9e+04; Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0; Oy 2 tttgctagatgctagg 17 | RESULT 2 AU104064 50 bp mRNA EST 05-APR-2001 LOCUS DEFINITION AU104064 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone HEP13823, mRNA sequence. ACCESSION AU104064.1 GI:13553585 KEYWORDS KEYWORDS HUMAN. ORGANISM Homo sapiens CORGANISM Homo sapiens CORGANISM Homo sapiens ENATYOTA: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (Dases 1 to 50) AUTHORS Suzuki,Y., Tsunoda,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo, K., Suyama,A. and Sugano,S. |
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| SCORP ACCOUNTABLES Query Score Match Length DB ID 12.8 64.0 23 241 AZ336049 12.6 63.0 50 107 AU104064 12.2 61.0 35 250 AZ841152 12 60.0 49 243 AZ421911 11.8 59.0 37 258 TAZ246020 | AA916137 TA3838120 AA916137 TA3838120 BE900863 BE900863 AL497988 AA275379 AA275379 AA275379 AA275379 AA275379 AA275379 AA275379 AA275379 AA275379 AA27588 AA2758837 AA2758837 AA2758837 AA2758837 AA27683 AA27683 AA27683 AA27683 AA277883 AA277883 AA37783 | 11 55.0 49 11 AA782046 AA782046 AA782046 11 55.0 49 246 AZ593107 AZ593108 54.0 27 247 AZ558164 BE276866 BE276866 AZ59310 AZ77363 AZ59310 AZ77363 AZ59310 AZ77363 | 10.6 53.0 34 10.6 53.0 37 10.6 53.0 37 10.6 53.0 38 10.6 53.0 40 10.6 53.0 46 | AZ336049/c AZ336049 23 bp DNA GSS 29-SEP-2000 DEFINITION 1M0066607F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0066607F, DNA sequence. AZ336049.1 GI:10404965 AZ336049.1 GI:10404965 SSS. SOURCE Nouse mouse. ORGANISM Mus musculus Eukaryota: Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi; Marmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. REFERENCE 1 (bases 1 to 23) AUTHORS Dunn, D., Aoyagi, A., Bearber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. |

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Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries Unpublished (2001)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
Fistiute of Medical Science, University of Tokyo
Banali: ysuzuki@ims.u-tokyo.ac.jp
Suzuki.Y., Yoshitomo-Nakagawa.K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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2M0139D06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0139D06 F, DNA sequence.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly and Wright, D., Weiss, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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/sex="Male"
/lab host=E. Coli strain XL10-Gold, Tl-resistant, F
/note="Vector: PWD42nv; Purified genomic DNA from M.
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84112, USA
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Insert Length: 10000 Std Error: 0.00
Plate: 0139 row: D column: 06
Seq primer: GGTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 35.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="HEP13823"
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/clone="UUGC2M0139D06"
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (qil4732114) gbl.REL29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 49)

1 (bases 1 to 49)

2 Dunn, D., Ayagai,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
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musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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/db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="tutscimc20mb22"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 12.2; DB 250; Length 35; Pred. No. 4e+04; 0; Mismatches 3; Indels 0;
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Insert Length: 10000 Std Error: 0.00
Plate: 0200 row: D column: 22
Seg primer: CGTTGTAAAACGACGCCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 49. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61.0%;
82.4%;
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Fax: 801 585 7177
Email: ddunn@genet
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Gaps

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/note-"Organ: breast; Vector: pCMV-SPORT4; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dr. Average insert size 1.2 kb. Life Technologies catalog #:10985-018"
                                                                                                                                                                                                                                 AA916137 46 bp mRNA EST 14-APR-1998 0932c10.s1 NCI_CGAP_BR7 Homo sapiens cDNA clone IMAGE:1441554 3' similar to SW.NU2M_HUMAN P03891 NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2'; mRNA sequence.
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T. brucei sheared genomic DNA clone 383e12, reverse sequence,
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Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
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Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
                                           Length 37;
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                                         Score 11.8; DB 258;
Pred. No. 6.5e+04;
0; Mismatches 2; 1
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86.7%; Pred. No. 6.7e+04;
ive 0; Mismatches 2;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1441554"
/clone=11b="NCI_GGAP_Br7"
/lab_host="DH108"
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AL497988 .1 GI:11873710
GSS.
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                                         59.0%;
86.7%;
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                                           Query Match
Best Local Similarity
Matches 13; Conserv
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                                                        (http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polywucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114)pblAR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli xil0.50ld (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hall, M., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G. Direct Submission Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
/note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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T. brucei sheared genomic DNA clone 254h02, reverse sequence,
genomic survey sequence.
AL483435
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60.0%; Score 12; DB 243; Length 49; ilarity 75.0%; Pred. No. 5.3e+04; Conservative 0; Mismatches 5; Indels
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/strain="TREU927"
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Matches 15; Conserv
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AUTHORS
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Length 44;

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (basea 1 to 50)

Suzuki, Y., Tsunoda, T., Taira, H., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Taira, H., Mizushima-Sugano, J., Sese, J., Hata, Y., Suyama, A. and Sugano, S.
Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries (Dupublished (2001)

Contact: Yutaka Suzuki Department of Virology
Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Bmail; ysuzuki@ims.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
               Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGGAGG(5. Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AU104334 50 bp mRNA EST 05-APR-2001
AU104334 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
REC00112, mRNA sequence.
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17 t
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Pred. No. 8.5e+04;
); Mismatches 4; Indels 0
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Pred. No. 8.4e+04;
); Mismatches 4; I
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/db_xref="taxon:9606"
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/clone_lib="Sugano Homo
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AA275379.1 GI:1915865
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Best Local Similarity 77.8
Matches 14; Conservative
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AA275379
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Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Direct Submission
Froject, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CBIO 18A, E-mail: barrell@sanger.ac.uk and
hl@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTTA 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and venter, J.C. (Makhing small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucel sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
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NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue procurement: ArCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Theyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCW833 row: k column: 09.
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/clone_lib="NIH_MGC_21"
/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming.
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Pred. No. 8.2e+04;
0; Mismatches 4; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Trypanosoma brucei"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:5691"
/clone="383e12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .ocation/Qualifiers
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ilarity 77.8%;
Conservative
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SOURCE

ORIGIN

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Gaps

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31-MAR-1997

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polymerase are the polymerase are the polymerase are Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil4732114 qipl4R129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the linsert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
                                                                                                                                                                                Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="E. Coli strain XLIO-Gold, T1-resistant, F-" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                        Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
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                                                                                                                                                                                                                            Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0160 row: J column: 20
Seg primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"/strain="C57BL/6J"
                                              plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:10090"
/clone="UUGC1M0160J20"
                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 25.
Location/Qualifiers
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  and Wright, D., Weiss, R.
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                                                                                                                    Marra, M. Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Marca, M., Hillier, L., Allen, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptce, M., Tan, F., Underwood, K., Moore, B., Thelsing, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
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                                                Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mouseest@watson.wustl.edu
This clone is available royalty.free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:467001
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Tel: 314 286 1800
Fax: 314 286 1810
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Pred. No. 1e+05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                          Unpublished (1996)
Contact: Marra M.YMouse EST Project
WashD-HHMI Mouse EST Project
WashIngton University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 31.
Location/Qualifiers
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/clone="lMAGE:766081"
/clone_lib="Barstead MPLRB1"
/sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/strain="BALB/c"
                                                                                                                                                                                                                                                                                     The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="Kidney"
/dev_stage="6 weeks"
/lab_host="DH10B"
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Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance. ^{\prime}_{7} c ^{\prime}_{7}
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                             Mouse whole genome scaffolding with paired end reads from 10kb
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AU006827 Schizosaccharomyces pombe late log phase cDNA Schizosaccharomyces pombe cDNA clone spc00499, mRNA sequence. AU006827.1 GI:3343285
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                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 11.2; DB 244; Length 34;
Pred. No. 1.3e+05;
0; Mismatches 3; Indels 0;
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Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
1 (bases 1 to 39)
                                                                                                                                                      Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                                                                      Plate: 0327 row: J column: 11
Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0327311"
                                                          Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualiflers
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81.2%;
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Best Local Similarity 81.2
Matches 13; Conservative
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11 TGTGCTACATGCCAGG 26
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Schizosaccharomyces pombe was prepared by cloning cDNA into the Smal site of Ml3mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, http://www.nirs.go.jp)"
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                                                                                                                                                                                                                                                                                    /organism="Schizosaccharomyces pombe"
/strain="912"
/db_xref="taxon:4896"
/clone="spc00499"
/clone_lib="Schizosaccharomyces pombe late log phase cDNA"
/sex="h minus"
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 41)
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Mouse whole genome scaffolding with paired end reads from 10kb
\begin{tabular}{ll} Morimyo, M. & and Mita, K. \\ Identification of expressed sequence tags of Schizosaccharomyces \\ \end{tabular}
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National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
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Insert Length: 10000 Std Error: (
Plate: 0363 row. P column: 15
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/strain="C57BL/6J"
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
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                                                                                                                  Contact: Mitsuoki Morimyo
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81.2%;
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Fax: 801 585 7177
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                                                                                                                                                                                      (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polymerase about end-repaired with 74 DNA polymerase and 74 polymerase to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarcse gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (4)14732114 (4)1618129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into adaptore for ampicillin resistance."

8 a 8 c 9 g 16 t
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Dunn,D., Aoyaqi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
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                                                                                                               /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                  /lab_host-"E. Coli strain XL10-Gold, T1-resistant, F-"
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/clone="UUGCIM0363P15"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
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Seq primer: CACACAGGAAACAGCTATGACC
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Fax: 801 585 7177
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셤 ò

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gelectrophoresis. Vector DNA was prepared from a derivative of pWDA2 (gil4732114 gblAR129072.1), a copy-number inducible derivative of pRDA2 (gil4732114 gblAR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                         /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-" /note="Weetcr: PWD42Nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                    /clone_lib="Mouse 10kb plasmid UUGC1M library"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                /clone="UUGC1M0397M06'
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5 gctagatgctaggtat 20

Search completed: October 2, 2001, 15:00:54 Job time: 10823 sec

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       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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A44595 Sequence 5 AR079892 Sequence A97844 Sequence 12 144719 Sequence 45 152125 Sequence 45 AX096725 Sequence E04774 Synthetic D

A97844 144719 152125 AX096725 E04774

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A84595 AR079892 AR084719

AR084719 Sequence

Description

DB

SUMMARIES

21-JAN-2000

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Unknown.
Unclassified.
Unclassified.
Unclassified.
Weinrich,S.L., Atkinson,E.M. III, Lichtsteiner,S.P., Vasserot,A.P.,
Pruzan,R.A. and Kealey,J.T.
Purified telomerase
Partent: US 5968506-A 5 19-OCT-1999,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68.0%; Score 13.6; DB 9; Length 30; 80.0%; Pred. No. 6.6e+03; ive 0; Mismatches 4; Indels
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Atkinson, E.M. and Kealey, J.T.
PURIED TELOMERASE
Patent: WO 9845450-A 5 15-OCT-1,998;
GERON CORP (US)
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Sequence 121 from Patent W09914377.
A97844
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Sequence 5 from patent US 5968506.
AR079892. GI:10006645
                                                                                                                                              /organism="unidentified"
        A84595 30 bp DNA
Sequence 5 from Patent W09845450.
A84595.1 GI:6733511
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/mod_base=OTHER
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AR016058 Sequence
AR025451 Sequence
AR075530 Sequence
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AX087933 Sequence
B12395 PCR Primer.
AR088301 Sequence
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160381 Sequence 28
185612 Sequence 25
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A97845 Sequence 12
A97843 Sequence 22
AR0800603 Sequence 28
A81398 Sequence 28
A82505 Sequence 29
AR064423 Sequence 29
AR064423 Sequence 29
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113041 Sequence 18
113042 Sequence 19
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191289 Sequence 48
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Unknown.
Unclassified.
1 (bases 1 to 30)
S Melsener. B. and Coleman, T.A.
Human cripin growth factor
AL Patent: US 5981215-A 6 09-NOV-1999;
Location/Qualifiers
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7 c 3 ~
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AR084719
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artificial sequence.

1 (bases 1 to 26)

1 (bases 1 to 26)

PRAFIDSHI, E., Kakhuuma, S., Takemoto, A., Miyoda, Y. and Fukuyama, S., PRAFIDSHI, E., Kakhuuma, S., Takemoto, A., Miyoda, Y. and Fukuyama, S., PROTEASE, ITS PRODUCTION AND USE
PATENT: JP 1993091876-A 13 16-APR-1993;
SHOWA DENKO KK.
OS Artificial gene
OC Artificial sequence; Genes.
ON Artificial sequence; Genes.
PN JP 1993091876-A/13
PD 16-APR-1993
PF 02-OCT-1991 JP 1991280313
                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 21)
Lander, E.S., Gargill, M., Ireland, J.S., Bolk, S., Daley, G.Q. and Mccarthy, J.J.
Single nucleotide polymorphisms in genes
Patent: WO 0118250-A 1903 15-MAR-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US); Millennium
Pharmaceuticals, Inc. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EU4774 26 bp DNA PAT 29-SEP-1997
Synthetic DNA for site directed mutagenesis of protease derived
from Bacillus NKS-21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64.0%; Score 12.8; DB 10; Length 21; 77.8%; Pred. No. 1.9e+04; ive 1; Mismatches 3; Indels
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Sequence 1903 from Patent WO0118250.
AX096725 GT:13512979
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JP 1993091876-A/13.
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Walsh, T.A., Hey, T.D. and Morgan, A.E.R.
Ribosome-inactivating proteins, inactive precursor forms thereof, a process for making and a method of using Patent: US 5635384-A 45 03-UNN-1997;
Location/Qualifiers
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Walsh,T.A., Hey,T.D. and Morgan,A.E.R.
Ribosome-inactivating proteins, inactive precursor forms thereof, a
process for making and a method of using
Patent: US 5646026-A 45 08-JUL-1997;
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unidentified
unclassified.
1 (Dasis 1 to 18)
Quint, W. and Kleter, B.
DETECTION AND IDENTIFICATION OF HUMAN PAPILLOMAVIRUS BY PCR AND TYPE-SPECIFIC REVERSE HYBRIDIZATION
PACENT: WO 9914377-A 121 25-MAR-1999;
INNOGENETICS NV (BE): DELETS DIAGNOSTIC LAB B V (NL)
Location/Qualifiers
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Pred. No. 8.4e+03;
0; Mismatches 2;
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Sequence 45 from patent US 5635384.
144719 GI:2469432
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152125.1 GI:2473326
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    /organism="unidentified"
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Best Local Similarity 87.5
Matches 14; Conservative
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Matches 14; Conservative
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WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US); Millennium
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 21)
Lander.E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and Mccarthy,J.J.
Single nucleotide polymorphisms in genes
Patent: WO 0118250-A 23 15-MAR-2001;
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 TAKINISHI EIKO, KAKINUMA SHINJI, TAKEMOTO AYANO, PI
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11 Similarity 78.9%; Pred. No. 2.6e+04;
15; Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                    Score 12.8; DB 10;
Pred. No. 1.9e+04;
0; Mismatches 2;
                                                                                                                                                    /organism="synthetic construct"/db_xref="taxon:32630"
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Unclassified.
1 (bases 1 to 32)
1 Thomas Jnr.K.A. and Linemeyer, D.L.
Mutant acidic fibroblast growth factor
Patent: EP 0319052-A2 27 07-JUN-1989;
Location/Qualifiers
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106269
106269.1 GI:590260
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Sequence 23 from Patent W00118250.
AX094845
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hypothetical: No;
anti-sense: No;
Location/Qualifiers
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Best Local Similarity 87.5%;
Matches 14; Conservative
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 3.3e+04;
1; Mismatches 2;
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Pred. No. 3.3e+04;
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Juan,S., Lichenstein,H.S. and Wright,S.D.
Anti-inflammatory CD14 polypeptides
Patent: US 5869055-A 24 09-FEB-1999;
Location/Qualifiers
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Sequence 640 from Patent WO0118250.
AX095462
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Pharmaceuticals, Inc. (US)
Location/Qualifiers
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81.2%;
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Best Local Similarity 81.2
Matches 13; Conservative
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Best Local Similarity 81.2
Matches 13; Conservative
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30-AUG-2000

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Unclassified.

1 (bases 1 to 25)
1 (bases 1 to 25)
Willeponteau, B., Feng, J., Funk, W. and Andrews, W.H.
Mammalian telomerase
Patent: US 5958680-A 27 28-SEP-1999;
Location/Qualifiers
    AKU75530 25 bp DNA
Sequence 27 from patent US 5958680.
AR075530
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                                                 AR075530.1 GI:10002278
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Best Local Similarity 82.4%;
Matches 14; Conservative
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Yazawa,K., Yamada,A., Kato,S. and Kondo,K.
Gene coding for eicosapentaenoic acid synthesizing enzymes and process for production of eicosapentaenoic acid
Patent: US 5798259-A 22 25-AUG-1998;
                                                  Gaps
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0
                        Score 12.4; DB 9; Length 39;
Pred. No. 3.4e+04;
0; Mismatches 1; Indels
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Pred. No. 4.4e+04;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                Length 25;
                                                                                                                                                                                                                                      Unknown.
Unclassified.
1 (bases 1 to 25)
1 (bases 2 to 25)
Villeponteau, B., Feng, J., Funk, W. and Andrews, W.H. Assays for the DNA component of human telomerase Patent: US 5776679-A 26 07-UUL-1998;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                               Score 12.2; DB 9; Length 2
Pred. No. 4.4e+04;
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                                                1; Indels
                                                                                                                                                                   PAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AR025451 25 bp DNA
Sequence 22 from patent US 5798259.
AR025451. GI:3978079
                                                                                                                                                               AR016058 25 bp DNA
Sequence 26 from patent US 5776679.
AR016058 G G:3972335
                                                                                                                                                                                                                                                                                                                                                 /organism="unknown"
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82.4%;
                      Query Match 62.0%;
Best Local Similarity 92.9%;
Matches 13; Conservative
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Best Local Similarity 82.4%;
Matches 14; Conservative
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Best Local Similarity 82.4
Matches 14; Conservative
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ACCESSION
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KEYWORDS
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AR016058
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ORGANISM
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AR025451
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ORIGIN
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AUTHORS
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RESULT

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Gaps

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Score 12.2; DB 9; Length 25; Pred. No. 4.4e+04; 0; Mismatches 3; Indels

| 12 13:2 66.0 29 21 AAA03899 Polyy 13 13.2 66.0 30 16 AAQ86352 Muta. 14 13.2 66.0 48 21 AAA13301 PCR | 16 12.8 64.0 21 22 AAF95258 Human gene | 12.8 64.0 21 22 AAF95875 Human gene singl 12.6 63.0 29 21 AAZ6252 PCR primer RP-6A 12.6 63.0 44 19 AAT78806 Kappa 11ght chal 12.6 63.0 44 19 AAV39247 Primer 0-551 use | 22 12.6 63.0 49 21 AAZ622001 O1199 24 12.4 62.0 27 20 AAZ01016 PCR [25 12.4 62.0 31 20 AAX06130 Human | 12.2 61.0 24 21 12.2 61.0 25 17 12.2 61.0 25 17 | 12.2 61.0 25 20 AAV20780 Human telomera 12.2 61.0 27 19 AAV21898 Nuclease resis | 33 12.2 61.0 32 19 AAV37859 34 12.2 61.0 32 19 AAV37859 35 12.2 61.0 32 19 AAV37851 | 12.2 61.0 40 18 AAN557948 12.2 61.0 49 18 AAN57947 12.2 61.0 49 18 AAN57947 12.2 61.0 49 20 AAN86109 | 40 12 60. 42 12 60. 43 12 60. 44 12 60. 45 12 60. | SIN | RESULT 1 AAC65542 ID AAC65542 standard; DNA; 20 BP. | AC AAC65542; XX DT 12-FEB:2001 (first entry) | XX DE Human focal adhesion kinase antisense sequence #8. XX KW Human, focal adhesion kinase; FAK; signal transduction; cancer; XW embryonic development disorder: angioenic disorder: wound healing: | nioate; ss. | PD 17-OCT-2000. XX PF 19-AUG-1999; 99US-0377310. | XX PR 19-AUG-1999; 99US-0377310. XX | PA (ISIS-) ISIS PHARM INC. XX PI Monia BP, Gaarde WA; | WPI; | PT New antisense compounds for inhibiting focal adhesion kinase PT expression, especially useful for inhibiting retinal PT neovascularization, or for diagnosing and treating e.g. colon cancer - |
|---|--|---|--|---|--|---|---|---|---|---|---|--|--|---|--|---|--|---|
| 4.5 Compugen Ltd. | | Search time 876.95 Seconds (without alignments) 14.320 Million cell updates/sec | | | | | | 4n/Na1980.DaT:* 4n/Na1981.baT:* 4n/Na1982.DaT:* | 'geneseqn'NA1984 | qn/Na1988.DaT:* eqn/Na1989.DaT:* eqn/Na1990.DaT:* eqn/Na1991.DaT:* | eqn/NA1993.DAT:* eqn/NA1994.DAT:* eqn/NA1995.DAT:* | eqn/NA1996.DAT:* eqn/NA1997.DAT:* eqn/NA1998.DAT:* eqn/NA1999.DAT:* | eqn/NA2001.DaT:* d by chance to have a the result being printed, re distribution. | : | Description Human focal adhesi | Sense primer used Human gene signatu Human focal adhesi | PCR primer for hum Human biallelic po Human criptin grow | H W |
| GenCore version 4.5 Copyright (c) 1993 - 2000 Compu | nucleic search, using sw model | October 2, 2001, 16:18:38 ; Sean (wit | US-09-757-100B-10 20 1 ggtaagcagctgccattatt 20 | IDENTITY_NUC Gapop 10.0 , Gapext 1.0 | 730101 seqs, 313950809 residues | 1: 50 1: 50 | Minimum Match 0% Maximum Match 100% Listing first 45 summaries | Geneseq_0601:* /SIDSB/gcgdata/geneseq,/SIDSB/gcgdata/geneseq,/SIDSB/gcgdata/geneseq,/SIDSB/gcgdata/geneseq, | 5: /SIDS8/gcgdata/geneseg/genesegn/NA1984.DAT: 6: /SIDS8/gcgdata/geneseg/genesegn/NA1985.DAT: 7: /SIDS8/gcgdata/geneseg/genesegn/NA1986.DAT: 8: /SIDS8/gcgdata/geneseg/genesegn/NA1987.DAT: | 9: /SIDS8/gcgdata/geneseg/genesec 10: /SIDS8/gcgdata/geneseg/genese 11: /SIDS8/gcgdata/geneseg/genese 12: /SIDS8/gcgdata/geneseg/genese 13: /SIDS8/gcgdata/geneseg/genese | 14: /SIDSB/gcgdata/geneseg/genese 15: /SIDSB/gcgdata/geneseq/genese 16: /SIDSB/gcgdata/geneseq/genese | /SIDS8/gcgdata/geneseq/geneseqn/NN1996.DAT:* /SIDS8/gcgdata/geneseq/geneseqn/NN1997.DAT:* /SIDS8/gcgdata/geneseq/geneseqn/NN1998.DAT:* /SIDS8/gcgdata/geneseq/geneseqn/NN1999.DAT:* /SIDS8/gcgdata/geneseq/geneseqn/NN1999.DAT:* | 22: /SIDSB/gcgdata/geneseq/geneseqn/N No. is the number of results predicted by greater than or equal to the score of the derived by analysis of the total score di | : | 20 | 22 20 29 16 15 22 | 49 21 31 20 30 18 | 69.0 40 20 AAX86412 68.0 30 19 AAV63648 68.0 30 20 AA223630 66.0 21 22 AAF97138 |
| | OM nucleic - nuc | Run on: | Title: Perfect score: Sequence: | Scoring table: | Searched: Total number of | um DB seq um DB seq | Post-processing: | Database : | | | | | Pred. No. score great and is der | ; ; | 20 | 2 16 3 15.2 4 15.2 | 14.4 14 13.8 | 8 13.8 9 13.6 10 13.6 c 11 13.2 |

BP

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Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 1163; 2245pp; Japanese.
                                                                              AAT22589 standard; cDNA to mRNA; 29
                                                                                                                                                             Human gene signature HUMGS04205.
 16 GGTAAGCAGCTGCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1995-206931/27.
                                                                                                                                                                                                                                                                                                                                                                           (MATS/) MATSUBARA K.
                                                                                                                                                                                                                                                                                                                                                                                         (OKUB/) OKUBO K.
                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                  Matsubara K,
                                                                                                                                                                                                                                                                                                                       11-NOV-1994;
                                                                                                                                   01-OCT-1996
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                       The present invention describes a number of phosphorothicate antisense sequences to the human focal adhesion kinase (FAK) protein. This protein is involved in integrin-mediated signal transduction, and is implicated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCR primers AAX36327-28 were used to amplify human FAK cDNA, in the course of the invention. The specification describes a method for altering the tumorigenicity or malignancy of brain cancer cells by changing the activity of glycosyltransferase in the cell so that glycosylation of cellular proteins is modified. The method is applied to glibma or maningioma, for prevention or treatment of brain tumours. Measuring the level of glycosyltransferase expression in brain cells is used to detect or predict their tumorigenicity.
                                                              in cancer, particularly colon, breast and oral tumours, embryonic development disorders, angiogenic disorders and wound healing. The antisense sequences, including the one shown here, can be used in the treatment of all of these.
                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                            Human; tumorigenicity; glycosyltransferase; malignancy; brain cancer cell; protein glycosylation; glioma; meningioma; brain tumour; FAK; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Altering tumorigenicity and malignancy of brain cancer cells
                                                                                                                                                                          22; Length 20;
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33;
                                                                                                                                                                          Score 20; DB 22
Pred. No. 0.29;
                                                                                                                                  Sequence 20 BP; 5 A; 4 C; 5 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                    Sense primer used to amplify human FAK cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 22 BP; 4 A; 7 C; 5 G; 6 T; 0 other;
                                                                                                                                                                                                   Mismatches
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100.0%; Pred. No.
ive 0; Mismatc
Example 2; Column 23; 30pp; English.
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                                                                                                                                                                        100.0%; Sc
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tive 0;
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                                                                                                                                                                                                                                                                                                                      AAX36327 standard; DNA; 22
                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 20; Conservative
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Best Local Similarity 100.
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-327411/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9924584-A1.
                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
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- e.g.

93JP-0355504. 94WO-JP01916

Okubo K;

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A single-stranded DNA (or its complementary strand or the corresp. Codouble-stranded DNA) which comprises one of the 7837 "GS" sequences given in AAT19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by using poly(T) as the sole primer since the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA shybridise with specific mRNAs Each library is constructed so as to reflect accurately the relative abundance of cifferent mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ed. No. 88;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 15.2;
Pred. No. 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          recognising different cell types
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85.0%;
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Matches 17; Conservative
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ID AAC6
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Gaps

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0; Indels

Mismatches

1 ggtaagcagctgccat 16

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fibrononectin collagen-binding domain. The amplified sequence was used to construct a collagen-binding physiologically active polypeptide. This polypeptide comprises a peptide from fibronectin ligated to a physiologically active peptide. The polypeptides are used in an agent for enabling topical retention or sustained release of a physiologically active peptide activity-imparting agent. They may used in gene therapy and in tissue regeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polymorphism; biallelic; paternity testing; forensic; genetic mapping; phenotypic typing; medicament; disease; marker; human; ss.
                                                                                                                                                                                                    Collagen-binding active polypeptide for use in an agent for enabling topical retention or sustained release of a physiologically active peptide or physiological activity-imparting agent comprises a fibronectin peptide -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid segments containing polymorphic sites - used for, e.g. detecting a disease phenotype, in forensics, paternity testing or genetic mapping of phenotypic traits
                                                                                                                                                                                                                                                                                                                                       PCR primers AAA64261-62 were used to amplify cDNA encoding a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 49;
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Pred. No. 2.4e+02;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 49 BP; 12 A; 16 C; 11 G; 10 T; 0 other;
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                                                                                                                                                                                                                                                                                                Example 1; Page 124; 135pp; English.
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21-FEB-2000; 2000WO-JP00964
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                                     99JP-0041913
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                                                                                                                            Ishikawa T, Kitajima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-080963/07.
                                                                                                                                                                 WPI; 2000-565375/52.
                                                                                         (TERU ) TERUMO CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 15; Conserv
                                     19-FEB-1999;
01-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a number of phosphorothioate antisense sequences to the human focal adhesion kinase (FAK) protein. This protein is involved in integrin-mediated signal transduction, and is implicated in cancer, particularly colon, breast and oral tumours, embryonic development disorders, anglogenic disorders and wound healing. The antisense sequences, including the one shown here, can be used in the treatment of all of these.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fibrononectin; collagen-binding domain; sustained release; gene therapy; physiologically active polypeptide; topical retention; PCR primer; tissue regeneration; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New antisense compounds for inhibiting focal adhesion kinase expression, especially useful for inhibiting retinal neovascularization, or for diagnosing and treating e.g. colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                          Human; focal adhesion kinase; FAK; signal transduction; cancer; embryonic development disorder; angiogenic disorder; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCR primer for human fibrononectin collagen-binding domain cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                         Human focal adhesion kinase antisense sequence #28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75.0%; Score 15; DB 22; 100.0%; Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 15 BP; 4 A; 4 C; 3 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 15; Column 25; 30pp; English.
                                                                                                                                                                 antisense; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP.
                                                                                                                                                                                                                                                                                                                 99US-0377310.
                                                                                                                                                                                                                                                                                                                                                     99US-0377310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA64261 standard; DNA; 49
                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 taagcagctgccatt 17
                                                                                                                                                                                                                                                                                                                                                                                          (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaarde WA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-006141/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200049159-A1
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                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                 19-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                     19-AUG-1999;
                                                    12-FEB-2001
                                                                                                                                                                                                                                     US6133031-A
                                                                                                                                                                                                                                                                          17-0CT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                               Monia BP,
                 AAC65562;
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Gaps

The PCR product

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biallelic polymorphic markers. The base occupying the polymorphic site is indicated by the appropriate IUPAC-IUB ambiguity code. These fragments can be used in a method for determining polymorphic forms in motividual. The invention further provides computer-readable storage medium for storing data for access by an application programme being executed on a data processing system. Such a method comprises a data structure stored in the computer-readable storage medium, the data structure including information resident in a database used by the application programme and including records, each record comprising information identifying a polymorphic side in the products and methods can be used for analysing polymorphic sites in includividuals for testing for the presence of a disease phenotype or in formatics, paternity testing or genetic mapping of phenotypic traits. They can also be used for the production of polymorphic animals. The nucleic acid segments can also be used in the manufacture of medicaments for the
                        Sequences AAX06101-X06558 represent human DNA fragments which contain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 31 BP; 5 A; 7 C; 6 G; 12 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treatment or prophylaxis of diseases
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Gaps
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                                                                                    ö
Score 14; DB 20; Length 31
Pred. No. 3.7e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human criptin growth factor 3' primer for COS expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAT51062 standard; cDNA; 30 BP.
70.0%;
ilarity 87.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                     5 agcagctgccattatt 20
                                                                                                                                                                                                           6 agcaggtgccrttatt 21
    Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAT51062;
                                                                                                                                                                                                                                                                                                                                                                        RESULT
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New isolated human Criptin Growth Factor polypeptide - which can be used to stimulate anglogenesis and develop products for use in
                                                                                                                                                                                                                                                                                                                          Example 3; Page 36; 52pp; English.
                                                     (HUMA-) HUMAN GENOME SCI INC
95WO-US07087
                                                                                                          Meissner PS;
                                                                                                                                                                                                                                                                       diagnosis and therapy
                                                                                                                                                             WPI; 1997-043055/04.
05-JUN-1995;
                                                                                                          Coleman TA,
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95WO-0S07087

05-JUN-1995;

12-DEC-1996.

WO9639420-A1

Synthetic.

A 3' PCR primer (AAT51062) contains a PvuII site followed by 15 nucleotides that are the reverse complement of human criptin growth factor (CGF) 3' DNA starting at the translational stop codon (see also AAT51058). It was used with a 5' primer (AAT51061) to

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PCR primers AAX86368-X86423 were used to amplify DNA encoding a human MMSC1 protein. The PCR templates were derived from tumour cell lines, and the amplicons were tested for mutations. The MMSC1 protein is a MMAC1 interacting protein which is involved in tumour suppression activity in the MMAC1 pathway. MMSC1, antigenic fragments or fusion proteins of these are used as immunogens for antibody production. Primers proteins of these are used as immunogens for antibody production. Primers proteins of freese are used as immunogens for identification of MMSC1 genes and for synthesis by amplification of MMSC1 denotes cancer. A germline an anteration in MMSC1 gene is indicative of a predisposition to cancer. A somatic mutation in an MMSC1 gene is indicative that the tissue is cancerous. Analysis of MMAC1 and MMSC1 (or PDZ domain 6 of MMSC1).

Cancerous. Analysis of MMAC1 and MMSC1 (or PDZ domain 6 of MMSC1) associated with cancer. Wild-type MMSC1 gene (a subply wild-type MMSC1 gene (a subply wild-type MMSC1) and the thousing the concernations in MMAC1 associated with cancer. Wild-type MMSC1 gene (a subply wild-type MMSC1) gene (a subply wil
                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; MMSC1 protein; MMAC1 interacting protein; tumour suppression;
MMAC1 pathway; immunogen; cancer; cell neoplastic growth; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             function) to a cell, which has lost the gene function due to a MMSC1 gene mutation. The gene suppresses neoplastic growth of the cell. Transgenic animals having an altered MMSC1 can be used as a model for identifying drug candidates useful in treating cancer.
                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MMSC1, an MMAC1 (tumour suppressor) interacting protein and related
amplify the CGF DNA clone deposited as ATCC 97142. The PCR proc was incorporated into plasmid pN346 to allow prodn. of CGF (see also AAW09111) in transfected COS cells.
                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCR primer PDZK5.5C used to amplify DNA encoding MMSC1 protein.
                                                                                                                                                                                                  Length 30;
                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                            Score 13.8; DB 18;
Pred. No. 4.6e+02;
; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 40 BP; 9 A; 12 C; 7 G; 12 T; 0 other;
                                                                                                               Sequence 30 BP; 11 A; 7 C; 3 G; 9 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 5; Page 51; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP.
                                                                                                                                                                                               69.0%;
88.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MYRI-) MYRIAD GENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US00995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAX86412 standard; DNA; 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-SEP-1999 (first entry)
                                                                                                                                                                                          Query Match
Best Local Similarity 88.2
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                            4 aagcagctgccattatt 20
                                                                                                                                                                                                                                                                                                                                      4 aaccagctgctattatt 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tavtigian SV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-458472/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W09936566-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-JAN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX86412;
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AAZ23630 standard; DNA; 30
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                                                                                                                                       AAZ23630;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents an antisense oligonucleotide
directed against the human telomerase RNA component gene sequences.
The oligonucleotide can be used as an affinity agent in the methods of
the invention, which are used to purify human telomerase. The methods
involve the use of several sequential steps, including the use of two
matrixes that bind molecules bearing negative charges, a matrix that
binds molecules bearing positive charges, an affinity purification step
and a size separation. Telomerase is a particular target of anticancer
therapies, and is useful in assays for characterizing (pre)cancerous
cells. Telomerase can also be used to screen for specific modulators,
for biochemical analysis of its activity, and in preparation of
antibodies. Fragments of telomerase, or nucleic acid encoding them,
are used in vaccines, and for treating over expression of telomerase,
particularly in cancer.
                                            ö
                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             e.g.
                                                                                                                                                                                                                                                                                                   Human; telomerase RNA component; anticancer therapy; purification; assay; vaccine; cancer; antisense oligonucleotide; ss.
                                                                                                                                                                                                                                                                        Antisense oligonucleotide 13 for human telomerase RNA component.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Purification of telomerase on affinity material - useful for,
            Length 40;
                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lichtsteiner SP, Pruzan RA;
            Score 13.8; DB 20;
Pred. No. 4.8e+02;
); Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 30 BP; 6 A; 6 C; 8 G; 10 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= a
/note= "biotinylated"
                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 24; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnosis and treatment of cancer
                                           ;
                                                                                                                                                                                AAV63648 standard; DNA; 30 BP.
            69.0%;
88.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97WO-US06012.
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Weinrich SL;
                                                                                                                                                                                                                                             (first entry)
                                                                       4 aagcagctgccattatt 20
                                                                                         16 acgcatctgccattatt 32
                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag=
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       Query Match
Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                 Key
modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Atkinson EM,
Vasserot AP,
                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-APR-1997;
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                                                                                                                                                                                                                                          15-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-OCT-1998
                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                               AAV63648;
                                                                                                                                                                    AAV63648
                                                                                                                                                  RESULT
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This invention describes a novel composition comprising human telomerase having at least 2000-fold (preferably at least 60000-fold) increased relative purity compared with crude extract of cells from adenovirus-transformed kidney cell line. The composition is useful for eliciting an immune response in animals and may therefore be used as a vaccine for treating diseases associated with the overexpression of telomerase e.g. cancer. AAZJ3626-Z3337 represent oligonucleotides used in the isolation of human clone 28-1 which contains a fragment of the human telomerase described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Compositions comprising human telomerase, useful for treating diseases associated with overexpression of telomerase e.g. cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kealey JT;
                                             Telomerase; human; immune response; cancer; vaccine; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pruzan RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
Human clone 28-1 telomerase oligonucleotide oligo-13,
                                                                                                                                                                                                                                           /*tag= a
/note= "5'-biotinylated guanosine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 13.6; DB 20;
Pred. No. 5.8e+02;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lichtsteiner SP, Weinrich SL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 30 BP; 6 A; 6 C; 8 G; 10 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Column 45-46; 34pp; English.
                                                                                                                                                                                              Location/Qualifiers
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80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ggtaagcagctgccattatt 20
|| || || || || || || 6
| ggccagcagctgacattttt 25
                                                                                                                                                                                                                                                                                                                                                                                                                     97US-0833377.
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Best Local Similarity
Las 16; Conserve
                                                                            disease; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-590379/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GERO-) GERON CORP.
                                                                                                                                                                                           Key
modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Atkinson EM,
Vasserot AP;
                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                   04-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-AUG-1995;
                                                                                                                                                                                                                                                                                                                     US5968506-A.
                                                                                                                                                                                                                                                                                                                                                                     19-0CT-1999
                                                                                                                    Synthetic.
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ID AAF971
XX
AC AAF971
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Gaps

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Query Match
68.0%; Score 13.6; DB 19; Length 30;
Best Local Similarity 80.0%; Pred. No. 5.8e+02;
Matches 16; Conservative 0; Mismatches 4; Indels

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The invention provides polymorphic fragments of genes associated with hypertension. The nucleic acids including the polymorphic sites can be used as probes or primers for expressing variant procedus. Detection of the polymorphisms is useful in designing prophylactic and therapeutic regimes customized to underlying abnormalities. The polymorphisms can be used for association studies for hypertension, and in hypertension of diagnostic assays. Where the polymorphisms have strong correlation with hypertension, within a gene, they are likely to have a causative role. In hypertension. This information can be used to find the precise role of a polymorphism in the disease, and this can be used to identify potential drugs which combat the disease. In polymorphisms can be tested for association with other diseases e.g. agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabrys disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrands disease, familial hypercholesterolemia.
                                                           Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus; Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome; Fabrys disease; familial hypercholesterolemia; hereditary spherocytosis; polycystic kidney disease; von Willebrands disease; forensic; human; tuberous sclerosis; hereditary hemorrhagica telangiectasia; familial colonic polyposis; osteogenesis imperfecta; porphyria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  colonic polyposis, Ehlers-Danios syndrome, osteogenesis imperfecta, and acute intermittent porphyria. The polymorphic forms can also be used in forensics to identify individuals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel nucleic acids containing polymorphisms used in the diagnosis of
Polymorphic fragment of hypertension associated gene AGT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66.0%; Score 13.2; DB 21;
llarity 75.0%; Pred. No. 9.3e+02;
Conservative 1; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 29 BP; 5 A; 4 C; 12 G; 7 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haluska MK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AFFY-) AFFYMETRIX INC. (UYCA-) UNIV CASE WESTERN RESERVE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 19; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0084641.
99US-0304232.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99EP-0250150
                                                                                                                                                                                                                                                                          Ehlers-Danlos syndrome; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ86352 standard; DNA; 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chakravarti A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-107928/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
Les 15; Conserv
                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-MAY-1998;
03-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypertension
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                        EP955382-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fan JB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAQ86352/c
   NO YOU COULD COULD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OXXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention provides a method of diagnosing a vascular disease in an individual, involving determining the sequence at various polymorphic sites within the human thrombospondin i and thrombospondin 4 genes. The sequences at a number of polymorphic sites are also provided in the specification. In particular, the method can be used in the diagnosis of atherosclerosis, myocardial infarction, coronary heart disease, stroke, peripheral vascular diseases, venous thromboembolism and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also useful in forensics, paternity teeting, genetic analysis and phenotype correlations to diseases. The present sequence is an example of one of
                                                                                                                                                          Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
polymorphism; vascular disease; coronary artery disease; forensics;
myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       McCarthy JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids comprising single nucleotide polymorphisms, useful in applications such as forensics, paternity testing, medicine, genetic analysis and phenotype correlations to diseases such as diabetes and atherosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /standard_name= "single nucleotide polymorphism"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Daley GQ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66.0%; Score 13.2; DB 22;
83.3%; Pred. No. 8.9e+02;
ive 0; Mismatches 3;
                                                                                                  Human gene single nucleotide polymorphism #1899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the human gene SNPS shown in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ireland JS, Bolk S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 21 BP; 8 A; 4 C; 4 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                   pulmonary embolism; paternity test; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (WHED ) WHITEHEAD INST BIOMEDICAL RES. (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers replace(11,T)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Examples; Page 177; 242pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0153357.
2000US-0220947.
2000US-0225724.
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                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-226749/23
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Best Local Similarity
Matches 15; Conserv
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26-JUL-2000;
                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-AUG-2000;
                               06-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-MAY-2000
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Variation
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21-SEP-1999;
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20-SEP-1999;
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                                                                                                         Synthetic.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                For preparing a protein S (PS) expression vector, partial cDNAs coding for human protein S were first isolated as described by Ploos van Amstel et al., FEBS Lett., 222:186-190 (1987) from a puc9 human liver cDNA library. The cDNA sequence is given in Q86-48. The PS nt sequence is also listed in GenBank having the accession number Y00692. The mRNA encodes a preprotein having 676 AAs. After post-translation processing the corresp. translated mature PS consists of 635 AAs as given in R72350. The AA sequence is also listed in GenBank having the accession no. A26157. PS can be modified without significant loss of anticoagulant activity by introducing one or more mutations in the region between residues 425 and 432 to reduce significantly or eliminate the ability of PS to bind C4BP. A variant protein S is claimed having AA residues substitutions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           K429E, 1425A/1426A and K432E (AA residue nos. corresp. to R72350).
Oligos Q86349-Q86350 were used to produce mutations
in the first disulfide loop in the sex hormone binding globulin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New recombinant protein S variants - having reduced C4b binding protein binding activity and anticoagulant activity for treating
                                         Protein S; PS; vitamin K-dependent protein; mutagenic oligo; ss.
                                                                                                                                                                  a
"nts for introducing desired AA substn."
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/note= "nts for introducing desired AA substn."
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Mutagenic oligo for human protein S variant I425A/I426A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 13.2; DB 16;
Pred. No. 9.3e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 30 BP; 16 A; 4 C; 7 G; 3 T; 0 other;
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                                                                                                                      Location/Qualifiers
13..14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example; Column 18; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Griffin JH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP.
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Best Local Similarity 83.3%;
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                       92US-0985691
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16.17
/*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bouma BN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1995-154630/20
                                                                                                                                            misc_difference
                                                                                                                                                                                                           misc_difference
                                                                                                                                                                                                                                                                                                                                                                              02-DEC-1992;
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                                                                                                                                                                                                                                                                                          US5405946-A.
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                                                                                                                                                                                                                                                                                                                                    11-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bertina R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     thrombosis
                                                                                 Synthetic
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NAME OF THE PROPERTY OF THE PR
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This sequence represents a PCR primer used in the construction of trans-splicing vectors to illustrate the invention. The present invention relates to the in vivo production of recombinant nucleic acid sequences. The method comprises expressing in a cell, two transcripts, one containing a first exon and first intron component, and a second transcript comprising a second intron component and a second exon. Transcript comprising a second intron component and a second exon. Transcript and transcript 2 are allowed to trans-splice, forming a product containing exon 1 and exon 2, but not the intron components. The invention makes use of the ability of intronic sequences derived from group 1 or group 1 introns to mediate specific cleavage and ligation of discontinuous nucleic acids, their products, or ribozymes in vivo. The method is preferably used for the preparation of exons are random. The method is preferably used for the assembly, or for the assembly of genes ordered at some exons but randomized at others. New genes can be second a product of a product of the sassembly of genes ordered arpidly and efficiently, and a very wide range of exons may be
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Recombinant nucleic acid production; combinatorial gene library; ordered gene assembly; trans-splicing; tissue plasminogen activator; vector production; PCR primer; ss.
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Synthetic.

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This sequence represents a PCR primer used in the construction of trans-splicing vectors to illustrate the invention. The present invention crelates to the in vivo production of recombinant nucleic acid sequences.

The method comprises expressing in a cell, two transcripts, one containing a first exon and first intron component, and a second cranscript comprising a second intron component and a second exon.

Transcript comprising a second intron component and a second exon.

Transcript and transcript 2 are allowed to trans-splice, forming a product containing exon 1 and exon 2, but not the intron components. The product containing exon 1 and exon 2, but not the intron components. The crombinant nucleic acid molecules. The method is used to produce crecombinant nucleic acids, their products, or ribozymes in vivo. The method is preferably used for the preparation of exons are random. The introducts is not into a second combinatorial gene contained is also used for ordered gene assembly, or for the assembly of genes ordered at some exons but randomized at others. New genes can be the preparation of exons may be the preparation of exons may be the preparation of exons may be presented in a part of the preparation of exons may be presented in a part of the preparation of exons may be presented in a part of the preparation of exons may be presented in the preparation of exons may be preparation.
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20-SEP-1999;
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Search completed: October 2, 2001, 16:18:39 Job time: 15483 sec 32 GAAAGCGCCCCCATTAT 15 g

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Gaps 0;

Score 13.2; DB 21; Length 48; Pred. No. 1e+03; 0; Mismatches 3; Indels (

Query Match 66.0%; Best Local Similarity 83.3%; Matches 15; Conservative

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| MRNAS using full-length enriched and 5'-end enriched cDNA libraries JOURNAL Unpublished (2001) COMMENT Contact: Yutaka Suzuki Department of Virology | Institute of medical Science, University of Yokyo 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Email: ysuzuki@ims.u.tokyo.ac.jp Suzuki.y y Soshitomo-Makagawa, K., Maruyama, K., Suyama, A. and Sugano , S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997). FEATURES Location/Qualifiers Ada.ref="Haxon:9606" Ada.ref="Hax | Query Match 76.0%; Score 15.2; DB 107; Length 50; Best Local Similarity 85.0%; Pred. No. 1.7e+03; Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0; Qy 1 ggtaagcagctgccattatt 20 | 2 45/c rion ION N DS | SUGREE FOREST MOUSE. ORGANISM Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. REFERENCE 1 (bases 1 to 41) AUTHORS Dun,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. | TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts JOURNAL Unpublished (2000) COMMENT Contact: Robert B. Weiss University of Utah Genome Center University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tal: 801 588 5606 | FEATURES FEATURES FEATURES FEATURES FEATURES FEATURES FATINDO FATINO F | /clone="UUGCIM0490012" /clone="UUGCIM0490012" /sex="Male" /lab_host="E. Coli strain XLI0-Gold, T1-resistant, F-" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson |
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| SUMMARIES QUETY QUETY | 76.0 50 107 AU103462 AU103462 AU103462 62.0 45 12 AA794942 AA794948 AA7948 A | 59.0 59.0 59.0 59.0 59.0 58.0 58.0 58.0 64.249 58.0 64.249 58.0 64.249 58.0 64.249 | 58.0 50 107 AU105748 AU105748 57.0 31 156 D18234 D18234 BU 57.0 31 249 AZ785014 57.0 47 143 BF036368 BF036368 57.0 50 107 AU103473 AU103473 56.0 20 249 AZ781008 AZ481008 56.0 20 249 AZ78105 56.0 22 245 AZ58125 56.0 24 | 56.0 39 250 AZ834606 AZ829485 56.0 43 241 AZ329485 AZ829485 56.0 50 0.0 AZ329485 AZ329485 56.0 50 107 AU107071 AU107071 AU107071 AU107071 56.0 50 107 AU107431 AU107431 56.0 50 107 AU107431 AU107431 56.0 50 173 BG077090 55.0 26 156 D21048 D21048 D21048 | 55.0 36 243 A2425719 AZ425719 55.0 36 244 AZ42058 AZ482058 55.0 40 247 AZ644893 AZ644893 55.0 41 258 TA386D04P AL498584 55.0 46 192 AK019062 AK019062 ALIGNMENTS | AU103462 50 bp mRNA AU103462 Sugano Homo sapiens CHEP14884, mRNA sequence. AU103462. GI:13552983 EST. Homo sapiens Eukaryota; Metazoa; Chordata; | Manmalia: Eutheria; Primates; 1 (bases I to 50) Suzuki, Y., Tsunoda, T., Taira, J. H., Ota, T., Isogai, T., Tanake , K., Suyama, A. and Sugano, S. Fine Structural analysis of th |
| Result | 00000000000000000000000000000000000000 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0000 00 | | οο ο 44444 Η σω 4υ | RESULT 1 AU103462/C LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM | REFERENCE AUTHORS TITLE |

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               (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pWD42 (qil4732114)[plARL29072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10.Gold (Stratagene) cells and selected for ampicillin resistance."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 45)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,

Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,

Schallenberg,K., Steptee,M., Tan,F., Underwood,K., Moore,B.,

Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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VIOSQUE TROWNESS SOLTER mouse blastcoyst B3 Mus musculus CDNA clone IMAGE:1110964 5' similar to 9b:M76124 Mus musculus EGP314 precursor mRNA, complete cds (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/strain="B6D2 F1/J"
/db_xraco:10090"
/clone="IMAGE:1110964"
/clone_lib="Knowles Solter mouse blastocyst B3"
/tissue_kype="blastocyst"
/dev_stage="embryo (pre-implantation)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marran MyMouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66.0%; Score 13.2; DB 247; Length 41; 83.3%; Pred. No. 1.7e+04; ive 0; Mismatches 3; Indels 0;
Laboratory Mouse DNA Resource
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 1. Location/Qualifiers
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Matches 15; Conserv
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ORIGIN
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AA794942/c
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VERSION
KEYWORDS
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hall, M., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                    Length 45;
                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                    Score 12.4; DB 12;
Pred. No. 4.4e+04;
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                                                                                                                                                                                                                                                                                                               0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:5691"
/clone="355f03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4
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                                                                                                                                                                                                                                                                 62.0%;
92.9%;
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Trypanosoma brucei
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Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                              2 gtaagcagctgcca 15
                                                                                                                                                                                                                                                                                                                                                                                                         45 GTTAGCAGCTGCCA 32
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cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 31)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AZ798762 31 bp DNA GSS 16-FEB-2001
2M0055C18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0055C18 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 40;
                                                                                                                                       Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Insert Length: 1216 Std Error: 0.00
Stq primer: -40ml3 Hwd. BT from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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Pred. No. 5.5e+04;
0; Mismatches 3;
                                                                                                                                                                                                                                                                               1. .40
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="1391624"
/clone_lib="Soares_testis_NHT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0055 row: C column: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plate: 0055 row: C column: 18
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AZ798762.1 GI:12949191
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82.4%;
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Best Local Similarity 82.4
Matches 14; Conservative
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ORIGIN
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AZ798762
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                            FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                          Trypanosoma.

1 (bases 1 to 30)

Hall, N., Bowman, S.,

Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,

Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,

Melville, S.E., Rajandream, M.A. and Barrell, B.G.

Direct Submission

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing

project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,

Cambridge CB10 LSA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                Constructed at the Institute for Genomic Research (TIGR),
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TRED27/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects.
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 40)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                            13-DEC-2000
TA272C09Q 30 bp DNA GSS 13-DEC-2000
T. brucei sheared genomic DNA clone 272c09, reverse sequence,
genomic survey sequence.
                                                                                                                                                                                                               Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61.0%; Score 12.2; DB 258; Length 30; 82.4%; Pred. No. 5.2e+04; tive 0; Mismatches 3; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Trypanosoma brucei"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:5691"
/clone="272c09"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="TREU927"
                                                                                                                  AL487818.1 GI:11852489
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Unpublished (1997)
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Best Local Similarity
Matches 14; Conserv
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                                                                                                                                                                                                                                                                                                (http://www.lax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with 74 DNA polymerase and 74 polywuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (qi|4732114 qiplaF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XE10-Gold (Stratagene) cells and selected for ampicilin resistance."
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 506
Fax: 801 585 7177
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AZ311284
AZ311284.1 GI:10354094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 33)
Dunn, D., Aoyagi, Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
                                                                                                                                                                                                           /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/G3 (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                /db_xref="taxon:10090"
/clone="UUGC2M0055C18"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 11.8; DB 249; Length 31;
Pred. No. 8.4e+04;
0; Mismatches 2; Indels 0;
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Insert Length: 10000 Std Error: 0.00
Plate: 0026 row: G column: 08
High quality sequence stop: 31.
Location/Qualifiers
                                                                                          /strain="C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59.0%;
86.7%;
                                                                                                                                                                                          /sex="Male"
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Best Local Similarity 86.7
Matches 13; Conservative
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is NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Stratagene, Inc.
CDNA Library Preparation: Stratagene, N.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarcise gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (qi|4732114|qib|ART29072.1), a copyrumber inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the linsert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/note="Weetcr: PWD42Dry; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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/clone="UUGCIM0026G08"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
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Pred. No. 8.5e+04;
); Mismatches 2; Indels 0;
Seq primer: CACACAGGAAACAGCTATGACC Class: plasmid ends
                                                                      High quality sequence stop: 33.
Location/Qualifiers
                                                                                                                                                                                                                       /strain="C57BL/6J
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86.7%;
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Best Local Similarity 86.7
Matches 13; Conservative
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sequences that lack an initiation codon; expression of lac2 is only provided by in frame fusion to yeast coding sequence. The yeast genomic DNA carrying the transposon was excised from piez6 and transplaced back onto the yeast chromosome. Yeast colonies expressing lac2 were screened for in a color assay. A plasmid containing the genomic DNA/lac2 fusion junction was recovered from each individual yeast colony that expressed lac2 activity. These recovered plasmids comprise 'The blue guys library'. The fusion junction was then sequenced to identify the expressed ORF upstream of the fusion. " a 13 c 8 g 10 t
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/organism="Homo sapiens"
/db_xref="texton:9606"
/clone="Inba08:1168126"
/clone="Inba WCI_CGAP_EW1"
/tissue_type="Ewing's sarcoma"
/lab_host="DH108"
/note="Vector: pAMP10; mRNA made from Ewing's sarcoma,
cDNA made by oligo-dT priming. Non-directionally cloned.
Size-selected on agarose gel, average insert size 600 bp.
Reference: Krizman et al. (1996) Cancer Research
56:3380-5383."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP chone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA662608 50 bp mRNA EST 12-NOV-1997 nr16a12.s1 NCI_CGAP_Ew1 Homo sapiens CDNA clone IMAGE:1168126 similar to SW:RL24_HUMAN P38663 608 RIBOSOMAL PROTEIN L24.;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lee Helman, M.D., Michael R. Emmert-Buck, M.D.
Ph.D.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Pred. No. 9.1e+04;
0; Mismatches 2; Indels
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www.bio.llnl.gov/bbrp/image/image.html
Seq primer: -40ml3 fwd. ET from Amersham.
Location/Qualifiers
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AA662608.1 GI:2615457
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86.7%;
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Matches 13; Conservative
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Best Local Similarity 86.7
Matches 13; Conservative
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1 (bases 1 to 45)
Burns, N., Grimwade, B., Ross-Macdonald, P.B., Choi, E.-Y., Finberg, K.,
Roeder, G.S. and Snyder, M.
Large-scale analysis of gene expression, protein localization and gene disruption in Saccharomyces cerevisiae
Genes Dev. 8, 1087-1105 (1994)
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//db_xref="taxon:4932"
//clone_lib="The blue guys library"
/lab_host="E.coli"
//note="Vector: pRECMTD; A yeast genomic DNA library was prepared in the vector pHSS6, and subjected to transposon mutagenesis with mTn3. This mini-transposon carries lac2
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So Cytoplasmic spots; Disruption phenotype: inviable, unbudded
so Cytoplasmic codon12 of ORF next to BRF1. Sequence below near
or adjacent to lac2.
Seq primer: Lac2 sequences in transposon.
Location/Qualifiers
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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0
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Pred. No. 8.8e+04;
0; Mismatches 2; Indels C
    Trace considered overall poor quality Insert Length: 660 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 1.
                                                                                                                   1. 41
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1420657"
/clone_lib="NCI_CGAP_CO12"
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Department of Biology
Yale University
New Haven CT 06520-8103
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T17561.1 GI:458583
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Best Local Similarity 86.7
Matches 13; Conservative
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Fax: 2034326161
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/clone="COLF4166"
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86.7%;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo,K., Suyama,A. and Sugano,S.
Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                Ontact: Yutaka Suzuki
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ilia.u-tokyo.ac.jp
Suzuki,Y., Yoshicomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
'S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 50)
Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogal,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo,K., Suyama,A. and Sugano,S.
Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries Contact: Yutaka Suzuki
Department of Virology
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                                                                                                                 AU102666 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone ADKA01276, mRNA sequence.
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AU103485 GI:13553006
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Pred. No. 9.1e+04;
); Mismatches 2; Indels 0;
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ENKaryota: Metazoa: Chordata; Craniata; Vertebrata; Enteleostomi; Bukaryota: Metazoa: Chordata; Craniata; Vertebrata; Enteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 50)

Suzuki, Y., Tsunoda, T., Taira, H., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Nakamura, Y., Morishita, S., Okubo, K., Suyama, A. and Sugano, S.

Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries on droublished (2001)

Ontact: Yutaka Suzuki
Department of Virology, Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
4 6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: Ysuzukifelims. "Lokyo.ac.; Jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Email: ysuzuki@ins.u-tokyo.ac.jp Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano S. Construction and characterization of a full length-enriched as 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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AU103486 Sugano Homo sapiens CDNA library Homo sapiens CDNA clone
COLF4166, mRNA sequence.
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Pred. No. 9.1e+04;
0; Mismatches 2; Indels 0
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla: Eutherla; Primates; Catarrhini; Hominidae; Homo.

Mammalla: Eutherla; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 50)

Suzuki, Y., Tsunoda, T., Taira, H., Mizushima-Sugano, J., Sese, J., Hata

H., Ota, T., Isogai, T., Tanaka, T., Nakamura, Y., Morishita, S., Okubo

K., Suyama, A. and Sugano, S.

Fine Structural analysis of transcription start sites of human

mRNAs using full-length enriched and 5'-end enriched cDNA libraries

To published (2001)

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: ysuzuki@ims.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano

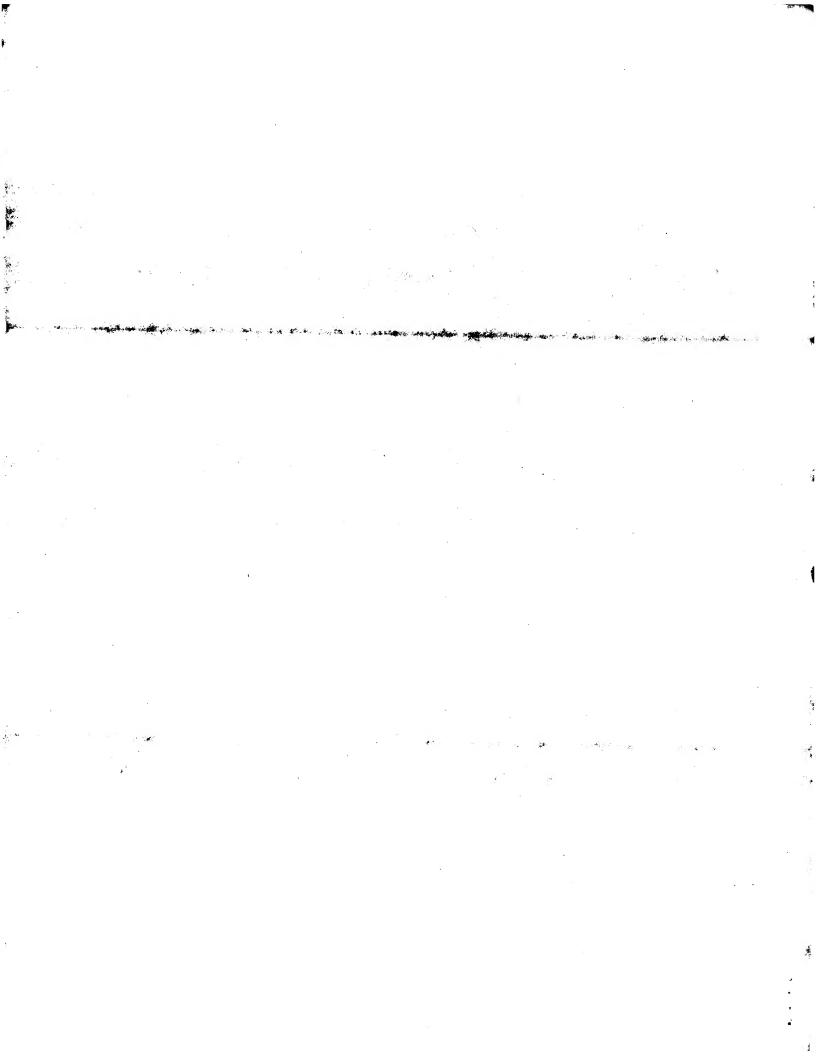
S. Construction and characterization of a full length-enriched and

a S'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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AU103487 50 bp mRNA EST 05-APR-2001
AU103487 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
CL0F6739, mRNA sequence.
AU103487.1 GI:13553008
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/db xref="taxon.9606"
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19 c 11 g 8 t
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Search completed: October 2, 2001, 15:00:56 Job time: 10825 sec

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Sequence:

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Database

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I30544 Sequence 7
I75320 Sequence 69
AR091705 Sequence
AR075823 Sequence
E30456 Method for
A3480 ARV probe.
AR067320 Sequence
AR067320 Sequence
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         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                    Title:
Perfect score:
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Description

03-APR-1998

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1 (bases 1 to 29)
Brown, S.Marie, Dean, D.Allen, Fromm, M.Ernest and Sanders, P.Rigden.
Synthetic DNA sequences having enhanced expression in
monocotyledonous plants and method for preparation thereof
Patent: US 5689052-A 69 18-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unknown.
Unclassified.
1 (bases 1 to 48)
Nadeau,J.G., Pitner,J.Bruce, Linn,C.Preston and Schram,J.L.
Detection of nucleic acids by fluorescence quenching
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 34)
Ting,J.Pan.Yung and Chin,K.
Forms of class II MHC transactivator (CIITA)
Patent: US 5994505-A 15 30-NOV-1999;
                                                                                                                                                                                                                                                                                                                           Score 12.8; DB 10;
Pred. No. 1.4e+04;
); Mismatches 2;
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Pred. No. 1.4e+04;
); Mismatches 2;
                                   US 5689052.
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Sequence 6 from patent US 5958700.
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AR07594 Oligonucleo
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AF0734 Sequence 11
AF0734 Sequence 34
AR01388 Sequence
AR042502 Sequence
AR04502 Sequence
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AR088208 Sequence
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AR013872 Sequence
AR013875 Sequence
AR033826 Sequence
AR042486 Sequence
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Hoke,G.D., Bradley,M.O., Williams,T.J. and Lee,C.
Antisense oligonucleotides directed against human ICAM-I RNA
Patent: US 5580969-A 7 03-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Pred. No. 6.4e+03;
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RESULT E30456/c

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COMMENT

REFERENCE

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Renard, A. and Thiry, M. Recombinant polypeptides of the haemorrhagical septicemia virus in
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unknown.
Unclassified.
Unclassified.
1 (bases 1 to 22)
Evans,62. and Smith,M.W.
Method for generation of sequence sampled maps of complex genomes Patent: US 5851760-A 668 22-DEC-1998;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Durkly, L.C., Chisholm, P.L., Thomas, D.W., Rosa, M.D. and Rosa, J.J. anti-CD4 antibody homologs useful in prophylaxis and treatment of AIDS, ARC and HIV infection
Patent: US 5871732-A 36 16-FEB-1999;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                              29-SEP-1999
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Pred. No. 2.6e+04;
0; Mismatches 1; Indels
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/organism="synthetic construct"
/db_xref="taxon:32630"
a 4 c 7 g 2 t
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Sequence 668 from patent US 5851760.
AR067320
                                              Patent: EP 0377349-A 20 11-JUL-1990;
EUROGENTEC S.A
Location/Qualifiers
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Sequence 36 from patent US 5871732.
AR035220 GI:5951888
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12 c 14 σ
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92.9%;
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Best Local Similarity 92.9
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14 CCCAGGTCAGTCTT 1
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AR067320/c
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AR035220/c
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PN 7P 199056880-A/6
PD 02-MAY-1998 JP 1998166141
PR 30-MAY-1997 US 08/865.675
PI JAMES G NADEAU, J BLUCE PITONA, C PRESTON RIN, JAMES L SHURAMU PC CL2N15/09, C1201/68, G01N33/566, C12N15/00 CC Strandedness: Single;
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Mathod for detecting target nucleic acid sequence and
Patent: JP 1999056380-A 6 02-MAR-1999;
                                                                                                                                                                                                                                                                                              E30456 48 bp DNA PAT 07-F
Method for detecting target nucleic acid sequence and
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                                                                                                                         Score 12.8; DB 9; Length 48;
Pred. No. 1.4e+04;
0; Mismatches 2; Indels

    .48
    /organism='Unidentified'.

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/organism="unidentified"
/db_xref="taxon:32644"
a 8 c 10 g 15
Patent: US 5958700-A 6 28-SEP-1999;
Location/Qualifiers
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                                              /organism="unknown"
a 8 c 10 g
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JP 1999055380-A/6.
unidentified.
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Best Local Similarity 87.5%;
Matches 14; Conservative (
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Best Local Similarity 87.5%;
Matches 14; Conservative
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synthetic construct
artificial sequence.
1 (bases 1 to 18)
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A34802
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BASE COUNT ORIGIN

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Gaps

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PROTEINS PREVENTING INTERACTION BETWEEN A FRAGMENT FC OF AN IMMUNOSLOBULIN AND ITS RECEIVER, AND THERAPEGTIC USE, PARTICULARILY IN TREATING AFFECTIONS LINKED TO THE HIV VIRUS PATENT: WO 9108301-A 6 13-JUN-1991; Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unclassified.
Unclassified.
1 (bases 1 to 41)
Thastrup,O., Tullin,S.slashed.ren, Poulsen,L.Kongsbak and Bj.o
slashed.rn,S.Petersen.
Method of detecting biologically active substances by using green
fluorescent protein
Fluorescent protein
Patent: US 5958713-A 8 28-SEP-1999;
Location/Qualifiers
       12-JUN-1995
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100.0%; Pred. No. 4.3e+04;
ive 0; Mismatches 0;
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/db_xref="taxon:32630"
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Sequence 8 from patent US 5958713.
AR075947
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Oligonucleotide xo123.
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synthetic construct
artificial sequence.
1 (bases 1 to 39)
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86.7%;
                                               A28774.1 GI:1248748
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Matches 12; Conservative
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Best Local Similarity 86.7
Matches 13; Conservative
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A49393/c
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1 (bases 1 to 44)

Burkly,L.C., Chisholm,P.L., Thomas,D.W., Rosa,M.D. and Rosa,J.J.

Burkly,A.C., Chisholm, P.L., Thomas,D.W., Rosa,M.D. and Kosa,J.J.

Burkly,A.C., Chisholm, P.L., Thomas,D.W., Rosa,M.D. and treatment of AIDS, ARC and HIV infection

Patent: US 5871732-A 59 16-PEB-1999;
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Unclassified.
Unclassified.
Eriksson, U., Olofsson, B., Alitalo, K. and Pajusola, K. Vascular endothelial growth factor-B Patent: US 5840693-A 53 24-Nov-1998;
Location/Qualifiers
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Pred. No. 3.2e+04;
0; Mismatches 3; Indels
                     Length 44;
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                  Score 12.2; DB 9;
Pred. No. 3.2e+04;
                                             0; Mismatches
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Sequence 59 from patent US 5871732.
AR035241
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14 c 12 g
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4 c 6 g
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US 5
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Sequence 53 from patent
AR060552
AR060552.1 GI:5987002
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Best Local Similarity 82.4%;
Matches 14; Conservative
                Query Match 61.0%;
Best Local Similarity 82.4%;
Matches 14; Conservative
                                                                         Local Similarity 100.
les 12; Conservative
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Unclassified.
Unclassified.
SE 1 (bases 1 to 26)
RS Gallatin,W.Michael and Vazeux,R.
Method to identify compounds which modulate ICAM-related protein interactions
INAL Patent: US 5773218-A 87 30-UUN-1998;
Location/Qualifiers
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PALENTE. WO 9915696-A 34 01-APR-1999;
OIN YUFEN (CA)
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1 (bases 1 to 23)
Edelman,L., Margaritte,C., Kaczorek,M. and Chaabihi,H.
MONOCLONAL RECOMBINANT ANTI-RHESUS D (D7C2) ANTIBODY
PATENT: WO 9607740-A 11 14-MAR-1996;
PASTEUR INSTITUT (FR)
Other publication FR 2724182 960308.
                                                                                                                                                                                                  Query Match 58.0%; Score 11.6; DB 9; Length 23; Best Local Similarity 77.8%; Pred. No. 7.8e+04; Matches 14; Conservative 0; Mismatches 4; Indels
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Sequence 87 from patent US 5773218.
AR013888 1 GI:3971342
                                                                                                                                                                                                                                                                                                                                                       A97534 26 bp DNA
Sequence 34 from Patent W09915696.
A97534. GI:6780880
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/organism="unidentified"
/db_xref="taxon:32644"
a 8 c 6 9
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/db_xref="taxon:32644"
1 8 c 9 9
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Best Local Similarity 77.8%;
Matches 14; Conservative
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unidentified
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1 (bases 1 to 26)
Qin,Y.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts JOURNAL Unpublished (2000) COMMENT Contact: Robert B. Weiss University of Utah Genome Center | Outversity of Utah Rm. 1907814 of Utah Rm. 19078 14 of Utah Rm. 19078 15 of 1005 Tel: 805 A107 Email: dudunmagementics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0347 row: C column: 11 Sea primer: CGTPGTPAAACGGCCAGT Class: plasmid ends ends High quality sequence stop: 25. 10-2150n/Qualificis: //CTGAIN="WANDER" was well and the Machine of M | Qy 5 cccaggtgagtcttag 20 | RESULT 2 AZ666528 AZ66528 AZ666528 AZ6668 AZ6668 AZ6668 AZ6668 AZ666 |
|---|--|------------------------------|--|
| SUMMARIES Result Query No. Score Match Length DB ID Description | 12.8 64.0 25 245 | ALIGNMENTS | AZ506197 AZ5 |

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gil4732114) iphaR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for amplcillin resistance."
                                                                                                                                                                                                                     Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Lee,C..C., Yazdani,A., Wehnert,M., Bailey,J., Couch,L., Xiong,M.,
  M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host-"E. Coli strain XLIO-Gold, Tl-resistant, F-" /note-"Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                      Mouse whole genome scaffolding with paired end reads from 10kb
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HUMXP1F11B Human placenta Homo sapiens cDNA clone XP6G6B, mRNA
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/clone="UUGCIMO003F19"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
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Pred. No. 3e+04;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                               Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0003 row: F column: 19
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
                                                                                                                                       Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 32
Location/Qualifiers
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                               and Wright, D., Weiss, R.
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Unpublished (2000)
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Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (qil4732114qiplaH23072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                           Rm.\ 308 , Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
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Makaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 32)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"/hote="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                       Mouse whole genome scaffolding with paired end reads from 10kb
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/clone="UUGCIM0548A18"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
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                                                                                                                                                                                                                                            Tel: 801 585 5606
Fax: 801 585 7177
Emall: ddunnegenetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0548 row: A column: 18
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Seg primer: CACACAGGAAACAGCTATGACC
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                                                                                                                                 University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                   Class: plasmid ends
High quality sequence stop: 37.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="C57BL/6J
                                                   plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
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and Wright, D., Weiss, R.
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1 (bases 1 to 50)

Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tamaka,T., Nakamura,Y., Morishita,S., Okubo,K., Suyama,A. and Sugano,S.
Fine Structural analysis of transcription start sites of human mensks using full-length enriched and 5'-end enriched cDNA libraries Contact: Yutaka Suzuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Institute of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
5-20 Suzukiélins.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library, Gene 200 (1-2), 149-156 (1997).

Location/Qualifiers
Coolbaugh, M.I., Chinault, C.A., Baldini, A., Lindsay, E.A., Zhao, Z.-Y. and Caskey, C.T.H.
Isolation of chromosome-specific genes by reciprocal probing of arrayed cDNAs and cosmid libraries
arrayed cDNAs and cosmid libraries
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AU105613 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HEP22150, mRNA sequence.
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/organism="Homo sapiens"
/db_xref="taxon:6606"
/map="xq27.3-q28"
/clone="xp6688"
/clone=lib="Human placenta"
/note="Arrayed cDNAs and cosmid libraries from human placental tissue"
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/db_xref="taxon.9606"
/clone="HEP22150"
/clone=lib="Sugano Homo sapiens cDNA library"
/ c 22 g 15 t
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Pred. No. 6.5e+04;
); Mismatches 2; Indels 0
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Pred. No. 4.8e+04;
0; Mismatches 5;
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                                                                                                             Contact: Caskey, C.T.H.
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86.7%;
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Best Local Similarity 75.09
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(http://www.jax.org/nscources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel. electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil4732114[gblAR129072.1], a copy.number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically competent E. coli XLLO-Gold (Stratagene) cells and selected for ampicillin resistance."
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Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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Mus recordia: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.

1 (bases 1 to 46)
1 (bases 1 to 46)
1 (bases 1 to 6)
1 (bases 1 to 86)
1 (bases 1 to
AZ826374 46 bp DNA GSS 20-FEB-2001
2M0102K06F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0102K06 F, DNA sequence.
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/sex="Male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0
Plate: 0102 row: K column: 06
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
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/db_xref="taxon:10090"
/clone="UUGC2M0102K06"
                                                                                                                                                                                                                      AZ826374.1 GI:12996282
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DEFINITION

D38689/c

RESULT

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ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

AUTHORS

TITLE

REFERENCE

MEDLINE COMMENT

FEATURES

JOURNAL

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(http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil4732114 [qib]48129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 33)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
.M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Welss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
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2M0056M03R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0056M03 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab host="E. Coli strain XLIO-Gold, T1-resistant, F-"/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Mouse 10kb plasmid UUGCIM library"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 11.2; DB 249; Length 31;
Pred. No. 1.3e+05;
0; Mismatches 3; Indels 0;
                                                 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0003 row: 0 column: 17
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 31.
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:10090"
/clone="UUGC2M0003017"
                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                           /strain="C57BL/6J"
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AZ799299.1 GI:12950275
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81.2%;
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Best Local Similarity 81.2
Matches 13; Conservative
Tel: 801 585 5606
Fax: 801 585 7177
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VERSION
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COMMENT
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Winyersity of Utah
Winyersity of Utah
Win 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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2M0003017R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0003017 R, DNA séquence.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 47)
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/note="Exon-like sequence on chromosome 8; exon-trapping
                                                                                                                                       D38689 47 bp mRNA EST 31-MAY-1995 HUMC1264 Human chromosome \theta Homo sapiens cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                             Koyama, K., Sudo, K. and Nakamura, Y.
Isolation of 115 human chromosome 8-specific expressed-sequence tags by exon amplification
Genomics 26, 245-253 (1995)
95324915
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          University of Tokyo
4-6-1, Shirokanedal, Minato-ku, Tokyo 108, Japan
Tel: 81-3-5449-5372
Fax: 81-3-5449-5433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: yusuke@ims.u-tokyo.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Yusuke Nakamura
Institute of Medical Science
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77.8%;
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Best Local Similarity 77.8
Matches 14; Conservative
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21 AGTTATCAGGTGTGTCTT
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DEFINITION

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (qilq732114 qiplAFL29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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Bunn,D., Aoyal,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longarer,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly and Wright,D., Weiss,R., Stokes,R., Tingey,A., von Niederhausern,A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host-"E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42Nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                               /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCIM0559C44"
/clone=lib="Mouse l0kb plasmid UUGCIM library"
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                                             Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0559 row: C column: 04
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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Contact: Robert B. Weiss
University of Utah Genome Center
                                                                                                                                                                                                                                              High quality sequence stop: 34.
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/note="Vector: PWAD2N: Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory whouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114gb AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Dunn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1M0559C04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0559C04 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon=10000"
/dcone="UGC2k0056k03"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
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                                                                                                   Std Error: 0.00
        Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.1
Plate: 0056 row: M column: 03
Seq primer: CACACAGGAAACACCTATGACC
Class: plasmid ends
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                            High quality sequence stop: 33.
Location/Qualifiers
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Best Local Similarity 81.2%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="Male"
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Gaps

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source

FEATURES

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(http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil4732114[gb]AR129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab_host="E. Coli strain XLIO-Gold, T1-resistant, F-" /note="Weetcor: PWD42nv; Purified genomic DNA from M. musculus C57BL/63 (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                          \rm Rm.~308,~Biomedical~Polymers~Research~Bldg.,~20~S.~2030~E.,~SLC,~84112,~USA
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T. bruce1 sheared genomic DNA clone 117f12, forward sequence, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Mouse 10kb plasmid UUGC1M library" /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 11.2; DB 249; Length 43; Pred. No. 1.3e+05; 0; Mismatches 3; Indels 0
                                                                                                               Tel: 801 585 5606
Fax: 801 585 7177
Email: ddundgenetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0069 row: O column: 06
                                                                                                                                                                                                                                                                 Seq primer: CGTTGTAAAACGACGCCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0069006"
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Location/Qualifiers
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81.2%;
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1 (bases 1 to 48)
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Matches 13; Conservative
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/67 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
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was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (qil4732114|qb]APL29072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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2M0069006F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0069006 F, DNA sequence.
AZ806794 GI:12970500
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                        Rm.\ 308 , Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 84112, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                           /db.xref="taxon:10090"
/clone="UUGCIM0302M10"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
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Pred. No. 1.3e+05;
); Mismatches 3; Indels 0;
                                                                                                                                        Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0302 row: M column: 10
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/strain="C57BL/6J"
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Contact: Robert B. Weiss
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81.2%;
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University of Utah
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Best Local Similarity 81.2
Matches 13; Conservative
                                                                                   Tel: 801 585 5606
Fax: 801 585 7177
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BASE COUNT ORIGIN

LOCUS AZ806794/c

ð g ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS

JOURNAL

COMMENT

TITLE

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Gaps

COMMENT

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1 (bases 1 to 34)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Kucaba, T., Leh.M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohling, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tissues representing the following areas of the brain: frontal, parietal, temporal and occipital cortex from the left and right hemispheres, subcortical white matter,
                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tal: 314 286 1800
Fax: 314 286 1810
Eamail: est@watson.wustl.edu
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (Info@image.llnl.gov) for further information.
Trace considered overall poor quality
                                                                                                                                                                                       Y038C05.rl Soares adult brain N2b4HB55Y Homo sapiens cDNA clone
IMAGE:180200 5' similar to gb:M92302 DIHYDROPRYRIDINE-SENSITIVE
L-TYPE, BRAIN CALCIUM CHANNEL (HUMAN);, mRNA sequence.
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Pred. No. 1.7e+05;
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/clone_lib="Soares adult brain N2b4HB55Y"
/sex="Male"
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Location/Qualifiers
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11 GTACCGCGCTGAGTCT 26
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Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo,K., Suyama,A. and Sugano,S.
Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries Unpublished (2001)
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Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Institute of Medical Science, Tokyo 108-8639, Japan
Email: ysuzukielims.u-tokyo.ac.jp
Suzuki.Y. Yoshitomo-Nakagawa.K., Maruyama.K., Suyama.A. and Sugano
'S. Construction and characterization of a full length-enriched and
a S'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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                    Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma bruce; (TREU927/4 GUTAT 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + 1 method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
                                                                                                                                                                                                                                    Email: nelsayed@tigr.org Details of T. brucel sequencing at the Sanger Centre are available
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AU106341 50 bp mRNA EST 05-APR-2001 UN 0106341 Sugano Homo sapiens CDNA library Homo sapiens CDNA clone AU106341, mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Pred. No. 1.4e+05;
0; Mismatches 3; Indels 0
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Location/Qualifiers
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81.2%; Pred. No. 1.4e+05;
live 0; Mismatches 3; I
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/strain="TREU927"
/db_xref="taxon:5691"
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DEFINITION

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REFERENCE AUTHORS JOURNAL

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BASE COUNT ORIGIN

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Search completed: October 2, 2001, 15:00:58 Job time: 10827 sec

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153690 Sequence 14
AX095079 Sequence
127043 Sequence 64
AR021414 Sequence
AR042976 Sequence
143923 Sequence 12
162967 Sequence 22
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        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Lander, E.S., Gargill, M., Ireland, J.S., Bolk, S., Daley, G.Q. and Mccarthy, J.J.
Single nucleotide polymorphisms in genes
Patent: WO 0118250-A 257 15-MAR-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US); Millennium
            07-OCT-1997
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1 (bases 1 to 17)

Stinchcomb.D.T., Draper,K., McSwiggen,J. and Jarvis,T.
C-myb targeted ribozymes

C-myb targeted ribozymes

Patent: US 5646042-A 1431 08-JUL-1997;

Location/Qualifiers
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           153690 17 bp DNA
Sequence 1431 from patent US 5646042.
153690 GI:2474893
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Sequence 257 from Patent W00118250.
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/db_xref="taxon:9606"
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1 (bases 1 to 17)
Stinchcomb, D.T., Draper, K., McSwiggen, J. and Jarvis, T.
C-myb ribozymes having 2'-5'-linked adenylate residues
Patent: US 5817796-A 1431 06-ocr-1998;
Location/Qualifiers
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Pred. No. 9.4e+03;
0; Mismatches 2; Indels
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AR046638
AR046638.1 GI:5968103
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188720
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AR020665
A51533
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AR021372
AR042934
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188678
AR077278
105886
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109165
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AR057887
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88.2%;
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REFERENCE

AUTHORS

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FEATURES TITLE

ACCESSION VERSION

KEYWORDS

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Unknown.
Unclassified.
1 (bases 1 to 42)
Lonbers.N.
Transgenic non-human animals capable of producing heterologous antibodies
Patent: US 5633425-A 12 27-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unclassified.

1 (bases 1 to 42)
Lonberg, N. and Kay, R.M.
Transgenic non-human animals capable of producing heterologous antibodies of various isotypes
Patent: US 56610.6-A 64 26-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Pred. No. 1.2e+04;
0; Mismatches 4;
80.0%; Pred. No. 1.2e+04;
tive 0; Mismatches 4;
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Sequence 64 from patent US 5661016.
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Best Local Similarity 80.0%;
Matches 16; Conservative
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Best Local Similarity 80.0
Matches 16; Conservative
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Unclassified.
I (bases I to 42)
Lonberg, N. and Ray, R.M.
Transgenic non-human animals for producing heterologous antibodies
Patent: US 5789650-A 64 04-AUG-1998;
Location/Qualifiers
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1 (bases 1 to 42)
Lobberg, N. and Agy, R.M.
Transgenic non-human animals for producing heterologous antibodies
Patent: US 5814318-A 64 29-SEP-1998;
Location/Qualifiers
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                                                                                                                                                 Length 30;
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         1 (bases 1 to 30)
Peterson, M.G., Baichwal, V.R. and Strulovici, B. Transcription factor-DNA binding assay
Patent: US 5563036-A 64 08-OCT-1996;
Location/Qualifiers
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Sequence 64 from patent US 5814318.
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US 5789650.
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Sequence 64 from patent
AR021414
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88.2%;
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Best Local Similarity 80.0
Matches 16; Conservative
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Best Local Similarity 88.2
Matches 15; Conservative
Unclassified
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Unclassified.
1 (bases 1 to 30)
Foulkes, J. Gordon, Liechtfried, F.E., Pieler, C., Stephenson, J.R. and
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Foulkes,J.Gordon, Liechtfried,F.E., Pieler,C., Stephenson,J.R. and
Case,C.C.
                                                                                                                                                                                                                                                                                                Case C.C. Methods of determining chemicals that modulate expression of genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Methods of determining chemicals that modulate transcriptionally expression of genes associated with cardiovascular disease Patent: US 5580722-A 17 03-DEC-1996;
                  Gaps
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Pred. No. 2e+04;
0; Mismatches 3; Indels 0
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Pred. No. 2e+04;
0; Mismatches 3;
   Pred. No. 1.2e+04;
                                                                                                                                                                                                                                                                                                                            associated with cardiovascular disease
Patent: US 5846720-A 17 08-DEC-1998;
Location/Qualifiers
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                0; Mismatches
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Sequence 17 from patent US 5846720.
AR063732.1 GI:5993040
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                16; Conservative
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Best Local Similarity 83.3
Matches 15; Conservative
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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V-region; antigen binding region; complementarity determining
region; immunoglobulin heavy chain; mu-immunoglobulin; processed
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chihara,Y., Matsuoka,H. and Kurosawa,Y.
)rganization of human immunoglobulin heavy chain diversity gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 45)
Raaphorst, F.M., Sanz, I., Vossen, J.M., Schuurman, R.K.B. and van
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunoglobulin heavy chain CDR3 regions in human fetal organs: Evidence for selection of rearrangements on the basis of CDR3
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Homo sapiens
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Sequence 64 from patent US 5719032.
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/gene="IGHM"
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/gene="IGHM"
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Vielkind, J.R.
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E 1 (bases 1 to 21)

S Audonnet, J.F., Bublot, M.J., Darteil, R.J., Duinat, C.V., Laplace, E.L.

and Riviere, M.A.

Live recombinant avian vaccine based on an avianherpes virus,
against Gumboro disease

RD Patent: EP 0728842-A 18 28-AUG-1996;

RONE MERICUY (FR)

Other publication FR 2728794 960705

Other publication AU 4063095 960711.
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RS Fowlkes, D.M., Broach, J., Manfredi, J., Klein, C., Murphy, A.J., Paul, J. and Trutheart, J.

"Yeast cells engineered to produce pheromone system protein surrogates, and uses therefor surrogates, and uses therefor "I ST 193184-A ST 90 4-Aug-1998;

"NAL Patent: US 578184-A ST 90 4-Aug-1998;

"ST 10-Cation/Qualifiers"
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0; Mismatches 2;
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              AR020665 23 bp DNA
Sequence 59 from patent US 5789184.
AR020665.1 GI:3975280
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Sequence 18 from Patent EP0728842.
A51533 GI:2304354
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Sequence 21 from Patent EP0719864.
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Madonnet,J.F., Bublot,M.J., Darteil,R.J., Duinat,C.V., Laplace,E.L. and Riviere,M.A.
Recombinant live avian vaccin, using an avian herpes virus as
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t
                                                                                        Patent: EP 0719864-A 21 03-JUL-1996;
RHONE MERIEUX (FR)
                                                                                                                              Other publication FR 2728795 960705 Other publication CA 2166367 960701 Other publication AU 4071595 960711.
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| TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts JOURNAL Onpublished (2000) CONTECT: Robert B. Weiss CONTECT: Robert B. Weiss University of Utah Genome Center Rm. 308 Biomedical Polymers Research Bidg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 506 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: Disamile ends High quality sequence stop: 19. Seq primer: CACACACACACACACACACACACACACACACACACACA | 10.5 Kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gil4732114) plAT129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance. and selected for ampicillin resistance. and selected for ampicillin resistance. BASE COUNT 2 a 4 c 7 g 6 t 7 g 6 t 6 t 7 g 7 g 7 g 7 g 7 g 7 g 7 g 7 g 7 g 7 | Oy 1 cctgacatcagtagcatc 18 | ACCESSION 49 bp mRNA EST 20-AUG-1998 DEFINITION ue31h01.yl Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1482001 5' similar to TR:P97298 P97298 STROMAL CELL DERIVED FACTOR 3; mRNA sequence. AI098615. I G1:3448140 KEYWORDS EST. 20-AUG-1998 ACCESSION A1098615 G1:3448140 KEYWORDS EST. 20-AUG-1998 AUGHOST 3; mRNA sequence. AI098615. I G1:3448140 EST. 20-AUG-1998 FACTOR 3; mRNA sequence. AI098615. I G1:3448140 EST. 20-AUG-1998 FACTOR 3; mRNA sequence. AI098615. I G1:3448140 EST. 20-AUG-1998 FACTOR 3; mRNA sequence. AINMAN SATURDAL CELL DERIVED FACTOR 3; mRNA SEQUENCE FACTO |
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| Result Ouery No. Score Match Length DB ID Description C 1 13.2 66.0 19 250 A2848554 A2848554 2M0149A07 C 1 13.2 66.0 19 250 A2848554 A2848554 2M0149A07 C 1 13.2 66.0 19 250 A2848554 A2848554 2M0149A07 C 1 13.6 63.0 49 14 AA975152 AA877812 AA910888 0x88501.s C 1 1.8 59.0 44 1258 HSWC04C05 AA877812 AA975120 CM99e07.s D 11.8 59.0 44 24 A277833 AA877812 AA77813 M055905.x D 11.8 59.0 49 24 AA777833 AA87812 AA77813 M059601.s D 11.6 58.0 49 14 AA979145 AA77813 M059601.x D 11.6 58.0 49 24 AA777833 AA77833 AM012X11 D 11.2 56.0 31 246 A2769305 A2769306 M050011.x D 11.2 56.0 31 249 A277633 AA77833 2M0012X21 D 11.2 56.0 49 AA77833 AA77833 AM012X21 D 11.2 56.0 49 AA77833 AA77833 AM012X21 D 11.2 56.0 49 AA77833 AA77833 AM012X21 D 11.2 56.0 49 AA78886 AA78812 AA77833 AM012X21 D 11.2 56.0 49 AA78888 AA78888 AA788881 AA75888 IM0260C01 D 11.5 50.0 49 AA78888 AA78888 AA78888 AA788881 AA75888 AA78881 AA75888 AA78881 AA75888 AA78881 AA75888 AA78881 AA75888 AA78881 AA75888 AU103398 AU103398 AU103398 C 22 11 55.0 43 AA78888 AA78888 AU103398 AU103398 AU103398 C 24 11 55.0 50 107 AU103398 AU103398 AU103398 AU103398 C 25 11 55.0 50 107 AU103398 AU103398 AU103398 AU103398 C 27 11 55.0 50 107 AU103398 AU103398 AU103398 AU103398 C 28 11 55.0 50 107 AU103398 AU103398 AU103398 AU103398 C 29 10.8 54.0 52 24 AA259115 AA789112 AA789115 AU104027 D 10.8 54.0 52 24 AA259115 AA789112 AA789115 AU104027 D 10.8 54.0 52 24 AA259115 AA789112 AA789115 AU104027 D 10.8 54.0 52 24 AA259115 AA789112 AA789115 AU104027 D 10.8 54.0 52 24 AA259115 AA789112 AA789115 AU104027 D 10.8 54.0 52 24 AA259115 AA789112 AA789115 AU104027 D 10.8 54.0 52 24 AA259115 AA789112 AA789115 AU104027 D 10.8 54.0 50 107 AU103398 AU103398 AU103398 AU103398 D 10.8 54.0 52 24 AA259115 AA789112 AA789112 AU104027 D 10.8 54.0 50 107 AU103398 AU103398 AU103398 D 10.8 54.0 52 24 AA789112 AA789112 AU104027 D 10.8 54.0 50 107 AU103398 D 10.8 54.0 52 24 AA789112 AA789112 AA789112 AU104027 D 10.8 54.0 50 107 AU103398 AU10309412 AU104027 D 10.8 54.0 52 24 AA78 | 10.8 54.0 34 250 AZ856611 AZ856611 10.8 54.0 39 104 AZ39886 AZ53986 10.8 54.0 43 246 AZ59784 AZ59784 10.8 54.0 46 189 T5359 Ya 10.8 54.0 46 189 T5359 Ya 10.6 53.0 28 17 AI188358 AI188358 10.6 53.0 34 17 AI188358 AZ389531 AZ389531 10.6 53.0 35 242 AZ389531 AZ659063 AZ659063 10.6 53.0 39 191 Z20226 Z20226 AZ659063 10.6 53.0 40 14 AA999748 AA999748 AA999748 10.6 53.0 40 10 AU013065 AU013065 AU013065 10.6 53.0 40 10 AU013075 AU013075 10.6 53.0 40 | ALIGNMENTS | AZ848554/C DEFINITION 2M01499A0TR Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0149A07 R, DNA sequence. DEFINITION Clone UUGC2M0149A07 R, DNA sequence. AZ848554 AZ848554.1 GI:13031758 AZ848554.1 GI:13031758 AZ848554.2 GI:13031758 AZ848554.1 GI:13031758 AZ84854.1 AZ84854.1 GI:13031758 AZ848554.1 GI:13031758 AZ8485747 AZ848574.1 GI:13031758 AZ8485747 AZ8485747 AZ8485747 AZ8485747 AZ8485747 |

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CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D. DNA Sequencing Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Mashington University Genome Sequencing Center Clone distribution: NCI-GAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: Kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI: 1st strand cDNA was primed with a Not I - oligo(dT) primer, double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. mRNA source: 2 pooled kidneys. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bummalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(Dases 1 to 40)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
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A1962543
A1962543.1 G1:5755256
EST.
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Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
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Pred. No. 4.5e+04;
0; Mismatches 1; Indels (
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Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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Mammalia; Butharia; Primates; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butharia; Primates; Catarrhini; Hominidae; Homo.

Mori-GAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                            This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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                                                                                                                                                                                                     4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                     Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: custom primer used
High quality sequence stop: 1.
Location/Qualifiers
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/db_xref="taxon:10090"
/clone="IMAGE:1482001"
/clone_lib="sugano mouse liver mlia"
                                                                        The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicinep
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                      Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="female"
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/lab_host="DH10B"
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Matches 15; Conserv
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SUBUNIT ;, mRNA sequence.
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                                                                                                                                                                                                                    60.0%;
75.0%;
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Best Local Similarity 75.0
Matches 15; Conservative
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                                                                                                                                                                 /tissue_rype="pooled germ cell tumors"
/lab_host="Pooled germ cell tumors"
/lab_host="DH10B"
/lab_host="Pooled germ cell tumors"
/lab_host="Wector: pT73D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library
NCI_CGAP_GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 146964-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo. "subtraction by B a 13 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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/clone="lmAGE:1555308"
/clone=lib="NLIGGAP_Kid3"
/lab_host="DHIOB"
/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       om99c07.s1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1555308 3' similar to TR:019048 019048 HNRNP-E1 PROTEIN. ;, mRNA sequence. AA975152.1 GI:3150944 EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 49)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Caneer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 12; DB 104;
Pred. No. 7.4e+04;
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High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ww-bio.llni.gov/bbrp/image/image.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2475032"
/clone_lib="NCI_CGAP_GC6"
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Seq primer: -40UP from Gibco
High quality sequence stop: 1
Location/Qualifiers
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75.0%;
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Best Local Similarity
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AA975152
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Rasborinae; Danio.

1 (bases I to 34)
Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hiller, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Rohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., Washu, Zebrafish EST Project 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AI657872 34 bp mRNA EST 06-MAY-1999 fc14f02.yl Zebrafish WashU MPIMG EST Danio rerio cDNA 5' similar to SW:T2D6_HUMAN Q15545 TRANSCRIPTION INITIATION FACTOR TFIID 55 KD
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double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. mRNA source: 2 pooled kidneys. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo.
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CDNA Library Preparation: Matthew Clark. CDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems. St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
Info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="26 somite embryos, adult livers, shield stage embryos"
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Fax: 314 286 1810
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Possible reversed clone: similarity on wrong strand
Seq primer: T3 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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/clone_lib="Zebrafish WashU MPIMG EST"
                                                                                                                                                                                                                                                                                                                                                      Score 12; DB 14; Le
Pred. No. 7.6e+04;
0; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1998)
Other_ESTs: fc14f02.x1
Contact: Stephen L. Johnson
Washington University School
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14 CAACAGGAGCATCTC 28
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double-stranded cDNA was ligated to Sal I adaptors (BRL), digested with Not I and cloned into the Not I and Sal I sites of the pSPORTI vector (BRL). Library was constructed by Matthew Clark (Lehrach lab; ICRF, London and Max Planck Institut fuer Molekulare Genetik, Berlin). CDNAs for EST analysis were selected following oligonuclectide hybridization fingerprinting of arrayed clones from zebrafish late somitogenesis (26 ss), adult liver or embryonic shield stage (5.6 h) libraries. Fingerprint data were used to computationally cluster cDNAs, and a single CDNA from each cluster was chosen for sequencing. In some cases multiple members of the same cluster were sequenced to assess clustering parameters or single clones were sequenced additional times to assess quality
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1 (bases 1 to 41)
Chen, H. M., Rossier, C., Chrast, R. and Antonarakis, S.E.
Cloning of trapped exons from human chromosome 21
(bases 1 to 41)
Antonarakis, S.E.
Antonarakis, S.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (17-MAR-1995) Stylianos E. Antonarakis, Division of
Medical Genetics, University and Cantonal Hospital of Geneva, CWU,
1 rue Michel-Servet, 1211 Geneva, SWITZERLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen, H., Chrast, R., Rossier, C., Morris, M.A., Lalioti, M.D. and Antonarakis, S.E. Cloning of 559 potential exons of genes of human chromosome 21 by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSMC04C05 41 bp DNA GSS 29-MAY-199
H.sapiens DNA for trapped exon (ID RMC04C05), genomic survey
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                                                                                                                                                                                                                                                                                                                                                                                   Score 11.8; DB 23; Length 34;
Pred. No. 9.1e+04;
0; Mismatches 2; Indels
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/db_xref="taxon:9606"
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97011340
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86.7%;
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8
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Best Local Similarity 86.7
Matches 13; Conservative
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Chen, H., Chrast, R.
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6 catcagtagcatete 20

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//delingst_b.coll Strain Allo Solu, il resistant, F. //note="Vector: PWAZIV; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Labotatory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil4732114 (pblA129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
University of Utah
WR. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Aslam, M., Longarers, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly M., Rose, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
AZ758330 46 bp DNA GSS 16-FEB-2001
1M0550115F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Mouse 10kb plasmid UUGCIM library"
/sex="Male"
/lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0550 row: I column: 15
                                                                       clone UUGC1M0550I15 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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/db_xref="taxon:10090"
/clone="UUGC1M0550115"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 46. Location/Qualifiers
                                                                                                                                           AZ758330.1 GI:12864016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 801 585 5606
Fax: 801 585 7177
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Mus musculus
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 49)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                    Waterston, R.
The WashU-HHMI Mouse EST Project
Unpublished (1994)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Possible reversed clone: similarity on wrong strand
Seq primer: -20ml3 rev1 Er from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Stratagene mouse lung 937302"
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Pred. No. 1.2e+05;
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  mRNA sequence.
AA087870
AA087870.1 GI:1631078
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Best Local Similarity 77.8%;
Matches 14; Conservative
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AI949145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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/db_xref="taxon:9606"
/clone="IMAGE:2401122"
/clone_lib="NCI_CGAP_Kid12"
/tlsue_type="2 pooled tumors (clear cell type)"
/lab_host="DH108"
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Pred. No. 9.6e+04;
0; Mismatches 2; Indels (
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ع.6e+04;
ع:
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86.7%;
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Unpublished (1997)
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Best Local Similarity 86.7
Matches 13; Conservative
4 gacatcagtagcate 18
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Gaps

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IMAGE:2470653 3'

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Email: buckler@helix.mgh.harvard.edu
                                                 Seq primer: T3.
    Fax: 6177265736
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A2769505
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                                                                                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note—Torgan: Kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCK-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1323912-1325831, 1471368-1472903 and H92104-1493255). Subtraction by Bento Soares and M. Fatima Bonaldo. "
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1 (bases 1 to 47)

Trofatter,J.A., Long,K.R., Murrell,J.R., Stotler,C.J., Gusella,J.F. and Buckler,A.J.

An expression-independent catalog of genes from human chromosome 22 denome Res. 5 (3), 214-224 (1995)
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CHR220319 Chromosome 22 exon Homo sapiens cDNA clone C22_405 5',
mRNA sequence.
H55380.1 GI:1108246
  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/db_xref="taxon:9606"
/clone="IMAGE:2470653"
/clone=lib="NCI_CGAP_Kid12"
/tlssue_type="2 pooled tumors (clear cell type)"
/lab_host="DH108"
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Pred. No. 1.2e+05;
0; Mismatches 4; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Molecular Neurogenetics Unit
Massachusetts General Hospital
Building 149, 13th St., Charlestown MA 02129
Tel: 6177249616
                                                                                                                                                                                                                                                                                                                             Trace considered overall poor quality Insert Length: 779 Std Error: 0.00 Seq primer: -40UP from Gibco High quality sequence stop: 1. Location/Qualifiers
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77.8%;
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Contact: Buckler AJ
                                        Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 77.8
Matches 14; Conservative
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AUTHORS
TITLE
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MEDLINE
COMMENT
                                                                 JOURNAL
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
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                                                                                       COMMENT
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H55380
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/organism="Homo sapiens"

/db_xref="taxon:9606"

/db="c22.405"

/clone="c22.405"

/clone="c22.405"

/lab_host="E. coli DH5a"

/note="Vector: pBluescriptIIKS+; Site_1: Sal I; Site_2: Bam HI (destroyed); Exons were isolated from human chromosome 22 specific cosmids using a modification of the method of exon amplification (Proc. Natl. Acad. Sci. USA 88:4005-4009, 1991). Amplified exons were digested with Sal I and Bgl II and subsequently cloned into pBluescriptIIKS+ at the Sal I and Bam HI sites:"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AZ769505 27 bp DNA GSS 16-FEB-2001
1M0570L17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
Lone UUGC1M0570L17 F, DNA sequence.
AZ769505 GI:12889709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone="UUGCIM0570L17"
/clone_"UUGCIM0570L17"
/clone_llb="mouse 10kb plasmid UUGCIM library"
/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.0%; Score 11.4; DB 158; Length 47; 92.3%; Pred. No. 1.5e+05;
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Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plate: 0570 row: L column: 17
Seg primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 27.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
Eukaryota; Metazoa; C
Mammalia; Eutheria; R
1 (bases 1 to 27)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12; Conservative
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/note-"Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia ) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
                                                                                                                                                                                                                                          T 3']; dobble-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into FNA Drovided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 31)
Dunn,D., Aoyaqi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 11.2; DB 17;
Pred. No. 1.8e+05;
0; Mismatches 3;
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                                   /tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
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t
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Insert Length: 10000 Std Error: C
Plate: 0452 row: P column: 14
Seg primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0452P14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
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Best Local Similarity 81.2%;
Matches 13; Conservative
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
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KEYWORDS
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musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AF129072.1), a copy-number inducable derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

I (bases 1 to 31)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,

Geisel,S., Kucaba,T., Lacy,M., Tan,M., Martin,J., Morris,M.,

Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,

Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A1174159 31 bp mRNA EST 07-OCT-1998 vz84e05.rl Soares_mammary_gland_NDMMG Mus musculus cDNA clone IMAGE:1333184 5' similar to SW:NUIM_MOUSE P03888 NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
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Contact: Marra M/Mouse EST Project
WashIn-HHI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fal: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 11.2; DB 249; Length 27;
Pred. No. 1.8e+05;
0; Mismatches 3; Indels 0:
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Possible reversed clone: similarity on wrong strand
Seq primer: -20ml3 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mouseest@watson.wustl.edu
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/db_xref="taxon:10090"
/clone="IMAGE:1333184"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56.0%;
81.2%;
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Best Local Similarity
Matches 13; Conserv
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δ q

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymerlectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114 [gilARL29072.1], a copy-number induible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into adaptors competent E. coll XL10-Gold (Stratagene) cells and selected for amplcillin resistance."
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ORIGIN
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ó Gaps ; 0 Query Match 56.0%; Score 11.2; DB 246; Length 31; Best Local Similarity 81.2%; Pred. No. 1.8e+05; Matches 13; Conservative 0; Mismatches 3; Indels 0;

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Search completed: October 2, 2001, 15:01:00 Job time: 10829 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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9b_htg16:*
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                                                           October 2, 2001, 15:56:47; Search time 3339.34 Seconds (without alignments) 92.640 Million cell updates/sec
                                                                                                                                                                                       423528
       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                    1344157 seqs, 7733874588 residues
                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                           OM nucleic - nucleic search, using sw model
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gb_htg8:* gb_htg9:* gb_htg10:*

Jb_htg7:

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b_htg1:

Searched:

Run on:

159963 Sequence 18
186044 Sequence 18
124249 Sequence 36
AX001078 Sequence
AR087980 Sequence
180198 Sequence
177110 Sequence 87

124249 AX001078 AR087980 180198 107710

AR016339 Sequence

AR016339 159963 186044

Length DB

Description

SUMMARIES

gb_pr7

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1 (bases 1 to 24)
Sheiness,D.K., Cangelosi,G.A. and Britschgi,T.B.
Nucleic acid probes useful for detecting microorganisms associated
with vaginal infections
Patent: US 5654418-A 18 05-AUG-1997;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 24)
Sheiness, D.K., Adams, T.H., Stamm, M.R., Cangelosi, G.A.,
Britschgi, T.B. and Dix, C.K.
Methods for selectively detecting microorganisms associated with
vaginal infections in complex blological samples
Patent: US 5700636-A 18 23-DEC-1997;
Location/Qualifiers
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                                 07-0CT-1997
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Pred. No. 1.8e+04;
0; Mismatches 2;
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Pred. No. 1.8e+04;
0; Mismatches 2;
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Sequence 18 from patent US 5700636.
186044
186044.1 GI:3205762
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                Sequence 18 from patent US 5654418.
159963.
159963.1 GI:2470rr.
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AR087948 Sequence
AR087956 Sequence
AR087974 Sequence
AR087978 Sequence
AR087978 Sequence
IR0116 Sequence
IR0116 Sequence 57
IR015 Sequence 57
IR0176 Sequence 65
IR0178 Sequence 65
IR0178 Sequence 65
IR0178 Sequence 65
IR0192 Sequence 67
IR0195 Sequence 83
IR0195 Sequence 83
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IR0195 Sequence 83
IR0196 Sequence 71
X74584 H.sapiens j
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A32693 Synthetic p
AX036877 Sequence
AX038887 Sequence
AR053527 Sequence
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Shelness, D.K., Addms,T.H., Stamm,M.R., Cangelosi,G.A.,
Britschgi,T.B. and Dix,C.K.
Diagnostic kits useful for selectively detecting microorganisms in
                                                                                                                                                                                                                                                                                                                                                                               AR009347 Sequence
AR060812 Sequence
I31591 Sequence 43
                                PCR primer
 A92270 Sequence 7
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AR083193 Sequence
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Pred. No. 1.8e+04;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent: US 5776694-A 18 07-JUL-1998;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 18 from patent US 5776694.
AR016339
AR016339.1 GI:3972616
                                                              AR087948
AR087958
AR087956
AR087976
AR087976
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88.2%;
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Best Local Similarity 88.2°
Matches 15; Conservative
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                                                                                                                                                                                                                                                            1 (bases 1 to 26)
Goh,S.Han, Chow,A.W. and Hemmingsen,S.
HSP-60 genomic locus and primers for species identification
Patent: US 5708160-A 87 13-JAN-1998;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 32)
Springer.T.A. and Larson,R.
The Alpha-subunit of the LFA-1 leukocyte adhesion receptor
Patent: EP 0362526-A2 15 11-APR-1990;
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            60.0%; Score 12; DB 9; Length 26;
75.0%; Pred. No. 1.6e+05;
Live 0; Mismatches 5; Indels
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Pred. No. 1.6e+05;
0; Mismatches 5; Indels
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Best Local Similarity 75.0%; Pred. No. 1.6e+05;
Matches 15; Conservative 0; Mismatches 5;
                                                                                                                                                       180198 26 bp DNA
Sequence 87 from patent US 5708160.
1180198 161:3208488
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                                                                                                                                                                                                                                                                                                                                                                          unidentified
unclassified.
1 (bases 1 to 34)
Sandig.V. and Loeser,P.
CLONING VECTORS FOR PRODUCING ADENOVIRAL MINIMAL VIRUSES
Patent: WO 9902647-A 3 21-JAN-1999;
HEPAVEC AG FUER GENTHERABLE (DE); SANDIG VOLKER (DE)
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Goh,S. Han, Chow,A. and Hemmingsen,S.
Universal targets for species identification
Patent: US 5989821-A 87 23-NOV-1999;
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                                                                                                                                                     Score 13.8; DB 10;
Pred. No. 1.7e+04;
0; Mismatches 2;
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Pred. No. 1.2e+05;
         1 (bases 1 to 30)
Gold, L. and Tasset, D.
DNA ligands of thrombin
Patent: US 5543293-A 36 06-AUG-1996;
Location/Qualifiers
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Sequence 87 from patent US 5989821.
AR087980
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Sequence 3 from Patent WO9902647..
AX001078
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/organism="unidentified"
/db_xref="taxon:32644"
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/organism="unknown"
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88.2%;
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Best Local Similarity 88.2
Matches 15; Conservative
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Best Local Similarity 82.4
Matches 14; Conservative
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(D3(TM4-del))-D3 dopamine receptor (3' region, alternatively spliced) [human, peripheral blood lymphocytes, mRNA Partial Mutant,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 45)
Nagal,Y., Ueno,S., Saeki,Y., Soga,F. and Yanagihara,T.
Expression of the D3 dopamine receptor gene and a novel variant transcript generated by alternative splicing in human peripheral blood lymphocytes
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PCR primer to detect polymorphism of Histamine H1 receptor gene.
E08846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="D3R"
/note="This sequence comes from Fig. 4; conceptual
translation presented here differs from translation in
publication"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GenBank staff at the National Library of Medicine created this entry [NCBI glubbsq 135517] from the original journal article. This sequence comes from Fig. 4.
Location/Qualifiers
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Shimizu,S., Shimazu,M., Habano,W. and Hayashi,T. .
HUMAN HISTAMINE H1 RECEPTOR GENE AND ITS UTILIZATION
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/db_xref="taxon:9606"
/cell_type="peripheral lymphocytes"
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/product="D3 dopamine receptor"
/protein_id="AAB27543.2"
/db_xref="G1:7704924"
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JP 1995067654-A/4.
unidentified.
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Best Local Similarity 75.0
Matches 15; Conservative
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E08846/c
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Jorgensen,J.L., Esser,U., de St Groth,B.F., Reay,P.A. and Davis,M.M.

Davis,M.M.

Immunization of single-chain transgenics
Nature 355 (6357), 224-230 (1992)
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/db_xref="taxon:10095"
<1. .>42
/jene="T-cell receptor beta chain V-J region"
/note="This sequence comes from FIG. 4 c; conceptual
translation presented here differs from translation in
publication"
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S77075 G1:242711
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/protein_id="AAB20961.2"
/db_xref="G1:9027588".
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                                                                                                                                Kajava, A. and Crameri, R. METHOD FOR THE OLIGOMERISATION OF PEPTIDES PATENT: WO 9818943-A 7 07-MAY-1998; CIBA GEIGY AG (CH).
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13 c 12 g 10 t
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/organism="unidentified"
/db_xref="taxon:32644"
a 14 c 13 g 4
Sequence 7 from Patent W09818943.
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A92270.1 GI:6741040
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Indels

Length 26;

Score 11.8; DB 9; Pred. No. 2.1e+05; 0; Mismatches 07-SEP-2000

PAT

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1 (bases 1 to 26)
Goh,S.Han, Chow,A. and Hemmingsen,S.
Universal targets for species identification
Patent: US 5989821-A 27 23-NOV-1999;
Location/Qualifiers
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Goh,S.Han, Chow,A. and Hemmingsen,S.
Universal targets for species identification
Patent: US 5989821-A 55 23-NOV-1999;
Location/Qualifiers
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Sequence 55 from patent US 5989821.
AR087948
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                                                                               /organism="unknown"
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86.7%;
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86.7%;
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                                       Artificial sequences.
JP 1995067654-A/4
JA-MAR-1993
03-SEP-1993 JP 1993219544
SHIMIZU SHOICHI, SHIMAZU MITSUNOBU, HABANO WATARU, PI
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                                                                                                                                                                                                    /organism='Artificial sequences'.
                                                                                                                                                                                                                                                                                                                      Score 11.8; DB 10; Length 20;
Pred. No. 2.2e+05;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 11.8; DB 9; Length 26;
Pred. No. 2.1e+05;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 26)
Goh,S. Han, Chow,A. and Hemmingsen,S.
Universal targets for species identification
Patent: US 5989821-A 5 23-NOV-1999;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAT
Patent: JP 1995067654-A 4 14-MAR-1995;
MITSUBISHI KAGAKU B C L:KK
OS None
OS Artificial sequences.
PN 1995067654-A/4
PD 14-MAR-1995
PI 14-MAR-1995
PI SHIMZU SHOICHI, SHIMAZU MITSUNOBU, B NIMZU SHOICHI, SHIMAZU MITSUNOBU, B C C12N15/09,C12Q1/68;
CC Strandedness: Single;
CC topology: Linear;
FH Key Location/Qualifiers
FT Source //organism='Artificia
                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AR087920 26 bp DNA
Sequence 27 from patent US 5989821.
AR087920 GI:10014683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AR087898 26 bp DNA
Sequence 5 from patent US 5989821.
AR087898
                                                                                                                                                                                                                              1. .20
/organism="unidentified"
/db_xref="taxon:32644"
                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AR087898.1 GI:10014661
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86.7%;
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Best Local Similarity 86.7
Matches 13; Conservative
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Unclassified.
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Unclassified.
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Best Local Similarity
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KEYWORDS
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KEYWORDS
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AR087898/C
LOCUS
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AR087920/c
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TITLE
JOURNAL
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ORIGIN
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                              COMMENT
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Gaps

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Indels

Length 26;

Score 11.8; DB 9; Pred. No. 2.1e+05; 0; Mismatches 2;

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New antisense compounds for inhibiting focal adhesion kinase expression, especially useful for inhibiting retinal neovascularization, or for diagnosing and treating e.g. colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Monia BP, Gaarde WA;
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Human focal adhesi
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                                                                                         (without alignments)
14.320 Million cell updates/sec
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                                                                          October 2, 2001, 16:18:41; Search time 876.95 Seconds
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Probe Gv003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /SIDSB/gcgdata/geneseq/geneseqn/NA1980. DAT: *
/SIDSB/gcgdata/geneseq/geneseqn/NA1981. DAT: *
/SIDSB/gcgdata/geneseq/geneseqn/NA1982. DAT: *
/SIDSB/gcgdata/geneseq/geneseqn/NA1983. DAT: *
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                     730101 seqs, 313950809 residues
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Maximum Match 100%
Listing first 45 summaries
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AAT89823
AAV36792
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AAF70762
AAZ40968
AAZ40969
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Match Length
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| Rho C antisense ph HMGCOA reductase t Extreme thermophil B-cell mRNA ribozy PCR Primer 378035 24-Hydroxylase gen Human T-cell recep C neoformans strai 24-Hydroxylase gen Potato dihydro-oro Probe for detectin Human ras oncogene Human ras oncogene Human fars I mRNA a PCR primer hymoRR Vector pMVX-BG oll: IGF: I oligonucleot Frimer for univers Untranslated regio | urin bindi istamine H us Yisi ho for univer for univer for univer for univer for univer |
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| AAF94689 AAC32833 AAC32833 AAC32833 AAC52003 AAV52003 AAV52003 AAV501423 AAT45956 AAV73114 AAC61223 AAC51105 AAC51105 AAC51105 AAC51106 AAC51106 AAC51106 AAC51106 AAC51106 AAC60649 AAC60649 | AAZ37033 AAQ87917 AAA71892 AAT69040 AAT69046 AAT68966 AAT68984 |
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ALIGNMENTS

Human; focal adhesion kinase; FAK; signal transduction; cancer; embryonic development disorder; angiogenic disorder; wound healing; antisense; phosphorothioate; ss. Human focal adhesion kinase antisense sequence #12. BP. 99US-0377310. 99US-0377310. AAC65546 standard; DNA; 20 (first entry) (ISIS-) ISIS PHARM INC ВР

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New flea protease genes and proteins - used in vaccine compositions for the prophylaxis and treatment of flea infestation, especially in cats or dogs
                                                                                                                                                                                                   Flea; Siphonaptera; protease; vaccine; prophylaxis; infestation; immunoglobulin protease; larvae; host animal; PCR primer; ss.
                                                                                                                                                                           Flea serine protease PCR primer SEQ ID NO:58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 23; Page 217; 318pp; English.
                                                                                                                                                                                                                                                                                                                                                            97US-0042945.
96US-0639075.
                                                                                                                                                                                                                                                                                                                                    97WO-US06121
                                                                                                                                                                                                                                                                                                                                                                                     960S-0749699
                                                                                           AAV20799 standard; DNA; 34
                                                                                                                                                 (first entry)
  3 ttagggatgqtqccq 17
                          1 ttagggatggtgccg 15
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaines PJ,
Stiegler GL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-076762/07
                                                                                                                                                                                                                                                                                                                                                                                                                 (HESK-) HESKA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                          Siphonaptera.
                                                                                                                                                                                                                                                                                                                                  24-APR-1997;
                                                                                                                                              02-JUL-1998
                                                                                                                                                                                                                                                                                  WO9740058-A1
                                                                                                                                                                                                                                                                                                                                                              04-APR-1997;
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15-NOV-1996;
                                                                                                                                                                                                                                                                                                           30-0CT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                          Frank GR,
Silver G,
                                                                                                                                                                                                                                          Synthetic.
                                                                                                                       AAV20799;
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                       The present invention describes a number of phosphorothioate antisense sequences to the human focal adhesion Kinase (FAK) protein. This protein is involved in integrin-mediated signal transduction, and is implicated in cancer, particularly colon, breast and oral tumours, embryonic development disorders, angiogenic disorders and wound healing. The antisense sequences, including the one shown here, can be used in the treatment of all of these.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a number of phosphorothioate antisense sequences to the human focal adhesion kinase (FAK) protein. This protein is involved in integrin-mediated signal transduction, and is implicated in cancer, particularly colon, breast and oral tumours, embryonic development disorders, anglogenic disorders and wound healing. The antisense sequences, including the one shown here, can be used in the treatment of all of these.
                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antisense compounds for inhibiting focal adhesion kinase expression, especially useful for inhibiting retinal neovascularization, or for diagnosing and treating e.g. colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                           Human; focal adhesion kinase; FAK; signal transduction; cancer; embryonic development disorder; anglogenic disorder; wound healing; antisense; phosphorothloate; ss.
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                                                                                                                                                                       100.0%; Score 20; DB 22; Length 20; 100.0%; Pred. No. 0.35;
                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                   ;
0
                                                                                                                                  Sequence 20 BP; 3 A; 3 C; 9 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 15 BP; 2 A; 2 C; 7 G; 4 T; 0 other;
                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; Column 25; 30pp; English
Claim 15; Column 23; 30pp; English.
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                                                                                                                                                                                                                            1 ggttagggatggtgccgtca 20
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                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 20; Conservative
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Grieve RB, Hunter SW, Rushlow KE;

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The present sequence represents a PCR primer for flea serine protease. The protease, its mimetopes, antibodies (Ab) and inhibitors of the protease, its mimetopes, antibodies (Ab) and inhibitors of the protease, its mimetopes, antibodies (Ab) and inhibitors of the protease as the DNA encoding the protease activity (especially improtease) and so reduce flea infestation, especially immunoglobulin protease) and so reduce flea infestation, especially in cats or dogs: Alternatively, flea larvae may ingest the faeces of adult in response to administration of the protein. Therapeutic compositions may further comprise a compound that reduces haematophagous ectoparasite in response to administration of the protein. Therapeutic compositions may further comprise a compound that reduces haematophagous ectoparasite activity. The novel flea DNA encoding the protein can also used to produce recombinant protein, and fragments of it are used as probes and primers for identification and isolation of related sequences, also as primers of the protein. Ab are also useful for screening expression libraries, to purify the protein and to target cytotoxins to fleas.
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Pred. No. 2.9e+02;
0: Mismatches 3;
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84.2%;
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Gaps

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Indels

0; Mismatches

Query Match 75.0%; Score 15; Best Local Similarity 100.0%; Pred. No. Matches 15; Conservative 0; Mismatch

Length 15;

DB 22; L 1.1e+02; 0

AAQ24636/

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The inventors claim a compsn. of at least one oligo probe for the detection of at least one microorganism found in vaginal samples. The sequence below is one such probe. The methods and compsns. can be used for the detection of microorganisms, partic. in vaginal fluid samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probe; hybridise; ribosomal RNA; vaginitis; infection; diagnostic; ribosomal RNA; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oligo:nucleotide probes for detecting microorganisms in vaginal samples - allows selective detection of vaginitis-causing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oligonucleotide probe GV003 specific for Gardnerella vaginalis.
                                                                                                                                                                     Detection of microorganisms, partic. in vaginal fluid samples by lysis of cells to release nucleic acid and hybridisation assays using probes
                                                                                             Sheiness DK;
                                                                                                                                                                                                                                                                                                                                                                                                           Score 13.8; DB 14;
Pred. No. 4.5e+02;
O; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                             Sequence 24 BP; 7 A; 7 C; 6 G; 4 T; 0 other;
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                                                                                           Cangelosi GA,
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                                                                                                                                                                                                                                   Claim 9; Page 42; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP.
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93WO-US05085.
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 69.0%;
Best Local Similarity 88.2%;
Matches 15; Conservative
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92US-0896094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BECT ) BECTON DICKINSON CO.
                               92US-0896094
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93US-0133598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
AAT89823/c
ID AAT89823 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Britschgi TB,
                                                            (MICR-) MICROPROBE CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
Gardnerella vaginalis.
                                                                                                                                       WPI; 1993-405847/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-401906/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Britschgi TB,
28-MAY-1993;
                               29-MAY-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-OCT-1990;
29-MAY-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US5654418-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-AUG-1997
                                                                                         Adams TH,
Stamm MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT89823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QQ
δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This oligonucleotide is one example of a probe suitable for diagnosing the presence of G.vaginalis. The preferred target for such probes is 16S rRNA, present in several thousand copies per coligonucleotides complementary to sequences in the G.vaginalis genome or in G.vaginalis plasmids may also be used.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probe; vaginal fluid microorganism; oligonucleotide; gram positive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence of probe GV003 for the detection of Gardnerella vaginalis
                                                                                                                                                      Dipstick; capture probe; 16S ribosomal RNA; vaginal infection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Detecting bacterial vaginitis infections - by contacting formed lysate with hybridisation soln. and dipstick comprising non-porous solid support and determining signal associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 13.8; DB 13;
Pred. No. 4.5e+02;
0; Mismatches 2;
                                                                                                                     Probe Gv003 specific for Gardnerella vaginalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 24 BP; 7 A; 7 C; 6 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 39; 62pp; English.
                             BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69.0%;
88.2%;
                                                                                                                                                                                                                                                                               91WO-US07763
                                                                                                                                                                                                                                                                                                              90US-0600334
                           AAQ24636 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAQ52752 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-JUN-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 ttagggatggtgccgtc 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15; Conservative
                                                                                                                                                                                                                                                                                                                                             (MICR-) MICROPROBE CORP
                                                                                                                                                                                                                                                                                                                                                                            Adams TH, Sheiness DK;
                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1992-167174/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                        05-NOV-1992
                                                                                                                                                                                                                                                                               21-OCT-1991;
                                                                                                                                                                                                                                                                                                              19-OCT-1990;
                                                                                                                                                                                                                 W09207096-A.
                                                                                                                                                                                                                                                30-APR-1992.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-DEC-1993
                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                          AAQ24636;
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RESULT 5 AAQ52752/c

Matches

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Gaps

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Length 24; Indels

Sequence 24 BP; 7 A; 7 C; 6 G; 4 T; 0 other;

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Sequences AAT89806-T89877 represent novel oligonucleotide probes which allow the detection of microorganisms associated with vaginal disorders e.g. Prevotella bylai, Prevotella melaninogenica, Gardnerella vaginalis, Trichomonas vaginalis, Mycoplasma hominis, Mobiluncus spp., Neisseria gonorrhoeae, Chlamydia trachomatis, Ureaplasma urealyticus, Neisseria gonorrhoeae, Chlamydia trachomatis, Ureaplasma urealyticus, microorganisms associated with vaginitis can be selectively detected using oligonucleotide probes specific for the organism and this can be incorporated into the design of diagnostic kits. These probes hybridise to regions of the ribosomal RNA with minimum secondary and tertiary interactions. Such hybridisation reactions do not require the additional step of heat denaturing the sample nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Probe; Gardnerella vaginalis; Candida albicans; Trichomonas vaginalis; dipstick; non-porous solid support; oligonucleotide-coated bead; vaginal disorder; hybridisation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This is the nucleotide sequence of the Gardnerella vaginalis probe used in the method of the invention which involves the production of Kits for simultaneously detection of Gardnerella vaginalis, Candida albicans and Trichomonas vaginalis, which comprised a dipstick with a non-prorus solid support having at least 3 capture oligonuclectide-coated beads attached to it. The kit can be used for detecting microorganisms associated with vaginal disorders.
                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Test kit for vaginal disorders - comprises dipstick with capture oligonucleotide-coated beads, specific for Gardnerella vaginalis. Candida albicans and Trichomonas vaginalis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sheiness DK;
                                                                                                                                                                                                                                                                            Length 24;
                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleotide sequence of the Gardnerella vaginalis GV003.
                                                                                                                                                                                                                                                                          Score 13.8; DB 18;
Pred. No. 4.5e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dix CK,
                                                                                                                                                                                                                           Sequence 24 BP; 7 A; 7 C; 6 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Britschgi TB, Cangelosi GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example; Column 32; 40pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP
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                                                                                                                                                                                                                                                                          69.0%;
88.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAV36792 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gardnerella vaginalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-398025/34.
                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US5776694-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-OCT-1990;
29-MAY-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Adams TH,
Stamm MR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequences given in AAT00202-25 and AAT00227-57 represent two groups of ligands to thrombin. These sequences were isolated using the single stranded DNA molecules given in AAT00201 and AAT00226 which comprise a 30N and a 60N variable region, respectively. These ligands were isolated using systematic evolution of ligands by exponential enrichment (SELEX). The selection was conducted in a buffer solution at 37 deg. C. After 12 rounds of selection, no additional improvement in binding was seen. By studying regions of homology between the isolated ligands, a truncated ligand of 38 nucleotides (see AAQ98403-04) was identified which retains high affinity binding and inhibits clotting. These ligands are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inhibitors of thrombin and are therefore useful in treating thrombin
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                 systematic evolution of ligands by exponential enrichment; SELEX; heparin; selection; region of homology; inhibitor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identification of ligands to basic fibroblast growth factor and thrombin - which can be modified for increased in vivo stability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mediated conditions and in studying the structure and binding of
                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
          24;
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           Length
                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
Score 13.8; DB 19;
Pred. No. 4.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 13.8; DB 16;
Pred. No. 4.6e+02;
O: Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 30 BP; 4 A; 1 C; 15 G; 10 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                   Family 1; family 2; ligand; thrombin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 39; Page 95; 236pp; English.
                                      ;
                                                                                                                                                                                                                                                        Thrombin DNA ligand, clone #14.
                                                                                                                                                                   BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Janjic N, Tasset D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94US-0195005.
90US-0536428.
91US-0714131.
93US-0061691.
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88.2%;
          69.0%;
88.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                             95WO-US01458
                                                                                                                                                                   AAT00210 standard; DNA; 30
                                                                                                                                                                                                                            (first entry)
                                                                3 ttagggatggtgccgtc 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NEXS-) NEXSTAR PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 88.2.
There is Conservative
          Query Match 69.0
Best Local Similarity 88.2
Matches 15; Conservative
                                                                                WPI; 1995-293073/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-FEB-1994;
11-JUN-1990;
10-JUN-1991;
                                                                                                                                                                                                                          14-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                      WO9521853-A1
                                                                                                                                                                                                                                                                                                                                                                                                                             06-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                  17-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-APR-1993
                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                               AAT00210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 thrombin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gold L,
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1 ggttagggatggtgccg 17

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Brooks DG;

Sasmor HM,

Freier SM, Vickers TA;

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A method has been developed of defining a set of compounds that modulate the expression of a target nucleic acid (tNA) sequence via binding of the compounds with the tNA sequence. The method comprises generating a library of virtual compounds in silico according to defined criteria, and evaluating in silico the binding of the virtual compounds with the tNA according to defined criteria. Also described are: (1) a method of defining a set of oligonuclectides (ONS) that modulate the expression of a tNA sequence via binding of the ONS with the tNA sequence comprising enerating a library of virtual compounds in silico according to defined criteria, and evaluating in silico the binding of the virtual ONS with the tNA according to defined criteria; and (2) a method of defining a set of compounds that modulate the expression of a tNA sequence via binding of the compounds with the tNA. The methods can be used for the generation and identification of synthetic compounds having defined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 physical, chemical or bioactive properties. Information gathered from assays of such compounds is used to identify nucleic acid sequences the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       are tractable to a variety of nucleotide sequence-based technologies, e.g. antisense drug discovery and target validation. AAZ40852 to AAZ41220, and AAX52701 to AAX52706, represent sequences used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying compounds which modulate expression of nucleic acids, us to provide compounds having defined physical, chemical or bioactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human RhoC phosphorothioate antisense oligonucleotide SEQ ID NO:121.
Identification; genetic target; gene modulation; human; probe; antisense oligonucleotide; phosphorothioate; PCR primer; nucleotide sequence-based technology; antisense drug discovery; target validation; sa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 13.4; DB 20;
Pred. No. 7e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 18 BP; 5 A; 8 C; 3 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 18; Page 96; 264pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   properties, e.g. antisense activity
                                                                                                                                                                                                                                                                                                                                                                                      , McNeil J,
Borchers AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAZ40969 standard; DNA; 18 BP.
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93.3%;
                                                                                                                                                                                                                                                                                     98US-0081483
98US-0067638
                                                                                                                                                                                                                                               99WO-US08268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-JAN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 67.0
Best Local Similarity 93.3
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                          Baker BF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wyatt JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-620446/53
                                                                                                                            Homo sapiens.
                                                                                                                                                               WO9953101-A1.
                                                                                                                                                                                                                                             13-APR-1999;
                                                                                                                                                                                                                                                                                     13-APR-1998;
                                                                                                                                                                                                                                                                                                          28-APR-1998;
                                                                                                                                                                                                       21-0CT-1999
                                                                                                                                                                                                                                                                                                                                                                                          Cowsert LM,
                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                             Ohasi C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAZ40969;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a purified and isolated non-naturally occurring DNA ligands to basic fibroblast growth factor (bFCF). The ligands are useful as part of gene therapy treatments and for diagnosing pathogenesis of vascular diseases including infitation and progression of atherosclerosis, acute coronary syndromes, vein graft disease and restenosis following coronary angloplasty. The ligands have improved stability in vivo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel nucleic acid ligands to basic fibroblast growth factor that are useful as inhibitors of basic fibroblast growth factors and 2'-amino modified RNA ligands, exhibit increased in vivo stability
                                                                                                                                                                                                                                                                                   Ligand; basic fibroblast growth factor; bFGF; gene therapy; vascular; atherosclerosis; angioplasty; stability; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human RhoC phosphorothioate antisense oligonucleotide SEQ ID NO:120.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 13.8; DB 22;
Pred. No. 4.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 30 BP; 4 A; 1 C; 15 G; 10 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 19; Column 57-58; 153pp; English.
                                                                                                                                                                                                                                           Thrombin high affinity ligand #9.
                                                                                                                       BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           910S-0714131.
920S-0973333.
940S-0195005.
940S-0219012.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gold L, Tasset D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69.0%;
88.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96US-0687421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90US-0536428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ40968 standard; DNA; 18
                                                                                                                   AAF70762 standard; DNA; 30
                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-JAN-2000 (first entry)
(NEXS-) NEXSTAR PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 88.2
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 ggttagggatggtagcg 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-158583/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-JUN-1991;
06-NOV-1992;
10-FEB-1994;
28-MAR-1994;
                                                                                                                                                                                                                                                                                                                                              Unidentified
                                                                                                                                                                                                                                                                                                                                                                                    US6177557-B1
                                                                                                                                                                                                   20-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                            23-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Janjic N,
                                                                                                                                                             AAF70762;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAZ40968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA240968/c
                                                                                                  AAF70762
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Length 18;

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WO200115739-A1.
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                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                   31-AUG-1999;
                                                                                                                                                                                                                     Roberts ML,
                                                                                                                 08-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAF94690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
   qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                               A method has been developed of defining a set of compounds that modulate the expression of a target nucleic acid (tMA) sequence via binding of the compounds with the tNA sequence. The method comprises generating a library of virtual compounds in silico according to defined criteria, and evaluating in silico the binding of the virtual compounds with the tNA according to defined criteria. Also described are: (1) a method of defining a set of oligonucleotides (ONS) that modulate the expression of a tNA sequence via binding of the ONS with the tNA sequence comprising generating a library of virtual compounds in silico according to defined criteria, and evaluating in silico the binding of the virtual ONS with the tNA according to defined criteria; and (2) a method of defining set of compounds that modulate the expression of a tNA sequence via binding of the compounds with the tNA. The methods can be used for the generation and identification of synthetic compounds having defined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              physical, chemical or bioactive properties. Information gathered from assays of such compounds is used to identify nucleic acid sequences that
                                                                                                                                                                                                                                                                                                           nseq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      are tractable to a variety of nucleotide sequence-based technologies, e.g. antisense drug discovery and target validation. AAZ40852 to AAZ41220, and AAX52701 to AAX52706, represent sequences used in the
                                                                                                                                                                                                                                             Sasmor HM, Brooks DG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                         Identifying compounds which modulate expression of nucleic acids, us to provide compounds having defined physical, chemical or bioactive properties, e.g. antisense activity
Identification; genetic target; gene modulation; human; probe; antisense oligonucleotide; phosphorothioate; PCR primer; nucleotide sequence-based technology; antisense drug discovery; target validation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rho C antisense phosphorothioate oligonucleotide SEQ ID 113.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67.0%; Score 13.4; DB 20; 93.3%; Pred. No. 7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                            Freier SM,
Vickers TA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18 BP; 6 A; 8 C; 3 G; 1 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                        Example 18; Page 96; 264pp; English.
                                                                                                                                                                                                                                           4, Baker BF, McNeil J,
Wyatt JR, Borchers AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAF94689 standard; DNA; 18 BP
                                                                                                                                                     99WO-US08268
                                                                                                                                                                            98US-0081483.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 67.0
Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                   (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 gttagggatggtgcc 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 GTTGGGGATGGTGCC
                                                                                                                                                                                                                                                                                 WPI; 1999-620446/53.
                                                                           Homo sapiens.
                                                                                                   WO9953101-A1
                                                                                                                                                     13-APR-1999;
                                                                                                                                                                            13-APR-1998;
28-APR-1998;
                                                                                                                            21-0CT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAY-2001
                                                                                                                                                                                                                                            Cowsert LM,
                                                            Synthetic.
                                                                                                                                                                                                                                                    Ohasi C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAF94689;
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Rho; GTP binding protein; phosphorothioate antisense oligonucleotide; RhoA; RhoB; RhoC; RhoC; Rac 1; cdc42; hyperproliferative condition; cancer; wound healing; clotting; ischaemia; reperfusion; reoxygenation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  An antisense compound targeted to a nucleic acid molecule encoding a member of the human Rho family of small GTP binding proteins useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rho; GTP binding protein; phosphorothioate antisense oligonucleotide; RhoA; RhoB; RhoC; RhoC; Rac 1; cdc42; hyperproliferative condition; cancer; wound healing; clotting; ischaemia; reperfusion; reoxygenation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rho C antisense phosphorothioate oligonucleotide SEQ ID 114.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67.0%; Score 13.4; DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ij
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18 BP; 5 A; 8 C; 3 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 16; Page 73; 156pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  treating e.g. cancer and ischaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP.
                                                                                                                                                                                                                                                                                                                                                                                                                               18-AUG-2000; 2000WO-US22808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0387341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-MAY-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 gttagggatggtgcc 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 GTTGGGGATGGTGCC
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oligonucleotides #1, #2 and #3 (AAZ22836-222838) to generate a four-way junction used to assay for any resolvase activity in an extreme thermophilic enzyme composition from Thermotoga maritima. Extreme thermophilic enzymes, such as TW-Endo V (from Thermotoga maritima) cleave at a mismatch formed between two polynucleotides in a duplex. It does not exhibit resolvase activity and does not require a GATC sequence to effect cleavage. TM-Endo V cleaves C/C G/G, T/C, A/A, and T/T mismatch. The enzyme does not cleave a perfectly complementary oligonucleotide pair (no mismatch), a T/G mismatch or a 3 base bubble. It
                                                                                              HWGCoA reductase is the enzyme which defines the rate limiting step in cholesterol biosynthesis. Expression of the gene may be prevented by the formation of a triplex between the duplex target DNA sequence and an anti parallel or parallel synthetic oligonucleotide. A suitable target sequence is the binding site for a repressor protein which appears to mediate end-prod. inhibition of transcription by cholesterol, from base -167 to -135 of HWGCoA reductase gene. Oligonucleotides targetted against this sequence will repress HWGCoA expression, and act as agonists of the cellular repressor. See also AAO36219-362.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated extreme thermophilic enzyme, which cleaves at a mismatch formed between two polynucleotides in a duplex \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermophilic; mismatch; cleavage; PCR; amplification; Taq polymerase; mutation; detection; pathogen; cancer; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence represents oligonucleotide #4 which was annealed to
Synthetic oligo-nucleotide(s), prodn. useful e.g. for HIV-1 inhibition - which bind to target sequence in duplex DNA forming colinear triplex by binding to major groove
                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Extreme thermophilic mismatch cleavage enzyme substrate oligo
                                                                                                                                                                                                                                                                                                                                                    Length 33;
                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                 Score 13.2; DB 14;
Pred. No. 9.3e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                              Sequence 33 BP; 3 A; 10 C; 13 G; 7 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    George AL;
                                                                 Example 9; Column 28; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 4; Fig 2; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP.
                                                                                                                                                                                                                                                                                                                                                   66.0%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US03274.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAZ22839 standard; DNA; 49
                                                                                                                                                                                                                                                                                                                                                                                                                      1 ggttagggatggtgccgt 18
||| || || |||||||| ||
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ggtgagagatggtgcggt 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-DEC-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chirikjian JG, Bazar LS,
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 83.3
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TREV-) TREVIGEN INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAZ22839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12
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                                                                                                                                                                                                                                                                                        This invention relates to an antisense compound targeted to a nucleic acid molecule encoding a member of the human Rho family of small GTP bidding proteins, where the antisense compound inhibits the expression of the member of the human Rho family. The invention includes antisense oligonucleotides AAF94580 - AAF94637 which target a RhoA nucleotide sequence, AAF94685 - AAF94684 which target a RhoC nucleotide sequence, AAF94759 which target a Rac 1 nucleotide sequence and AAF9476 - AAF94790 which target a Rac 1 nucleotide sequence and AAF94759 - AAF94809 which target a Rac 1 nucleotide sequence and AAF94755 - AAF94809 which target a Cdc42 nucleotide sequence. The antisense compound is useful for treating hyperproliferative conditions, especially cancer, abnormal wound healing or clotting conditions and ischaemia/reperfusion or recoxygenation injury. The compound may also be used to diagnose the above conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                        An antisense compound targeted to a nucleic acid molecule encoding a member of the human Rho family of small GTP binding proteins useful for treating e.g. cancer and ischaemia -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cholesterol; repressor protein; transcription; agonist; cellular;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 13.4; DB 22;
Pred. No. 7e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 18 BP; 6 A; 8 C; 3 G; 1 T; 0 other;
                                                                                                                                                                                                                                                             Example 16; Page 73; 156pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HMGCOA reductase target sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BAYU ) BAYLOR COLLEGE MEDICINE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67.0%;
93.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    triplex; target; duplex; ss
                18-AUG-2000; 2000WO-US22808
                                                   99US-0387341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 67.0
Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                      Roberts ML, Cowsert LM;
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                                                                                   (ISIS-) ISIS PHARM INC
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Gaps

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can be used to detect mutations in a target nucleotide or to detect the presence of a non-mutated sequence. In particular, the enzyme can be used for detecting mutations in HIV, sickle cell anaemia hypoxanthine transferase gene, and in genes associated with cancer e.g., p53 and BKCA1. TM-Endo V can be used to cleave mismatches that are created during polymerase, incorporates approximately one incorrect base per 500 bases, which is unacceptable if DNA greater than 500 bp is to be amplified. TM-Endo V cleaves at the mismatch, either on the template or the durther amplification. A chimera of an extreme thermophilic DNA polymerase and TM-Endo V can accomplish the dual roles of PCR plus correction of erroneous base incorporation.
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Sequence 49 BP; 13 A; 15 C; 12 G; 9 T; 0 other;

ö 0; Gaps Length 49; Score 13.2; DB 20; Length 4 Pred. No. 9.6e+02; 0; Mismatches 3; Indels Query Match
Best Local Similarity 83.3%;
Matches 15; Conservative

2 gttagggatggtgcgtc 19 ò

31 GTTAGGGCTCGTGCTGTC 14 g Search completed: October 2, 2001, 16:18:42 Job time: 15486 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts JOURNAL Unpublished (2000) COMMENT Contact: Robert B. Weiss University of Utah Genome Center | Paris 101 0010 Rm. 308, Biomedical Polymers Research Bidg., 20 S. 2030 E., SLC, UT 84112. USA Tel: 801 585 5606 Fax: 801 585 5177 Email: ddunn@qenetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0429 row: K column: 17 Seq primer: CACACACACACATATGACC Class: plasmid ends High quality sequence Stop: 27. Location/Oualifiers Source //Organism="Wus musculus" //Stram="C7BL/G7BL/G7" //Clone="UncC1M0429X17" //Lob.Date="E. Coll strain XLI0-Gold, T1-resistant, F-" //Ab.Date="UncC1M0429X17" //Clone="Uncc1" Publication Strain Strain Annowants/Anaresy) //Ab.Date="Uncc1" Publication Strain Strain Annowants/Anaresy) //Ab.Date="Uncc1" Publication Strain Annowants/Anaresy through a was hydrodynamically sheared by the sheared by was but end-repaired with T4 DBM polymnerase and T4 //Waw Jax.org/resources/documents/Annowa | damptored vector DNA, and transformed into chemically-competent E. coll XLIO-Gold (Stratagene) cells and selected for ampicillin resistance." BASE COUNT 5 a 9 c 6 g 7 t CORIGINA CORIGINA S A 10 CORIGINA S COURTY MATCH TI.0%; Score 14.2; DB 246; Length 27; Best Local Similarity 84.2%; Pred. No. 6.7e+03; Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0; | Oy 1 ggttagggatggtgcgtc 19 | RESULT 2 AZ592004 LOCUS AZ592004 LOCUS LOCUS MO402106R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0402H06 R. DNA sequence. ACCESSION AZ592004 VERSION AZ592004 AZ592004 AZ592004 CSS SOURCE Nouse mouse. ORGANISM Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus. REFERENCE 1 (bases 1 to 29) AUTHORS Dunn, D., Aoyagi, A., Barber, M., Meenen, E., Pedersen, T., Reilly M., Rose, M., Rose, R., Tingey, A., von Niederhausern, A. |
|---|--|--|--------------------------------|--|
| SUMMARIES Result Query No. Score Match Length DB ID | c 1 14.2 71.0 27 246 Az592004 Az5607381 IM0429K17 2 12.8 6.0 4 45 12.8 Az602041 IM04029K17 4 12.2 61.0 4.9 246 Az59204 Az6020311 Maccoll 100020K1 6 12.2 61.0 4.9 Az602031 Az602081 IM0429K17 7 12.2 61.0 4.9 Az760994 Az601048 Az601148 6 12. 60.0 2.4 Az760007 Az760007 Az760007 11.8 59.0 37 24.9 Az760007 Az760007 Az760007 11.8 59.0 30.7 Az1345513 Az760007 Az760007 Az760007 11.0 51.0 41.1 51.0 Az100007 Az100000 Az100000 Az100000 11.1 58.0 40.7 Az100000 Az1000000 Az100000 Az1000000 Az1000000 Az1000000 Az1000000 Az1000000 | 37 11 55.0 50 107 AU103102 AU303102 38 11 55.0 50 107 AU106713 AU106713 39 10.8 54.0 21 247 AZ399828 AZ399828 40 10.8 54.0 22 247 AZ647408 AZ647408 41 10.8 54.0 30 250 AZ833673 AZ647408 43 10.8 54.0 34 10 AG655488 AA6655488 43 10.8 54.0 40 258 TA130E05P AL464109 45 10.8 54.0 42 188 R97402 R97402 | ALIGNMENTS | AZ607381/C LOCUS LOCUS MO429K17R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0429K17 R, DNA sequence. ACCESSION AZ607381.1 GI:11729571 AZ607381.1 GI:11729571 GSS. SOURCE OKGANISM Mus musculus Eukaryota: Marmalia: Butheria; Rodentia; Sciurognathi; Muridae; Mus. REFERENCE Dun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. |

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Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 12.8; DB 1;
Pred. No. 3.4e+04;
0; Mismatches 2;
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Trace considered overall poor quality
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                                                                                               The WashU-HHMI Mouse EST Project
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High quality sequence stop: 1.
Location/Qualifiers
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Best Local Similarity 87.5%;
Matches 14; Conservative
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                                                                            Waterston, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (qil4732114(pblAF129072.1), a copy-number inducible derivative of plasmid Rl. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-GOld (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                           Rm.\ 308 , Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112 , USA
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="E. Coli strain XLI0-Gold, Tl-resistant, F-" /note="Vector: PW042nv; Purified genomic DNA from M. musculus G57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA009110 45 bp mRNA EST 26-JUL-1996 mg92g09.rl Soares mouse embryo NbME13.5 14.5 Mus musculus CDNA clone IMAGE:446512 5' similar to gb:X05021 Murine mRNA with homology to yeast L29 ribosomal protein (MOUSE);, mRNA sequence.AA009110
                      Mouse whole genome scaffolding with paired end reads from 10kb
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIM0402H06"
/clone_lib-"Mouse 10kb plasmid UUGCIM library"
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                                                                                                                                                                                                                                                             Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0402 row: H column: 06
                                                                                                                                                                                                                                                                                                                             Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 29.
Location/Qualifiers
                                                                                                              University of Utah Genome Center
University of Utah
                                                                    Unpublished (2000)
Contact: Robert B. Weiss
Wright, D., Weiss, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="Male
                                                                                                                                                                                                            Tel: 801 585 5606
Fax: 801 585 7177
                                              plasmid inserts
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 27)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacres,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly

M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AZ607381 27 bp DNA GSS 13-DEC-2000
1M0429K17R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0429K17 R, DNA sequence.
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashurHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="IMAGE:440512"
/clone_lib="Soares mouse embryo NDME13.5 14.5"
/sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 45;
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Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
                        Waterston, R.
The WashU-HHMI Mouse EST Project
Unpublished (1986)
Contact: Marra M/Mouse EST Project
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashU-HHMI Mouse EST Project
WashU-HHMI Mouse EST Project
WashU-HMI Mouse EST Project
WashU-HMI Mouse EST Project
Fast 144 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:520583
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Knowles Solter mouse inner cell mass"
/dev_stage="embryo (post-implantation)"
/lab_host="DH10B"
              Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/strain="B6D2 F1/J"
/db_xref="taxon:10090"
/clone="IMAGE:892623"
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5066
Fax: 801 585 7177
Email: ddunn@qenetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 042 row: K column: 17
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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Mus musculus musculus substance substance mouse.

Mus musculus substance s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIM0429K17"
/clone="UUGCIM0429K17"
/clone="UuGCIM0429K17"
/clone="UuGCIM0429K17"
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AA501145.1 GI:2236112
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Best Local Similarity 82.4
Matches 14; Conservative
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(http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with 74 DNA polymerase and 74 polymerase at a polymerase and 74 polymerase to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarcse gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gild/32114 gblaka129072.1), a copy-number inducible derivative of plasmid Rl. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
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84112, USA
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1M0553C23F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC1M0553C23 F, DNA sequence.
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Mouse whole genome scaffolding with paired end reads from 10kb
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Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                  /sex="Male"
/lab_host="E. Coli strain XLIO-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                         /organism="Mus musculus"
/strain="057BL/64"
/db_xref="taxon:10090"
/clone="UGCIMO571A14"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 47;
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100.0%; Pred. No. 8.3e+04;
ive 0; Mismatches 0;
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0571 row: A column: 14
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
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University of Utah Genome Center
University of Utah
                                                                                                                                               High quality sequence stop: 47
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Matches 12; Conservative
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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1M0571A14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0571A14 F, DNA sequence.
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                                                                                                                                                                                                                                                                                                                                        /sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC.
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75.0%; Pred. No. 8e+04;
Live 0; Mismatches
                             Plate: 0220 row: K column: 22
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                              /organism-"Mus musculus"
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/db_xref="taxon:10090"
/clone="UUGC1M0220K22"
                                                                                                               High quality sequence stop: 23.
                                                                                                                                            Location/Qualifiers
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Fax: 801 585 7177
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Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries Contact: Yutaka Suzuki
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Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedal, Minatoku, Tokyo 108-8639, Japan
Email: ysuzukiéins.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
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AU103569 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
CASO0968, mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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Pred. No. 1e+05;
0; Mismatches 2; Indels 0
                 Email: ddunn@genetics.utah.edu
Insert Lenqth: 10000 Std Error: 0.00
Plate: 0553 row: C column: 23
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 37.
Location/Qualifiers
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0553C23"
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86.7%;
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Fax: 801 585 7177
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997). Location/Qualifiers
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1M0080J04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0080J04 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Welss, R.
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                sapiens cDNA library"
10 t
                                                                                                                                                                                                                                                                                                                                                            Score 11.8; DB 107; Length 50; Pred. No. 1e+05; 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 801 585 5606
Fax: 801 585 7177
Brall: ddnnn@qentics.utah.edu
Insert Length: 10000 Std Brror: 0.00
                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CAS00968"
/clone="CAS00968"
a 14 c 22 9 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: CGTTGTAAAACGACGGCCAGT Class: plasmid ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/db_xref="taxon:10090"
/clone="UUGC1M0080J04"
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Best Local Similarity 86.7%;
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              row: J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 gggatggtgccgtca 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39 GGGATGCTGCCGACA 25
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1 (bases 1 to 41)
Hiliar, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston X., Williamson, A., Wohldmann, P. and Wilson, R.
The Wash-Werck EST Project
Unpublished (1995)
                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality
Seq primer: Promega -21ml3
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                    H84363 41 bp mRNA EST 13-NOV-1995 yv85c09.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:249520 3' similar to gb:L06505 60S RIBOSOMAL PROTEIN L12 (HUWAN); , mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58.0%; Score 11.6; DB 158; Length 41; 77.8%; Pred. No. 1.3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_"IMAGE:249520"
/clone_lib="Soares melanocyte 2NbHM"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4
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/db_xref="GDB:3867226"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: est@watson.wustl.edu
                                                                                                                                                                                                                                           H84363.1 GI:1063034
    2 gttagggatggtgccgtc 19
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H84363/c
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KEYWORDS
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electrophoresis. Vector DNA was prepared from a derivative electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114[gb]AF129072.1), a coopy-number inductble derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into adaptoretent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A1188838 40 bp mRNA EST 13-OCT-1998 401112.x. Soarses_placenta_Eto9weeks_2NbHP8tc9W Homo sapiens cDNA clone IMAGE:1774399 3' similar to SW:EXTN_TOBAC P13983 EXTENSIN PRECURSOR; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; In Bases 1 to 40)

NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumor Gene Index
Unpublished (1997)
Contact: Roberts Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: -40Up from Gibco
High quality sequence stop: 1.
Location/Qualifiers
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                                                                                                                                                                                                                                                         Score 11.6; DB 242; Length 20; Pred. No. 1.2e+05;
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ilarity 77.8%; Pred. No. 1.3e+05;
Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                   0; Mismatches
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                                                                                                                                                                                                                                                            58.0%;
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Matches 14; Conservative
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Best Local Similarity
Matches 14; Conserv
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AUTHORS
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Gaps

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Indels

DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS

JOURNAL

COMMENT

TITLE

AZ399400/c

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 21)

S Dunn,D., Aoyaqi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Menen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Waiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 94112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunnegenetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0031 row: L. column: 23
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                 AZ786429 21 bp DNA GSS 16-FEB-2001
2M0031L23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0031L23 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/strain="c57BL/64"
/db_xref="taxon:10090"
/db_cref="taxon:10090"
/clone="UGGC2M0031L23"
/clone=lib="Mouse 10kb plasmid UGGIM library"
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Pred. No. 1.6e+05;
0; Mismatches 1; Indels 0;
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Location/Qualifiers
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ilarity 92.3%;
Conservative (
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                                                                                                                                                                                                                  house mouse.
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Best Local Similarity
Matches 12; Conserv
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                      RESULT 1.
AZ786429
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/60 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114) [plARL29072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the linsert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. B. (Dases 1 to 21)

E. (Dases 1 to 21)

E. (Dases 1 to 21)

B. (Dases 1 to 21)

S. (Ban, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Stoke, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

I. (Dupublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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AZ399400 21 bp DNA GSS 03-OCT-2000 1M0165C13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0165C13 F, DNA sequence.
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGGCIM0165C13"
/clone=lib="Mouse 10kb plasmid UUGCIM library"
/sex="Male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0165 row: c column: 13
Seg primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Class: plasmid ends
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
                                                                                                                                       AZ399400.1 GI:10514474
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92.3%;
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Fax: 801 585 7177
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Matches 12; Conserv
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FEATURES

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### 84112, USA
Tel: 801 585 5606
Fax: 801 585 56
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University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
                                                         AZ822907 38 bp DNA GSS 20-FEB-2001
ZM0096M03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0096M03 R, DNA sequence.
AZ822907.1 GI:12992815
                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 30)
Lunn,D., Aoyaqi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly, M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. Mouse whole genome scaffolding with paired end reads from 10kb Unbublished (2000)
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house mouse.
RESULT 15
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DEFINITION
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AUTHORS
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ORIGIN
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KEYWORDS
SOURCE
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Query Match 57.0 Best Local Similarity 92.3 Matches 12; Conservative

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Search completed: October 2, 2001, 15:01:02 Job time: 10831 sec

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9.071 Million cell updates/sec
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l to the score of the result being printed,
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Sequence 224, Sequence 11, A
Sequence 11, A
Sequence 11, A
Sequence 12, A
Sequence 339, A
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/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
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Compugen Ltd.
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US-09-377-310-34

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US-08-140-18

US-08-140-18

US-08-160-999-18

US-08-150-12

US-09-156-807-11

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                                                                                                                                                                   hits satisfying chosen parameters:
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GenCore version
(c) 1993 - 2000
                                                   2001, 16:03:50
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Maximum Match 100%
Listing first 45 summaries
                                  - nucleic search, using sw model
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Maximum DB seq length: 50
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Fatent NO. 6133031
GENERAL INFORMATION:
APPLICANT: Monia, Brett P.
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
TITLE OF INVENTION: WHERE: US/09/377,310B
CURRENT APPLICATION UNMBER: US/09/377,310B
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SEQ ID NOS: 43
LENGTH: 15
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Patent No. 6133031
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Monia, Brett P.
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0389
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
            Sequence
                       Sequence
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Pred. No. 0.072;
Mismatches 0; Indels
                            US-09-003-067-81
US-09-003-067-83
US-08-09-003-067-83
US-08-219-012-50
US-08-619-012-50
US-08-619-012-50
US-08-619-012-50
US-08-619-998-709
US-08-859-998-709
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US-08-811-492-113
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US-08-418-613-43
US-09-003-067-55
US-09-003-067-65
US-09-003-067-67
                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: antisense sequence US-09-377-310-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20; Conservative
  Query Match
Best Local Similarity
 RESULT 2
US-09-377-310-34
                                                                                                                                                                                                                                              US-09-377-310-14
                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 14
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
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FLEA PROTEASE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
                               APPLICANT: Wu Hunter, Shirley
APPLICANT: Stiegler, Gary
APPLICANT: Stiegler, Gary
APPLICANT: Gaines, Patrick J.
TITLE OF INVENTION: FLEA PROTEASE PROTEINS,
TITLE OF INVENTION: MOLECULES AND USES THERE
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 58:
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84.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear; MOLECULE TYPE: DNA (primer)
US-08-749-699-58
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Best Local Similarity 84.2
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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ADDRESSEE: Townsend
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: sing
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                                                                                                                                                                                                                Colorado
: USA
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                      GENERAL INFORMATION:
                                                                                                                                                                                                 CITY: Denver
   Patent No. 6210920
                                                                                                                                                                                                                             COUNTRY: US
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US-08-460-344-18/c
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                                                                                                                                                                                                                                                                                                                                                                                          NUCLEIC ACID
                                                                                      DB 3; Length 15; 25;
                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,731
                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wu Hunter, Shirley
APPLICANT: Stiegler, Gary
APPLICANT: Gaines, Patrick J.
TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCTITLE OF INVENTION: MOLECULES AND USES THEREOF
                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 71;
0; Mismatches
                                                                                      Score 15;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REGISTRATION NUMBER: 2618-25-C3
TELECOMMUNICATION:
TELEPHONE: (303).863-9700
                ; OTHER INFORMATION: antisense sequence US-09-377-310-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                   Sequence 58, Application US/09004731 Patent No. 6177258 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-749-699-58; Sequence 58, Application US/08749699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                      75.0%;
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs
                                                                                   Query Match 75.0
Best Local Similarity 100.
Matches 15; Conservative
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Matches 16; Conservative
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STRANDEDNESS: single
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: USA
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: 11;
; MOLECULE TYPE:
US-09-004-731-58
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COUNTRY:
                                                                                                                                                                                                                                                                    .09-004-731-58
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FEATURE:
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Patent No. 56544

GENERAL INFORMATION:
APPLICANT: SHEINESS, Diana K.
APPLICANT: STAMM, Michael R.
APPLICANT: CANGELOSI, Gerard A.
APPLICANT: CANGELOSI, Theresa B.
APPLICANT: DIX, CONNIE K.
TITLE OF INVENTION: METHODS AND DIAGNOSTIC KITS USEFUL FOR
TITLE OF INVENTION: INFECTING MICROORGANISMS ASSOCIATED WITH VAGINAL
TITLE OF INVENTION: INFECTIONS
NUMBER OF SEQUENCES: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/749,699 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 14.2;
                                                                                                                                                                    CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-25-C3
TELECOMMUNICATION INFORMATION:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: ADAMS, Trevor H.
APPLICANT: STAMM, Michael R.
APPLICANT: STAMM, Michael R.
APPLICANT: GANGELOSI, Gerard A.
APPLICANT: DIX, Connie K.
APPLICANT: DIX, Connie K.
TITLE OF INVENTION: DETECTING MICROORGANISMS ASSOCIATED WITH VAGINAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 13.8; DB 1; Length 2
Pred. No. 1.1e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/886,999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature

: LOCATION: 1.24

: OTHER INFORMATION: /standard_name= "GV003"

US-08-133-598A-18
                    APPLICATION NUMBER: US/08/133,598A
FILING DATE: 08-0CT-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATE: CS-0MAY:
APPLICATION NUMBER: US 07/896,094
FILING DATE: 29-MAY-1992
PRIOR APPLICATION DATE: 29-MAY-1990
ATTORNER, DATE: 19-0CT-1990
ATTORNER, AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia REGISTRENCE/DOCKET NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 11652-73-2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEG ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/458,319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 18, Application US/08886999
Patent No. 5776694
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ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: SHEINESS, Diana K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69.0%;
88.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 ttagggatggtgccgtc 19
     CURRENT APPLICATION DATA:
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Best Local Similarity 88.2
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC OPERATING SYSTEM: SOFTWARE: Patent1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
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US-08-886-999-18/C
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APPLICANT: ADAMS, Trevor H.
APPLICANT: STAMM, Michael R.
APPLICANT: STAMM, Michael R.
APPLICANT: CANGELOSI: Gerard A.
APPLICANT: CANGELOSI: Grand A.
APPLICANT: DIX, Connie K.
TITLE OF INVENTION: METHODS AND DIAGNOSTIC KITS USEFUL FOR
TITLE OF INVENTION: DETECTING MICROORGANISMS ASSOCIATED WITH VAGINAL
TITLE OF INVENTION: INPECTIONS
NUMBER OF SEQUENCES: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US/08/460,344 FILING DATE: 02-JUN-1995 CLASSIFICATION: 536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 13.8; DB 1;
Pred. No. 1.1e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION: 1..24
; OTHER INFORMATION: /standard_name= "GV003"
US-08-460-344-18
                                                                                                                                                                                CLASSIFICATION: 330
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,598
FILING DATE: 08-007-1993
APPLICATION NUMBER: US 07/896,094
FILING DATE: 29-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/600,334
APPLICATION NUMBER: US 07/600,334
FILING DATE: 19-007-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 11652-73-2
TELECOMMUNICATION INFORMATION:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-133-598A-18/c
; Sequence 18, Application US/08133598A
Patent No. 5700636
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PC-DOS/MS-DOS
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: PatentIn Release #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (415) 543-9600
TELERAX: (415) 543-5643
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARATERISTICS:
LENGTH: 24 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69.0%;
88.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 69.0
Best Local Similarity 88.2
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94105-1493
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Fatent No. 5543293
GENERAL INFORMATION:
APPLICANT: Larry Gold
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 92
CORRESPONDENCE ADDRESS:
ADDRESSEE: Beaton & Swanson, P.C.
STREET: 4582 South Ulster Street Parkway, Suite #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPOTER READABLE FORM:

WIDDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordberfect 5.1

SOFTWARE: Wordberfect 5.1

APPLICATION DATA:

APPLICATION NUMBER: US/08/219,012
                                                                                                                                                                    Score 13.8; DB 5;
Pred. No. 1.1e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 13.8; DB 1;
Pred. No. 1.1e+02;
0; Mismatches 2;
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; Patent No. 6177557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA: none
ATORNEY/AGENT INFORMATION:
AMME: BALTY J. SWANSON
REGISTRATION NUMBER: 33,215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 850-9900
                                         linear
E: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (303) 850-9900
TELEFAX: (303) 850-9401
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                    69.0%;
88.2%;
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                                                                                                                                                                      Query Match 69.0
Best Local Similarity 88.2
Matches 15; Conservative
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Best Local Similarity 88.2
Matches 15; Conservative
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                                                                                                                                                                                                                                                                               18 TTTGGGATGGAGCCGTC 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 30 base pairs
nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Denver
: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                           ; TOPOLOGY: line; MOLECULE TYPE: I; HYPOTHETICAL: NCPCT-US93-05085-18
                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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US-08-687-421-224
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US-08-219-012-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: CC
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY:
US-08-219-012-36
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TITLE OF INVENTION: METHODS AND PHARMACEUTICAL KITS USEFUL
TITLE OF INVENTION: POR DETECTING MICROORGANISMS ASSOCIATED WITH VAGINAL
TITLE OF INVENTION: INFECTIONS
NUMBER OF SEQUENCES: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 13.8; DB 1; Length 24; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: Steuart Street Tower, One Market Plaza CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: 1..24
OTHER INFORMATION: /standard_name= "GV003"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                   FILING DATE: 08-007-1993
APPLICATION NUMBER: US 07/896,094
FILING DATE: 29-MAY-1992
PRIOR APPLICATION NUMBER: US 07/806,034
FILING DATE: 19-007-1990
APPLICATION NUMBER: US 07/600,334
FILING DATE: 19-007-1990
ATTORNEY AGENT INFORMATION:
NAME: GALFELT-WACKOWSKI, EUGENIA
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 11652-73-2
TELECHONE: (415) 543-9600
TELECHONE: (415) 543-9600
TELECHONE: (415) 543-9600
TELECHONE: (415) 543-9600
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDENRESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US93/05085 FILING DATE: 28-MAY-1993
                   JMBER: US 08/133,598
08-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCT-US93-05085-18/c
; Sequence 18, Application PC/TUS9305085
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,762
REFERENCE/POCKET NUMBER: 1165:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69.0%;
88.2%;
02-JUN-1995
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Best Local Similarity 88.2
Matches 15; Conservative
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                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA
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Gaps

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Sequence 339, Application US/08961083
Patent No. 6159469
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                  Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: COWSET, LEX M.
TITLE OF INVENTOR: ANTISENSE MODULATION OF RhOC EXPRESSION
FILE REFERENCE: RTS-0014
CURRENT APPLICATION NUMBER: US/09/156,807
CURRENT FILING DATE: 1998-09-18
NUMBER OF SEQ ID NOS: 47
TITLE OF INVENTION: ANTISENSE MODULATION OF RhoC EXPRESSION
                                                                                                                                                                                                                                                                                                                                       Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATION SYSTEM: MSDOS Version 6.2
                                                                                                                                                                                                                                                                                             Score 13.4; DB 3;
Pred. No. 1.7e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 13.4; DB 3;
Pred. No. 1.7e+02;
0; Mismatches 1;
                                                                                                                                                                                          ; FEATURE:
... OTHER INFORMATION: Antisense Oligonucleotide
US-09-1156-807-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Antisense Oligonucleotide US-09-156-807-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Human Genome Sciences, Inc. STREEF: 9410 Key West Avenue CITY: Rockville STATE: Maryland
                                   CURRENT APPLICATION NUMBER: US/09/156,807
CURRENT FILING DATE: 1998-09-18
NUMBER OF SEQ ID NOS: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12, Application US/09156807 Patent No. 6030786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67.0%;
93.3%;
                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                             Query Match 67.0%;
Best Local Similarity 93.3%;
Matches 14; Conservative
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Matches 14; Conservative
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                     FILE REFERENCE: RTS-0014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-961-083-339/c
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US-09-156-807-12/c
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                                                                                                       SEQ ID NO 11
LENGTH: 18
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LENGTH: 18
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                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage COMPUTER: TBM compatible OPERATING SYSTEM: MS-DOS SOFTWARE: WordPerfect 6.0 CURRENT APPLICATION DATA:
FILING DATE: 08-MAY-1996
CLASSIFICATION: 435
                                   APPLICANT: Janjic, Nebojsa
PEDLICANT: Tarsset, Diane
TITLE OF INVENTION: HIGH-AFFINITY LIGANDS OF BASIC
TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR AND
NUMBER OF SEQUENCES: 445
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 13.8; DB 4;
Pred. No. 1.1e+02;
0; Mismatches 2;
                                                                                                                                                                               ADDRESSEE: Swanson & Bratschun, L.L.C. STREET: 8400 E. Prentice Avenue, Suite 200 CITY: Englewood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEX07/PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 07/973,333
FILING DATE: 11-NOVEMBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Sequence 11, Application US/09156807
; Sequence 11, Application US/09156807
; Patent No. 6030786
; GENERAL INFORMATION:
; APPLICANT: COWSert, Lex M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/195,005
FILING DATE: 10.FEBRUARY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 22-APRIL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/219,012
FILING DATE: 28-MARCH-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (303) 793-3333
TELERAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 224:
SEQUENCE CHARACTERISTICS:
LENGHH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NE:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69.0%;
88.2%;
                   : Gold, Larry
: Janjic, Nebojsa
: Tasset, Diane
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Best Local Similarity
Matches 15; Conserv
GENERAL INFORMATION:
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US-09-418-641-75
Sequence 75.
Sequence 75.
Sequence 75.
Patent No. 6124133
GENERAL INFORMATION:
APPLICANT: Jennifer K. Taylor
TITLE OF INVENTION: ANTISENSE MODULATION OF FRA-1 EXPRESSION
FILE REPERBERE: FYS-0105
CURRENT FILING DATE: 1999-10-15
CURRENT FILING DATE: 1999-10-15
SEQ ID NO 75
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
63.0%; Score 12.6; DB 3; Length 37;
Best Local Similarity 78.9%; Pred. No. 4.7e+02;
Matches 15; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 12.6; DB 6; Length 50;
Pred. No. 4.9e+02;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: MUTATED STREPTOKINASE PROTEINS
APPLICATION NUMBER: US/08/961,083
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTARATION NUMBER: 86,33
REFERENCE/DOCKET NUMBER: PB340P2
TELECOMMUNICATION INFORMATION:
TELEPHORE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 339:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 base pairs
TYPE: nucleic acid
STRANDENNES: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 65
CURREWY APPLICATION DATA:
APPLICATION NUMBER: US/07/549,049
FILING DATE: 06-JUL-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63.0%;
78.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 gttagggatggtgccgtca 20
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Best Local Similarity 78.9
Matches 15; Conservative
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5240845-45
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US-08-961-083-339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;SEQ ID NO:45:
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                                                         Length 20;
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                                                        Score 12.2; DB 3;
Pred. No. 6.9e+02;
0; Mismatches 3;
; OTHER INFORMATION: Antisense Oligonucleotide US-09-418-641-75
                                                                                                                                                                                                          Search completed: October 2, 2001, 16:03:50 Job time: 14594 sec
                                                      Ouery Match 61.0%;
Best Local Similarity 82.4%;
Matches 14; Conservative
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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9b_htg12::#
9b_htg12::#
9b_htg12::#
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Match Length DB
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gb_sts1:*
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9b_ht91::*
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Score
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                                                         2, 2001, 15:56:48; Search time 3339.34 Seconds (without alignments) 92.640 Million cell updates/sec
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        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                            1344157 seqs, 7733874588 residues
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Maximum Match 100%
Listing first 45 summaries
                                          OM nucleic - nucleic search, using sw model
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em_htg_hum7:*
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em_hum1:*
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em_hum7:*
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em_om:*
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Maximum DB seq length: 50
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Perfect score:
Sequence:
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109246 Sequence 12 109244 Sequence 10 109247 Sequence 13 AR109705 Sequence A56687 Sequence 6 E03267 Primer for AX023416 Sequence AX052544 Sequence

109246 109244 109247 AR109705 A56687 E05267 AX023416

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Description

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SUMMARIES

| RESULT 2 109244/c LOCAL | Query Match Best Local Similarity 80.0%; Score 13.6; DB 10; Length 37; Best Local Similarity 80.0%; Pred. No. 8.1e+03; Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps Qy 1 tgttggttccaatcggacc 20 Qy 1 tgttggttccaatcggacc 20 Db 28 TgTTGGATTCCAGCAGGACC 9 | RESULT 3 109247 LOCUS LOCUS LOCUS DEFINITION Sequence 13 from Patent WO 8901940. ACCESSION 109247 VERSION 109247.1 GI:588031 KEYWORDS COIDCE COLORDOR COLORD | Unknown. Unclassified. Unclassified. Unclassified. I (bases 1 to 38) Fisher,R.A., Glibert,W., Sato,V.L., and Liu,T.R. DNA SEQUENCES, RECOMBINANT DNA MOLE PRODUCING SOLUBLE T4 PROTEINS PATENT WO 8901940-A 13 09-MAR-1989 Location/Qualifiers 1. 38 /organism="unknown" | BASE COUNT 8 a 9 c 12 g 9 t ORIGIN OUGLY Match Best Local Similarity 80.0%; Pred. No. 8.16+03; Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps Qy 1 tgttggtttccaatcggacc 20 | RESULT 4 |
|--|--|--|--|--|---|
| E32827 Novel compo 169336 Sequence 8 A0019232 Sequence 6 A43528 Sequence 6 A43528 Sequence 8 AR052465 Sequence 8 AR011952 Sequence AR093800 Sequence AR09380 Sequence S59402 TCR beta =T A21431 Oligonucleo A43129 Sequence 15 AR091842 Sequence 15 AR019138 Sequence 15 AR0109138 Sequence E25881 Blastocyst A26514 PT-261 muta AX091842 Sequence AX090859 Sequence AX092613 Sequence AX092613 Sequence AX082611 Sequence AX082611 Sequence AX082613 Sequence AX0826 | 40 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 | AR012356 Sequence AX006548 Sequence AX030256 Sequence AX049934 Sequence | PAT 02-DEC-1994 | Flavell,R.A., Maraganore,J.M. ULES AND PROCESSES FOR | DB 10; Length 36; le+03; s 4; Indels 0; Gaps 0; |
| 10 12 60.0 26 10 E32827 11 12 60.0 30 10 I69336 11 12 60.0 42 9 AX019232 11 18 59.0 24 9 A4528 11 1.8 59.0 24 9 AR05465 11 1.8 59.0 24 9 AR011952 11 1.8 59.0 35 9 AR011952 11 1.6 58.0 27 9 AX02890 11 1.6 58.0 27 9 AX02890 11 6 58.0 27 9 AX02890 11 6 58.0 27 9 AX02890 11 6 58.0 27 9 AX0129 11 6 58.0 30 9 A43129 11 6 58.0 30 9 AX3129 11 6 58.0 30 9 AX0129 11 6 58.0 27 9 AX0138 11 6 58.0 30 9 AX0129 11 7 57.0 21 10 AX09332 11 4 57.0 21 10 AX09351 11 2 56.0 21 10 AX082615 11 2 56.0 21 10 AX082615 | 2 56.0 28 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 | 2 56.0 34 2 56.0 34 2 56.0 34 2 56.0 34 2 56.0 34 | | MEFERENCE I (0368 I to 3b) AUTHORS FISHET.R.A., Gilbert,W., Sato,V.L., Flave and Liu,T.R. TITLE DNA SEQUENCES, RECOMBINANT DNA MOLECULES JOURNAL PACENT: WO 8901940-A 12 09-MAR-1989; FEATURES Location/Qualifiers Source 136 Aorganism="unknown" 8 to 08161 | Ouery Match 68.0%; Score 13.6; DB 10 Best Local Similarity 80.0%; Pred. No. 8.1e+03 Matches 16; Conservative 0; Mismatches 4 I tgttggtttccaatcggacc 20 Y Igttggtttccaatcgacc 20 |

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Maraganore, J.M.

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Maraganore,J.M.

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synthetic construct.
synthetic construct
artificial sequence.
1 (bases 1 to 21)
Lipford,G.B., Heeg,K. and Wagner,H.
G-motif oligonucleotides and uses thereof
Patent: WO 0014217-A 31 16-MAR-2000;
LIPFORD GRAYSON B (DE); HEEG KLAUS
CPG IMMUNOPHARMACEUTICALS GMBH (DE)
OS Artificial gene
OC Artificial sequence; Genes.
PN JP 1993192200-A/37
PD 073-AUG-1993
PF 19-AUG-1991 JP 1991230839
PR 20-AUG-1990 JP 90P 217067
PI OKAZAWA KAZUHIDE, SHIMADA MASAMITSU, KATOU IKUNOSHIN, PI FUKUSHIMA MICHIO,
PI FUZINAGA KEI
PC C12Q1/70,C12Q1/68;
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-SEP-2000
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/db_xrsf="taxon:32630"
/note="synthetic, no natural origin"
5 5 3 9 11 t
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Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 0;
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/db_xref="taxon:32630"
4 c 5 g 3 t
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Sequence 31 from Patent WO0014217.
AX023416
AX023416.1 GI:10183816
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Sequence 6 from Patent WO0071668.
AX052544 AX052544.1 GI:12226774
                                                                                                                                         C12Q1/70,C12Q1/68;
strandedness: Single;
topology: Linear;
hypothetical: No;
anti-sense: No;
Location/Qualifiers
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           Unclassified.

1 (bases 1 to 30)
Hinuma, S., Hosoya, M., Fujli, R., Ohtaki, T., Fukusumi, S. and Ohgi, K.
Hinuma, S., Hosoya, M., Fujli, R., Ohtaki, T., Fukusumi, S. and Ohgi, K.
G-protein coupled receptor protein and a DNA encoding the receptor Patent: US 611413-A 129 05-SEP-2000;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 26)
Daban, M., Espuna, E., Medrano, A., Querol and Enrique.
Daban, M., Espuna, E., Medrano, A., Querol and Enrique.
Transferrin-binding protein 1 (Tbpl) gene of Actinobacillus pleuropneumoniae, its use in vaccines for pleuropneumonia and as diagnostic reagents
Patent: EP 0733708-A 6 25-SEP-1996;
HIPRA S A LAB (ES)
Other publication ES 2092960 961201
Cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Primer for amplifying Human papillomavirus Sapporo gene.
E05267.1 GI:2173457
JP 1993192200-A/37.
synthetic construct.
synthetic construct
artificial sequence.
1 (bases 1 to 19)
DETECTION OF HUMAN PAPILLOMA VIRUS
PARARA SHUZO CO LTD
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Pred. No. 1.1e+04;
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/organism="unidentified"
/db_xref="taxon:22644"
a 6 c 9 g
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Sequence 6 from Patent EP0733708.
A56687.1 GI:3712729
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Best Local Similarity 75.0
Matches 15; Conservative
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                                                                                                         Method for identifying components involved in signal transduction pathways in higher plants
Patent: Wo 0071668-A 6 30-NOV-2000;
The Board of Regents of the University of Nebraska (US)
Location/Qualifiers
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Example: JP 1999137263-A 3 25-MAY-1999;

SMITHKLINE BEECHAM CORP, SMITHKLINE BEECHAM CORP PUBLIC LTD CO
OS Unidentified
PN JP 1999137263-A/3
PN JP 1999137263-A/3
PN 1999137263-A/3
PN 1999137263-A/3
PR 20-JUN-1999
PF 18-JUN-1999
PF 18-JUN-1999
PF 20-JUN-1999
PF 20-JUN-199
PF 2
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Pred. No. 4.1e+04;
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/organism="unidentified"
/db_xref="taxon:32644"
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E32827. G:13026860
JP 1999137263-A/3.
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92.9%;
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synthetic construct
artificial sequence.
1 (bases 1 to 24)
Rhoades, D.M.
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Nicola, G.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 62.0
Best Local Similarity 92.9
Matches 13; Conservative
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nes 15; Conservative
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11 TGGTTTCAAATCGG 24
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synthetic construct.
synthetic construct
artificial sequence.

1 (bases 1 to 42)
Huels,C., Muellner,S., Boehnisch,B. and Gallert,K.C.
Expression vector for the production of dead proteins
Patent: WO 9941390-A 12 1999;
HUELS CHRISTOPH (DE); MUELLMER STERAN (DE); AVENTIS RES & TECH GMBH
& CO (DE); BOEHNISCH BRITTA (DE); GALLERT KARL CHRISTIAN (DE)
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                                                                                                                                              1 (bases 1 to 30)
Makarow,M.
Method for production of proteins in yeast
Patent: US 5677172-A 8 14-OCT-1997;
Location/Qualifiers
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="pl35-NT5C"
a 13 c 6 g 11 t
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Sequence 6 from Patent EP 0334004.
108124
169336 30 bp DNA
Sequence 8 from patent US 5677172.
169336 GI:2831458
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Sequence 12 from Patent W09941390.
AX019232
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/organism="unknown"
9 c 8 9
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  Unknown.
Unclassified.
1 (bases 1 to 48)
Smith J.A. and Lee,F-J.S.
Isolation, purification, characterization, cloning and sequencing of N alpha-acetyltransferase Patent: EP 0334004-A1 6 27-SEP-1989;
Location/Qualifiers
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Pred. No. 9e+04;
0; Mismatches 2; Indels
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**synthetic construct
artificial sequence.
1 (bases 1 to 24)
Schweighoffer, F. and Tocque, B.
Schweighoffer, F. and Tocque, B.
GRB3-3 GENE, VARIANTS AND USES THEREOF
Patent: WO 9507981-A 8 23-WAR-1995;
RHONE POULENC RORER SA (FR)
Other publication PL 313445 960708
Other publication FI 961202 960314
Other publication R2 960708
Other publication A 9407059 950518
Other publication A 9407059 950518
Other publication R9 950789
Other publication R9 950308
Other publication R9 2169938 950318
Other publication R8 2710074 950403
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/organism="synthetic construct"
/db_xref="taxon:32630"
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Sequence 9 from patent US 5831048.
AR052465
AR052465.1 GI:5975829
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Sequence 8 from Patent WO9507981.
A43528
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86.7%;
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Best Local Similarity 86.7
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60d/b., Willis, M., Koch, T., Ringquist, S., Jensen, K. and Atkinson, B.
Systematic evolution of ligands by exponential enrichment: photoselection of nucleic acid ligands and solution selex Patent: US 5763177-A 29 09-UNN-1998;
Location/Qualifiers
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86.7%; Pred. No. 9e+04;
iive 0; Mismatches 2; Indels
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Pred. No. 9e+04;
0; Mismatches 2;
Schweighoffer, F. and Tocque , B. Grb3-3 cDNA and polypeptides
Patent: US 5831048-A 9 03-NOV-1998;
Location/Qualifiers
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Sequence 29 from patent US 5763177.
AR011952.1 GI:3969942
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86.7%;
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Best Local Similarity 86.7
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17.508 Million cell updates/sec
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          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Theising, B., Mylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R. TITLE The Washu-HHMI Mouse EST Project JOURNAL Unpublished (1996) COMMENT Contact: Marra M/Mouse EST Project Washu-HHMI Mouse EST Project | MASTINGTON UNIVERSITY SCHOOL OI MEDICINE MASTINGTON UNIVERSITY SCHOOL OI MEDICINE THE 131 286 1800 Fax: 314 286 1800 Fax: 314 286 1800 Fax: 314 286 1810 FEATURES FEATURE | Oy 2 gttggtttccaatcgg 17 I |
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| SUMMARIES Sult Query No. Score Match Length DB ID 1 12 8 64 0 46 12 38720750 | 50 AA790739 AA790739 40 AZ388877 AZ388877 42 AZ388025 AA497861 45 AZ380625 AA497861 45 AZ380625 AA497861 46 AZ37286 AA895268 4AZ37390 AA897263 4AZ377390 AA8972739 AZ3277390 AZ327739 AZ452673 AZ452673 AA652673 AZ65363 AA652673 AZ65673 AA75000 AZ752739 AZ75010 AZ752739 AZ75010 AZ752739 AZ77959 AZ623308 AZ623308 AZ623308 AZ623308 AZ623308 AZ77965 AZ623308 AZ77965 AZ623308 AZ77965 AZ623308 | SULT 1 790759/c CUS AA790759 46 by ERINITION WA18912.r1 Soares_m HENYY-CHAIN H2.;, I RESTON AA790759. GI:2850 WWORDS EST. MOUSE MOUSE DUCE MOUSE MOUSE. DUCE MOUSE MOUSE. DUCE MOUSE MOUSE. |

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/clone_lib="Mouse lokb plasmid UUGCIM library"
/sex="Male"
//lab_host="be: Coli strain XLIO-Gold, Tl-resistant, F-"
//note="Vector: PWDAINY; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orlifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymcleotide kinase Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114 giplahz29072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the linsert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
chemically-competent B. coli XLIO-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Dunn,D., Aoyaqi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. Mouse whole genome scaffolding with paired end reads from 10kb
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                                               Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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Pred. No. 2.4e+04;
0; Mismatches 3; Indels 0
                                                                                                                                                                                                                                                                                                                Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0568 row: C column: 10
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends

    .30
    /organism="Mus musculus"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="c57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M056BC10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 30.
Location/Qualifiers
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           Unpublished (2000)
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Best Local Similarity 82.4
Matches 14; Conservative
                                                                                                                                                                                                                                            Tel: 801 585 5606
Fax: 801 585 7177
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                                                                                                              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
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1M0568C10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0568C10 R, DNA sequence.
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
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                                                                                                                                                                                                                                                                                                                    Std Error: 0.00
                                                                                                                                                                                                                                                                                                                Insert Length: 10000 Std Error: (Plate: 0134 row: E column: 10 Seq primer: CACACAGGAAACAGCTATGACC Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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                                                                                                                                                                                                                                                                            Email: ddunn@genetics.utah.edu
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82.4%;
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Best Local Similarity 82.4
Matches 14; Conservative
                                                                                                                                                                                                 Tel: 801 585 5606
Fax: 801 585 7177
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Aurora Biosciences Corp.

Autora Biosciences Corp.

11010 Torreyana Road, San Diego, CA 92121, USA
Tel: 8584046719

Email: henkelg@aurorabio.com
Pools of cells were isolated from a GenomeScreen(TM) library. The
library of cells was generated by retroviral integration of a gene
tagging element consisting of: 1) A promoterless beta-lactamase
proceeded by a splice acceptor as a reporter for gene expression;
2) A promoter driving neomycin resistance followed by a splice
donor to trap downstream exons. 3' RACE from neomycin gene was
performed using total RNA from isolated pools. Output was shotgun
cloned in pamp-1 and used to transform mediated pools.

by splice donor from the trapping construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 40)

1 (bases 1 to 40)

Durick, K. and Pollok, B.
Exon-trap tags from a PC-3 GenomeScreen(TM) Library
Unpublished (2000)
Gontact: Greg Henkel
Gene Expression
                                                                            Trypanosoma brucei (TRED), was mechanically sheared to give a tight size distribution (Trypanosoma brucei (TRED)27/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
                                                                                                                                                                                                                                                                                                                                            Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
  Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AZ537263 40 bp DNA GSS 06-NOV-2000 AZ57-2203160 Genetrap PC-3 Human Prostatic Carcinoma Library Homo sapiens genomic 5', DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60.0%; Score 12; DB 258; Length 37; 75.0%; Pred. No. 3.2e+04; ive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Trypanosoma brucei"
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/clone="379b06"
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Matches 15; Conservative
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114)pblARL29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampleillin resistance."
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                                                                                                                                     E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-" /note="Vector: PWD42nv; Puiffied genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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T. bruce1 sheared genomic DNA clone 379b06, reverse sequence, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Trypanosoma.

1 (bases 1 to 37)

Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,

Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,

Melville, S. E., Rajandream, M.A. and Barrell, B.G.

Direct Submission
                                                                                                                       Run 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., 84112, USA
Tel: 801 585 5606
Fax: 801 585 5177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0136 row: G column: 10
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Trypanosoma brucei
Trypanosoma brucei
Bukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGGLM0136G10"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 12; DB 242; Length 28;
Pred. No. 3e+04;
0; Mismatches 5; Indels
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Best Local Similarity 75.0%;
Matches 15; Conservative 0
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TA379B06Q/c
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house mouse.
                       12 a
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Eukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Musculua; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 43)
Marrah M., Hiller, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Marrah M., Hiller, T., Levy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
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Alab_host="SOLR (kanamycin resistant)"
//note="Organ: lung; Vector: pBluescript SK-; Site_1: EcoRI ; Site_2: AhoI; Cloned unidirectionally. Primer: Oligo site_2: AhoI cloned unidirectionally. Primer: Oligo were source of meNA. Average insert size: 1.5 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCACGAG 3' -3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vx49c02.rl Stratagene mouse lung 937302 Mus musculus cDNA clone MAGE:1278530 5' similar to TR:002754 C/EBP ALPHA PROTEIN.;, mRNA sequence.
AA895268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                               /cell_type="Epithelial"
/cell_type="Epithelial"
/cell_line="PC-3"
/note="Organ: Prostate; Vector: pAmp-1; 3' RACE of tot
RNA from genetrap pools; shotgun clone in pAmp-1 and
to transform DH5-alpha competent bacteria."
                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-APR-1998
/db_xref="taxon:9606"
/clone_lib="Genetrap PC-3 Human Prostatic Carcinoma
                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashIngton University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fat: 314 286 1810
                                                                                                                                                                                                                                                                                       60.0%; Score 12; DB 245; Length 40; 75.0%; Pred. No. 3.3e+04; Live 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28ml3 revl ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="IMAGE:1278530"
/clone_lib="Stratagene mouse lung 937302"
                                                                   /tissue_type="Adenocarcinoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
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The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="C57BL/6 x CBA"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA895268.1 GI:3031687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                  1 tgttggtttccaatcggacc 20
                                                                                                                                                                                                                                                                                                                                                                                                       5 TGTTGATTTCCACTGAAACC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43 bp
                                                                                                                                                                                                                                                                                       Query Match 60.0
Best Local Similarity 75.0
Matches 15; Conservative
                                            Library
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AA895268/C
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ORIGIN
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COMMENT

SOURCE

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/noce="vector: PMP42TUF, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resources/documents/dnares/). The DNA (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarcse gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil47321Hqb)AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longare, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AZJ19753 43 bp DNA GSS 29-SEP-2000 HA0039BOZR Mouse 10kb plasmid UUGCIM library Mus musculus genomic Clone UUGCIM0039BOZ R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 84112, USA
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                                                                                                                                                                                                                          Gaps
adaptor sequence: 5' CTCGACTTTTTTTTTTTTTTT 3'^n
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/db_xref="taxon:10090"
/clone="UGGCIM0039B02"
/stone_lib-"Mouse 10kb plasmid UGGCIM library"
/sex="Male"
                                                                                                                                                      Score 12; DB 13; Length 43;
Pred. No. 3.3e+04;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0039 tow: B column: 02
Seq primer: CACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AZ319753.1 GI:10370842
                                                                                                                                                          60.0%;
75.0%;
                                                                                                                                                                                                                                                                                1 tgttggtttccaatcggacc 20
                                                                                                                                                                                                                                                                                                                       32 TGTTCGGTTCCCAGCGTACC 13
                                                                                                                                                                                       Best Local Similarity 75.0
Matches 15; Conservative
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Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            plasmid inserts
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Б

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114[pl5ART29072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
'M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
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AZ822425
AZ822425.1 GI:12992333
                                                                                                                                                        Unpublished (2000)
Contact: Robert B. Weiss
Contract: Yof Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 1
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: PWD42ny; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                        Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59.0%; Score 11.8; DB 241; Length 19; 86.7%; Pred. No. 3.6e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                    Std Error: 0.00 column: 09
                                                                                                                                                                                                                                                                                                                                               Email: ddunnégenetics.utah.edu insert Length: 10000 Std Error: (Plate: 0050 row: L column: 09 Seg primer: CACACAGGAAACAGCTATGACC
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/db_xref="taxon:10090"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                               Tel: 801 585 5606
Fax: 801 585 7177
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Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata
.H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo
.K., Suyama,A. and Sugano,S.
.Fine Structural analysis of transcription start sites of human
mRNAs using full-length enriched and 5'-end enriched cDNA libraries
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Institute of Medical Science, University of Tokyo 4-6-1, Shizokanedai, Minatoku, Tokyo 108-8639, Japan Email: ysuzuki@ins.u-tokyo.ac.jp Email: ysuzuki@ins.u-tokyo.ac.jp Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance." 11\ c 13\ g \ t
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AU107355 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
CASO7628, mRNA sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                       Length 43;
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clone UUGCIM0050L09 R, DNA sequence.
AZ327390
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/db_xref="taxon:9606"
/clone="CAS07628"
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/G1 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonicleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarcse gel
electrophoresis. Vector DNA was prepared from a derivative
of pwD42 (414732114 (191-AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicilin resistance."
                                                                                                                                                                                                                                                                             E., SLC, UT
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 27)
Dunn, D., Acyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longarce, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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/sex="Male"
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Pred. No. 5e+04;
0; Mismatches 4; Indels 0;
                                                                                                                                                                                                                                                                 Rm. 308, Biomedical Polymers Research Bldg., 20
84112, USA
                                                                                                                                                                                                                                                                                                      Tel: 801 585 5606
Fax: 801 585 7177
Emall: ddunnegenetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0095 row: M column: 09
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Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
                                                                                                                                                                               Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/clone="UUGC2M0095M09"
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                                        1 (Dases 1 to 46)
Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Marca, M., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
Other_ESTs: uj06e03.yl
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G0114A01-3 Mouse E7.5 Embryonic Portion cDNA Library Mus musculus cDNA clone G0114A01 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                        Contact: Marra M.Washu-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Fal: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: custom primer used
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:10090"
/clone="IMAGE:1891132"
/clone_lib="Sugano mouse liver mlia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      primer CGACCTGCAGCTCGAGCACA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .46
/organism="Mus musculus"
/strain="C57BL"
                                                                                                                                                                                                                                                                                                                                                                                                             Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="female"
/dev_stage="adult"
/lab_host="DH10B"
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/dev_stage="45 years old"
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/lab_host="DHILDS"
/lab_host="DHILDS"
/lab_host="DHILDS"
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/note="Vector: pAMPIO; Site_1: Not1; Site_2: EcoRI; ist
strand cDNA was primed with oligo(dT)17 on 50 ng of
DNAse-treated, total cellular RNA obtained from 5,000-10
,000 microfissected preneoplastic cells
histologically-deremined to be prostatic intraepithelial
neoplasia 2 (PIN2) cells. Double-stranded cDNA was
ligated to EcoRI adaptors, 5 cycles of PCR applied to the
cDNA with an adaptor-specific primer, and the resulting
PCR product succloned into pAMPIO by the UDG-cloning
method (Life Technologies). Average insert size is 600
bp. NOTE: Not directionally cloned. This library was
constructed by a payid Krisman."
                                                                                                                                                                      Email: cgapDs-remail.nib.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D.
Michael Brumert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AZ822833 43 bp DNA GSS 20-FEB-2001
MO0965723F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCZM0096323 F, DNA sequence.
AZ822833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 43)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longare, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 40)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56.0%; Score 11.2; DB 10; Length 40; 81.2%; Pred. No. 8.9e+04; ive 0; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                      Trace considered overall poor quality Insert Length: 1233 Std Error: 0.00 Seq primer: -40m13 fwd. ET from Amersham High quality sequence stop: 1. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1188909"
                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AZ822833.1 GI:12992741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="Male"
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Matches 13; Conservative
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III, Becker, K.G. and Ko, M.S. H. Genome-wide expression profilling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /Clone_lib="Mouse E7.5 Embryonic Portion cDNA Library"
//sex="unknown"
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//lab_host="DH10B"
//lab_host="Vector: pSPORT1 (Gibco/BRL Life Technology);
Site_l: Sall; Site_2: Not!; Total RNAS were extracted from 6 Embryo. The double-stranded cDNA was synthesized by
gibco's kit with an Oligo(dT) primer [NotI primer-adapter
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AA652673.1 G1:2584325
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                                                                                                                                                                                                               Laboratory of Generics National Institutes of Health National Institute on Aging/National Institutes of Health 313 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA Email: cdnad[gsun.grc.nia.nih.gov Plate: G0114 row: A column: 01 Seq primer: -21M13 Forward
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Pred. No. 7.3e+04;
0; Mismatches 1; Indels 0
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/organism="Mus musculus"
/orstrain="C57BL/6J"
/db_xref="taxon:10090"
/clone="G0114A01"
                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 50 POLYA=Yes.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                  Contact: George J. Kargul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from GibcobRL]
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92.3%;
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Best Local Similarity 92.3'
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Gaps

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/sex="Male" rouse two presmits observed interests //sex="Male" //lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
//note="Vector: PWD42Nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was hydrodynamically sheared by repeated by the sheared DNA was purified and size-selected for a 9.5 to 10.5 Nb range using preparative agances gal electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AF129072.1), a copy-number inductable derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
Rel: 801 585 5606
Fax: 801 585 717
Fax: 801 585 717
Fax: 801 585 717
Fax: Banati: ddunn@enetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .43
/organism="Mus musculus"
/strain="c57BL/6J"
/db_xref="taxon:10000"
/clone="UGC2M0096J23"
/clone_lib="Mouse l0kb plasmid UUGCIM library"
                                                                                                                                                                                                                                                                                                                                                                         Plate: 0096 row: J column: 23
Seq primer: CGTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 43.
Location/Qualifiers
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ORIGIN
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Query Match 56.0%; Score 11.2; DB 250; Length 43; Best Local Similarity 81.2%; Pred. No. 9e+04; Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps

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ò ద completed: October 2, 2001, 15:01:04 Search com Job time:

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AR100356 Sequence
AR032663 Sequence
129403 Sequence 27
191077 Sequence 27
119158 Sequence 21
AR032673 Sequence
129413 Sequence 28
191087 Sequence 28
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AR032663
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gb_htg21:*
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gb_sts2:*
gb_sts3:*
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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1 (bases 1 to 47)
Edwards,C.A., Cantor,C.R., Andrews,B.M., Turin,L.M. and Fry,K.E. Sequence-directed DNA-binding molecules compositions and methods Patent: US 5578444 - 275 26-NOV-1996;
Location/Qualifiers
                                                                                     Edwards, C.A., Cantor, C.R., Andrews, B.M., Turin, L.M. and Fry, K.E. Method of determining DNA sequence preference of a DNA-binding molecule
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Unclassified.
1 (bases 1 to 47)
Edwards, C.A., Cantor, C.R., Andrews, B.M. and Turin, L.M.
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Pred. No. 4.8e+04;
0; Mismatches 3;
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Pred. No. 4.8e+04;
); Mismatches 3;
                                                                                                                                 Patent: US 5869241-A 275 09-FEB-1999;
Location/Qualiflers
                                                                                                                                                                                                                                                                                                     Sequence 275 from patent US 5578444. I29403.1 GI:182012.
             ARU32663 47 bp DNA
Sequence 275 from patent US 5869241.
AR032663
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Sequence 275 from patent US 5726014.
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Best Local Similarity 83.3
Matches 15; Conservative
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AR063468 Sequence
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Baker, B. F., Bennett, C. Frank, Butler, M.M. and Shanahan, W.R. Jr. Antisense oligonucleotide modulation of tumor necrosis factor. alpha. (TWF. alpha.) expression Patent: US 6080580-A 87 27-JUN-2000;
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Sequence 87 from patent US
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1 (bases 1 to 47)
Edwards,C.A., Cantor,C.R., Andrews,B.M., Turin,L.M. and Fry,K.E.
Sequence-directed DNA-binding molecules compositions and methods
Patent: US 5578444-A 285 26.NOV-1996;
Location/Qualifiers
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Edwards,C.A., Cantor,C.R., Andrews,B.M. and Turin,L.M.
Screening assay for the detection of DNA-binding molecules
Patent: US 5726014-A 285 10-MAR-1998;
Location/Qualifiers
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Matches 14; Conservative 0; Mismatches 2;
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Sequence 285 from patent US 5726014.
191087. GI:3935557
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Sequence 285 from patent US 5578444.
129413
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Sequence 2 from patent US 5851529.
AR066591 GI:5997813
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Edwards,C.A., Cantor,C.R., Andrews,B.M., Turin,L.M. and Fry,K.E.
Method of determining DNA sequence preference of a DNA-binding
molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                     07-0CT-1996
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Screening assay for the detection of DNA-binding molecules Patent: US 5726014-A 275 10-MAR-1998; Location/Qualifiers
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Pred. No. 8.4e+04;
0; Mismatches 2;
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Pred. No. 4.8e+04;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 30)
Tenen, D.G., Pahl, H.L. and Burn, T.C.
Myeloid cell specific promoter
Patent: US 5502176-A 21 26 MAR-1996;
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                Sequence 21 from patent US 5502176.
119158
119158.1 GI:1599513
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13 c 5 g
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15 c 12 g
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15 c 13 q
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Best Local Similarity 87.5%;
Matches 14; Conservative (
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Best Local Similarity 83.3%;
Matches 15; Conservative
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ORIGIN

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RESULT I19158/c

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VERSION KEYWORDS

ORGANISM

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106858
106858.1 GI:589980
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21-MAK-1988 L70.515
HALLEY E GRABAR, DOUGLAS J JOLY, JAMES G RESPESU, PAUL K REIKAIND
C12N15/09, A01K67/027, A61K31/00, A61K31/00, A61K35/12, A61K35/76,
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C12N5/10,C12N7/00,C12P21/00//(C12P21/00,C12R1:91),C12N15/00,
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           Unclassified.
Unclassified.
Unclassified.
1 (bases 1 to 28)
Guber.H.E., Johly, D.J., Respess, J.G. and Laikind, P.K.
Recombinant retroviruses
Patent: US 5851529-A 2 22-DEC-1998;
Locaton/Qualifiers
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Pred. No. 1.1e+05;
0; Mismatches 4; Indels (
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1 (bases 1 to 28)

Recombinant retrovirus with defective replication
RE 1999562397-A/2
RP 24-ReP-1999
RP 24-ReP-1999
RP 21-MAR-1988 US
RP
                                                                                                                                                                                                                                                                                                      63.0%; Score 12.6; DB 9; Length 28; 78.9%; Pred. No. 1.1e+05; Live 0; Mismatches 4; Indels

    .28
    /organism='Artificial Sequence'

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Sequence 2 from Patent EP 0334301.

    .28
    /organism="unidentified"
    /db_xref="taxon:32644"

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13 c 3 g
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78.98;
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Best Local Similarity 78.99
Matches 15; Conservative
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Best Local Similarity 78.9°
Matches 15; Conservative
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Virus resistant transgenic plants comprising cells transformed with a polynucleotide encoding a potyviridae Pl protein or Pl protein
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Pehu, E., Pehu, T., Maki-Valkama, T., Valkonen, J., Koivu, K. and Lehto, K.
Virus-resistant transgenic plants
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1 (bases 1 to 28)
Gruber, H. E., Jolly, D. J., Respess, J.G. and Laikind, P.K.
Recombinant retroviruses
Patent: Bp 0334301 Al 2 27-SEP-1989;
Location/Qualifiers
                                                                                                                                                                                                                  Length 28;
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Pred. No. 1e+05;
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Pred. No. 1.1e+05;
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Sequence 2 from patent US 5968828.
AR080756 GI:10007486
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Location/Qualifiers
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Sequence 2 from patent US 5576202.
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8 c 9 g
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Best Local Similarity 78.9%;
Matches 15; Conservative (
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78.9%;
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29 CTAGGTGAGACTCATTGAG 11
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Best Local Similarity 78.9
Matches 15; Conservative
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E 1 (bases 1 to 42)

S Uyemura, K., Klotz, J., Pirmez, C., Ohmen, J., Wang, X.H., Ho, C., Hoffman, W.L. and Modlin, R.L.

Microanatomic clonality of gamma delta T cells in human leishmaniasis lesions

L J. Immunol. 148 (4), 1205-1211 (1992)

E 92148143

GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 80775] from the original journal article.

This sequence comes from Figure 4.
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S80775.1 GI:244965
                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 33)
Lonberg, N. and Kay, R.M.
Transgenic non-human animals capable of producing heterologous antibodies
Patent: US 5633425-A 76 27-MAY-1997;
                                                                                                                                                         Gaps
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                                                                                                                       Score 12.6; DB 10; Length 32;
Pred. No. 1e+05;
0; Mismatches 4; Indels (
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Patent: US 5576202-A 2 19-NOV-1996;
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                                            /organism="unknown"
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Perfect score:
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em_gss_pln1: *

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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gb-gss24:*
gb-gss24:*
gb-gss26:*
gb-gss27:*
gb-gss28:*
gb-gss31:*

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Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 50)

Suzuki, Y., Tsunoda, T., Tanaka, T., Makamura, Y., Morishita, S., Chubo, K., Suyama, A. and Sugano, S.

Fine Structural analysis of transcription start sites of human

MRNAs using full-length enriched and 5'-end enriched cDNA libraries

Ontact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: ysuzuki@ims.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Makagawa, K., Maruyama, K., Suyama, A. and Sugano

S. Construction and characterization of a full length-enriched and

a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
                               Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
Email: ysuzukiéms.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., suyama,A. and Sugano
y.S. Construction and characterization of a full length-enriched and
a S'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
mRNAs using full-length enriched and 5'-end enriched cDNA libraries Unpublished (2001)
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AU107336 Sugano Homo sapiens CDNA library Homo sapiens CDNA clone
LNG11142, mRNA sequence.
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/organism="Homo sapiens"
/db_xref="taxon.9606"
/clone="KAT02360"
/clone="Lib="Sugano Homo sapiens cDNA library"
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/db_xref="taxon:9606"
/clone="LNG11142"
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AZ417155 1M0192P07
AL45976 T. brucei
T95881 Ye47b02.s1
BE386700 601274107
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A160975 qy02fi2.x
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A1000255 ov10a02.s
A264367 1M0310C14
A2597058 1M0410M08
A2815328 1M0410M08
A2815328 2M0089N10
A2815328 2M0089N10
A2815328 2M0143B2
A2815328 1M0147F19
A28592675 1M02047F19
A2592675 1M020315
A2592675 1M060521
A2623308 1M0606721
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AL488871 T. brucel
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                               Description
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0 AZ815328
2 AZ815329
2 AZ8229
6 AZ592675
AAZ38745
9 AZ683308
8 TA177A100
                       SUMMARIES
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AU107335 Sugano Homo sap
KAT02360, mRNA sequence
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DEFINITION

AZ826713

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VERSION KEYWORDS

ORGANISM

SOURCE

REFERENCE AUTHORS JOURNAL

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TITLE

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M.D., Louis M. Staudt, M.D., Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   n2498822 42 bp DNA GSS 05-OCT-2000 IM036I17F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0336I17 F, DNA sequence. AZ498822 AZ498822.1 GI:10677034 GSS.
                                                                                                                                                                                                                                                                                             Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 46)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                           wh76cl0.xl NCI_CGAP_CLL1 Homo sapiens CDNA clone IMAGE:2386674 3' similar to TR:Q40402 Q40402 EXTENSIN ; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Emall: cgapbs rfemail.nih.gov
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63.0%; Score 12.6; DB 102; Length 46; llarity 78.9%; Pred. No. 7.1e+04; Conservative 0; Mismatches 4; Indels 0;
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11 CTAGGTGCCGCGCAGTGTG 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       plasmid inserts
Unpublished (2000)
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Binnedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, M., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly M., Rose, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                      A2826713 33 bp DNA GSS 20-FBB-2001
2M0102H12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0102H12 R, DNA sequence.
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/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0102 row: H column: 12
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends

    .33
    /organism="Mus musculus"
    /strain="C57BL/6J"

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/clone="UUGC2M0102H12"
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High quality sequence stop: 33.
Location/Qualifiers
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Fax: 801 585 7177
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JOURNAL COMMENT

TITLE

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AUTHORS

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (qi|4732114|qp)ART29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the innest adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                        E 1 (bases 1 to 48)

S Dun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/note="Weetcr: PWD42nv; Purified genomic DNA from M.
musculus C57BL/G3 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Fax: 801 585 7177
Email: ddun@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0113 row: P column: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends

    .48
    /organism="Mus musculus"
    /strain="C57BL/6J"

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/clone="UUGC2M0113P15"
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Location/Qualifiers
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                            house mouse.
                                                               Mus musculus
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Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymerase at the polymerase and T4 polymerase at the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (qil4732114) pblAR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                         Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
WRN. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 42)

Dunn, D., Aoyai, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AZ833039 48 bp DNA GSS 20-FEB-2001
2M0113P15R Mouse 10kb plasmid UUGClM library Mus musculus genomic
clone UGGCZM0113P15 R, DNA sequence.
AZ833039.1 GI:13002947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /note="Vector: PWD42nv; Puiffed genomic DNA from M. musculus G57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGGCIM0336I17"
/sox="Male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 801 585 5606
Fax: 801 585 7177
Email: ddun@qenetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0336 row: I column: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 42.
Location/Qualifiers

    .42
    /organism="Mus musculus"

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Best Local Similarity 75.03
Matches 15; Conservative
                               Mus musculus
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AZ833039

RESULT

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VERSION

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In (bases 1 to 50)

Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo,K., Suyama,A. and Sugano,S.

Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries Unpublished (2001)

Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Bmail: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched CDNA library. Gene 200 (1-2), 149-156 (1997).
                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 50)

Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata, H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo,K., Suyama,A. and Sugano,S.
Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries Contact: Yutaka Suzuki
                                                                                                                                                                                                                                                                                                                                                                                                          Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
5-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
5-8-1, Shirokanedai, Minatoku, Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

Location/Qualifiers
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AU105603 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HSIO0510, mRNA sequence.
AU105603. GI:13555124
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/clone_lib="Sugano Homo sapiens cDNA library"
11 c 20 g 11 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"
/clone="HSI00510"
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AU104075
AU104075.1 GI:13553596
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86.7%;
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                                                                                                              Homo sapiens
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Best Local Similarity
Matches 13; Conserv
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AU105603/c
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COMMENT
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                                                     KEYWORDS
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                                                                                                                                                                                                                                                                                                                             plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Han 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (21)
Dunn,D., Aoyal,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
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AU104075 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HEP14513, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Mouse 10kb plasmid UUGCIM library"
/sex="Male"
/lab_nost="E. Coli strain XLIO-Gold, TI-resistant, F-"
/note="Nostc="F. Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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Pred. No. 1.6e+05;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0538 row: M column: 09
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0538M09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 21.
Location/Qualifiers
AZ660221.1 GI:11797367
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Fax: 801 585 7177
Email: ddunn@qenet
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Best Local Similarity 86.7
Matches 13; Conservative
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                                                                            Mus musculus
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Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata, H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo, K., Suyama,A. and Sugano,S.
Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries Unpublished (2011)
Contact: Yutaka Suzuki
Department of Virology Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y. Yoshitomorakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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1 (bases I to 50)

Suzuki, Y., Tsunoda, T., Taira, H., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Nakamura, Y., Morishita, S., Okubo, K., Suyama, A. and Sugano, S.
Fine Structural analysis of transcription start sites of human Unpublished (2001)

Contact: Yutaka Suzuki
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Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
5-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
6-5-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
7-6-1, Shirokanedai, Minatoku, Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library, Gene 200 (1-2), 149-156 (1997).

Location/Qualifiers
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AU105606 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
AU105606 AU2061 GI:13555127
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); Mismatches 2; Indels
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/db_xref="taxon:9606"
/clone="HSI05558"
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            AUTHORS
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Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Suzukitute of Medical Science, University of Tokyo
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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Suzukl, Y., Tsunoda, T., Talra, H., Mizushima-Sugano, J., Sese, J., Hata
N., Ota, T., Isogai, T., Tanaka, T., Nakamura, Y., Morishita, S., Okubo
N., Suyama, A. and Sugano, S.
Fine Structural analysis of transcription start sites of human
mRNAs using full-length enriched and 5'-end enriched cDNA libraries
Unpublished (2001)
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AU105604 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HSI01710, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 1.7e+05;
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Pred. No. 1.7e+05;
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/db_xref="taxon:9606"
/clone="HSI01710"
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SOURCE ORGANISM

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COMMENT

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Constructed at the Institute for Genomic Research (TIGR), Constructed at the Institute for Genomic Research (TIGR), Constructed at the Institute for Isolated from a cloned population of Rockville, MD. Genomic DNA isolated from a cloned population of to give a tight size distribution (4 kb). The v + 1 method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Trypanosoma.

1 (bases 1 to 26)

Hall, N. Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,

Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,

Melville, S.E., Rajandream, M.A. and Barrell, B.G.

Direct Submission

Submitted (10-DEC-2000) Trypanosoma brucel genome sequencing

project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,

Cambridge CBI0 1SA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T95881 40 bp mRNA EST 27-MAR-1995 ye47b02.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:120843 3' similar to gb|M87923|HUMALCE12 Human carcinoma cell-derived All RNA transcript, (FRNA); gb:M57627 INTERLEUKIN-10 PRECIRSOR (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                         13-DEC-2000
                                                                                                                                                                                                                                                   TA91B03P 26 bp DNA GSS 13-DEC-200
T. brucei sheared genomic DNA clone 91b03, forward sequence,
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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Pred. No. 2e+05;
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  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
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                                                                                                                                                                                                                      AZ417155 20 bp DNA GSS 03-OCT-2000
1M0192P07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0192P07 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longarce, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly and Wright, D., Weiss, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Mouse 10kb plasmid UUGC1M library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0192 row: P column: 07
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIM0192P07"
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Fax: 801 585 7177
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                             5 gggaggctcagtgtg 19
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source

FEATURES

BASE COUNT

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Gaps

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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Email: st@watson.wustl.edu
Insert Size: 2754
Source: IMAGE Consortium, LLNL This clone is available royalty-free
through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov)
Insert information: Trace considered overall poor quality
Insert Length: 2754 Std Error: 0.00
1 (bases 1 to 40)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hullman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., R. Ifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
The Washu-Warck EST Project
Conpublished (1995)
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/db_xref="GDB:47338"
/db_xref="taxon:9606"
/clone="IMAGE:120843"
/clone_lib="Soares fetal liver spleen lNFLS"
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High quality sequence stop: 1.
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Search completed: October 2, 2001, 15:01:06 Job time: 10835 sec

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         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                         1344157 segs, 7733874588 residues
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 50
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Perfect score:
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AR012105 Sequence AR014544 Sequence AR059098 Sequence M96133 Human hybri A73580 Sequence 4 AR0770795 Sequence Z50819 H.sapiens m

AR014544 AR059098 HUMTCIGC1A

AR012105

AR067419 AR070795 HSCD85706

A73580

Description

SUMMARIES

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HUMTCIGCIA 46 bp DNA PRI 13-JaN-1995 Human hybrid T cell receptor/immunoglobulin protein, clone 1 V-D-J segment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                       1 (bases 1 to 40)
Sukhatme, V.P.
Methods and materials relating to the functional domains of DNA binding proteins
Patent: US 5773583-A 52 30-JUN-1998;
Location/Qualifiers
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Location/Qualifiers
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                   PAT
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Pred. No. 1.5e+05;
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M96133.1 GI:339188
T'ccell receptor/immunoglobulin protein.
Homo sapiens
Homo sapiens
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US 5837854.
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                                                                                                                                                      /organism="unknown"
14 c 13 g
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7 c 4 a
                 AR014544 40 bp
Sequence 52 from patent
AR014544
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Sequence 16 from patent
AR059098
AR059098.1 GI:5984675
                                             AR014544.1 GI:3971998
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84.2%;
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AR108637 Sequence
AR058955 Sequence
AR105229 Sequence
AX098901 Sequence
AX099321 Sequence
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AR078900 Sequence
AR106304 Sequence
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AR103323 Sequence
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AR051920 Sequence
AR049382 Sequence
AR095543 Sequence
A83263 Sequence
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AR050042 Sequence
AR064551 Sequence
AR013956 Sequence
                                                                                        Sequence 4
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I25985 Sequence 2
                                              125076 Sequence 3
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A82993 Sequence 3
AX027268 Sequence
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AR068600 Sequence
AR095952 Sequence
        AX044138 Sequence
AX044178 Sequence
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Sukhatme, V.P.
Methods and materials relating to the functional domains of DNA
binding proteins
Patent: US 5763209-A 52 09-JUN-1998;
Location/Qualifiers
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Pred. No. 4.6e+04;
); Mismatches 3; Indels
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AR064551
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AR065636
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AR078900
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171129
A82991
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85.0%; Pred
0; )
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Sequence 52 from patent
AR012105
AR012105.1 GI:3970095
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Best Local Similarity 85.0
Matches 17; Conservative
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Unclassified.
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DEFINITION ACCESSION VERSION

KEYWORDS

ORGANISM

AUTHORS TITLE JOURNAL

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Brunker, P., Minas, W., Kallio, P. and Bailey, J.E.
Methods and compositions for increasing production of erythromycin
Patent: US 5908764-A 2 01-JUN-1999;
Location/Qualifiers
                                                                                                                                                                                                                                                                       1 (bases 1 to 18)
Heym.b., Cole, S., Young, D., Zhang, Y., Honore, N., Telenti, A. and
Bodmer, T.
Rapid detection of antibiotic resistance in mycobacterium
                                                                Gaps
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                                      Length 32;
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                                                              4; Indels
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Pred. No. 3.5e+05;
0; Mismatches 1;
                                   68.0%; Score 13.6; DB 9; 70.0%; Pred. No. 2.4e+05; Live 2; Mismatches 4;
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ب
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Patent: US 5851763-A 16 22-DEC-1998;
Location/Qualifiers
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Sequence 16 from patent US 5851763.
AR067419
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AR070795
AR070795.1 GI:7221683
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/organism="unknown"
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93.3%;
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Best Local Similarity 70.0
Matches 14; Conservative
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Best Local Similarity 93.3
Matches 14; Conservative
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Unclassified.
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Matches 14; Conserv
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AR070795/c
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1 (bases 1 to 46)
Kobayashi,Y., Tycko,B., Soreng,A.L. and Sklar,J.
Transrearrangements between antigen receptor genes in normal human
Transrear and in ataxia telangiectasia
J. Immunol. 147 (9), 3201-3209 (1991)
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unclassified.
E ( Dases 1 to 32)
AS Nemeth, E.F. and Brown, E.M.
CALCIUM RECEPTOR-ACTIVE MOLECULES
NAL Patent: WO 9418959-A 4 OI-SEP-1994;
BRIGHAM & WOMENS HOSFITAL (US); NPS PHARMA INC (US)

Location/Qualifiers
32 "...identified"
7 others
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Pred. No. 1.8e+05;
0; Mismatches 2;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Sequence 4 from Patent W09418959.
A73580 GI:6064168
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36..46
/gene="TCRD"
/note="G00-120-406"
16 c 11 g
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'gene="IGH@"
'note="G00-118-731"
                                                                                                                                                                                                                                                                                                                                                                                                                     31. .35
/gene="TCRD"
/note="G00-120-406"
                                                                        Location/Qualifiers
                                                                                                                                                                                    'note="G00-128-528"
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/note="G00-120-406"
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/map="14q11.2"
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/gene="TCRD"
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88.2%;
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Best Local Similarity 88.2%,
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18; Conservative
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ORIGIN
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Sw synthetic construct
artificial sequence.
1 (bases 1 to 23)
S Hawkes, T.R., Warner, S.A., Andrews, C.J., Bachoo, S. and Pickerill, A.P.
Herbicide resistant plants
L Patent: WO 0066746-A 30 09-NOV-2000;
ZENECA LIMITED (GB)
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artificial sequence.
1 (bases 1 to 23)
Hawkes,T.R., Warner,S.A., Andrews,C.J., Bachoo,S. and Pickerill,A.P.
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100.0%; Pred. No. 4.8e+05;
tive 0; Mismatches 0;
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="primer" 5 9 6 t
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/db_xref="taxon:32630"
/note="Primer"
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="primer"
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Patent: WO 0066747-A 38 09-NOV-2000;
ZENECA LIMITED (GB)
Location/Qualifiers
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Sequence 38 from Patent WO0066747.
AX044138 GI:11343016
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Sequence 30 from Patent WO0066746.
AX044178 GI:11343056
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Matches 13; Conservative
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Matches 13; Conserv
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AXO44138/c
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AX044178/c
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                                                                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Wang, E.C.; Moss, P.A., Frodsham, P., Lehner, P.J., Bell, J.I. and
Borysiewicz, L.K.
Oligoclonal CD8+, CD57+ T cells in normal, healthy individuals and
Unpublished
                                                 HSCD85706 39 bp mRNA for T cell receptor (ID CD85706). 250819. 250819. GI:1004241 constant region; T cell receptor; variable region.
                                                                                                                                                                                                                                                                                                                       Wang, E.C.

Direct Submission

Submitted (17-AuG-1995) Eddie CY Wang, Medicine, University of Wales of College of, Medicine, Heath Park, Cardiff, South Glamorgan, CF4 4XN, Wales UK

3 (bases 1 to 39)

Wang, E.C., Moss, P.A., Frodsham, P., Lehner, P.J., Bell, J.I. and Borystewicz, L.K.

CD8highCD57+ T lymphocytes in normal, healthy individuals are oligochonal and respond to human cytomegalovirus
J. Immunol. 155 (10), 5046-5056 (1995)
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(I bases I to 23)
Hawkes, T.R., Warner, S.A., Andrews, C.J., Bachoo, S. and Pickerill, A.P.
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/isolate-"FW"
/db_xref-"taxon:9606"
1. 12
/note-"end T cell receptor V beta 24"
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Pred. No. 2.7e+05;
0; Mismatches 1;
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Patent: WO 0066748-A 40 09-NOV-2000;
ZENECA LIMITED (GB)
Location/Qualifiers
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/note="beginning J beta 2.
9 a 11 c 15 g 4
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Sequence 40 from Patent WO0066748.
AX044085.1 GI:11342963
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93.3%;
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Best Local Similarity 93.3
Matches 14; Conservative
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/note="Cl
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19 CCTCTGCTGGTGG 5
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HSCD85706/c
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BASE COUNT ORIGIN

AX044085/c DEFINITION

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ORGANISM

REFERENCE AUTHORS JOURNAL

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FEATURES

ACCESSION VERSION KEYWORDS

AUTHORS TITLE JOURNAL

JOURNAL REFERENCE

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JOURNAL MEDLINE

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Kawasaki, H., Tsuchiya, M., Miwa, K. and Kawahara, Y.
Coryneform bacteria deficient in a cell surface protein
Patent: US 5547864-A 3 20-AUG-1996;
Location/Qualifiers
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                                                                                                         63.0%; Score 12.6; DB 9; Length 20; 78.9%; Pred. No. 7.5e+05; Live 0; Mismatches 4; Indels
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Kawasaki, H., Tsuchiya, M., Miwa, K. and Kawahara, Y.
DNA encoding novel cell surface protein
Patent: US 5681717-A 3 28-OCT-1997;
Location/Qualifiers
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Sequence 3 from patent US 5681717.
171129
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Sequence 3 from patent US 5547864.
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125076.1 GI:1604946
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/organism="unknown"
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/organism="unknown"
a 9 c 7 g
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Matches 15; Conservative
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1 (bases 1 to 20)

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1 (bases 1 to 20)

Antisenet., Frank, Ackermann, E.J. and Cowsert, L.M.

Antisense modulation of X-linked inhibitor of apoptosis expression Patent: US 6087173-A 43 11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (12-PEB-1998) Silins S.L., Queensland Institute of
Medical Research, The Bancroft Centre, 300 Herston Road, Brisbane,
                                                                                                                                                                        HSA224214 48 bp mRNA PRI 23-FEB-2001
Homo sapiens mRNA for T cell receptor beta chain V-D-J junctional
region (TCRBV6BJ1S5).
                                                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 48)
Silins,S.L., Cross,S.M., Krauer,K.G., Moss,D.J., Schmidt,C.W. and
                                                             Gaps
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T cell receptor; T cell receptor beta chain; variable region
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/haplotype="A1, A3, B8, B35"
/cell_line="JS11"
/cell_type="cytotoxic T lymphocyte"
/rearranged
/rearranged
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                        Query Match 65.0%; Score 13; DB 9; Le Best Local Similarity 100.0%; Pred. No. 4.8e+05; Matches 13; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 13; Conservative 0; Mismatches 0;
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Sequence 43 from patent US 6087173.
AR103323
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Silins, S.L.
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R. TITLE The WashU-HHMI Mouse EST Project JOURNAL Unpublished (1996) COMMENT Contact: Marra M/Mouse EST Project | Washington Quiversity School of Medicinep Washington Quiversity School of Medicinep Text: 314 286 1800 Fax: 315 281 281 Fax: 315 281 281 Fax: 315 281 281 Fax: 316 281 Fax: 316 281 Fax: 316 281 Fax: 316 381 Fax: 317 Fax: 316 381 Fax: 317 Fax | RESULT 2 A2473098 LOCUS A2473098 LOCIMO288114 R. DNA sequence. A2473098 LOCIMO28 LOCIMO38 LOCIMO |
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| * Query Match Length DB ID Description | 76.0 37 11 AA734467 AA734467 vC9400B.r 76.0 37 11 AA734467 AA734467 vC9400B.r 66.0 50 107 AU107725 AU107725 AU107725 65.0 50 107 AU107724 AU107732 AU107732 65.0 50 107 AU107732 AU107732 AU107732 65.0 50 107 AU107734 AU107732 AU107732 65.0 50 107 AU107734 AU107732 AU107732 65.0 50 107 AU107734 AU107734 AU107734 65.0 50 107 AU107736 AU107734 AU107734 <td>AAJ34467 37 bp mRNA EST 07-JAN-1998 vt94a08.rl Soares_mammary_gland_NbMMG Mus musculus cDNA clone INAGE:1178774 5' similar to TR:Q09472 Q09472 ElA-ASSOCIATED PROTEIN P300. ;, mRNA sequence. AA734467 AA734467 AA734467 AA734467 GI:2756134 EST. house mouse. Mus musculus musculus Ext. house musculus Exteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases I to 37) Marray. , Jacy. M. Hillier, L. Allen, M. Bewles, M. Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy. M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,</td> | AAJ34467 37 bp mRNA EST 07-JAN-1998 vt94a08.rl Soares_mammary_gland_NbMMG Mus musculus cDNA clone INAGE:1178774 5' similar to TR:Q09472 Q09472 ElA-ASSOCIATED PROTEIN P300. ;, mRNA sequence. AA734467 AA734467 AA734467 AA734467 GI:2756134 EST. house mouse. Mus musculus musculus Ext. house musculus Exteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases I to 37) Marray. , Jacy. M. Hillier, L. Allen, M. Bewles, M. Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy. M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., |
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Institute of Medical Science, University of Tokyo
Suzukiéins.u-tokyo.ac.jp
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Suzukifix. Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Email: ysuzukieins.u-tokyo.ac.jp
Suzuki/Y. Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
S. Construction and characterization of a full length-enriched and
a 5'-end-enriched CDNA library. Gene 200 (1-2), 149-156 (1997).
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Suzukl, Y., Taunaka, T., Taira, H., Mizushima-Sugano, J., Sese, J., Hata
'H., Ota, T., Isogai, T., Tanaka, T., Nakamura, Y., Morishita, S., Okubo
'K., Suyama, A. and Sugano, S.
Fine Structural analysis of transcription start sites of human
mRNAs using full-length enriched and 5'-end enriched cDNA libraries
Unpublished (2001)
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AU107726 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
COL02114, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
/clone="BX3A0030"
/clone_llb="Sugano Homo sa
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/clone="COL02114"
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Matches 13; Conservative
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  Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
1711: 0158 5606
Fax: 801 585 7177
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AU107725 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
BX3A0030, mRNA sequence.
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/clone_lib="Mouse 10kb plasmid UUGCIM library"
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Pred. No. 3.9e+04;
0; Mismatches 3; Indels 0
                                                                                                                                                                                     Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0288 row: I column: 14
                                                                                                                                                                                                                                                                         Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 32.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
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AU107725.1 GI:13557246
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Best Local Similarity 83.3
Matches 15; Conservative
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
5-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
5-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
7-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
7-1, Shirokanedai, Minatoku, Gene 200 (1-2), 149-156 (1997).

1-1, Shirokanedai, Minatoku, Gene 200 (1-2), 149-156 (1997).
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HEP13686, mRNA sequence.
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AU107733 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HP119813, mRNA sequence.
AU107733 GI:13557254
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/db_xref="taxon:9606"
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AU107732/c
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Bummalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 50)

Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata
'H., Ota,T., Isogai,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata
'H., Ota,T., Isogai,T., Tanaka,T.; Nakamura,Y., Morishita,S., Okubo
'K., Suyman,A. and Sugano,S.
Fine Structural analysis of transcription start sites of human
mRNAs using full-length enriched and 5'-end enriched cDNA libraries
Upublished (2001)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
108-8639, Japan
Email: ysuzuki@ims u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
'S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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Eukaryota, Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 50)
Suzukli,Y. Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isongai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo,K., Suyama,A. and Sugano,S.
Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries
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Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Hof-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki@ims.u-tokyo.ac.jp
Suzukif,iv. Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
A. Construction and characterization of a full length-enriched and 5'-end-enriched cDNa library. Gene 200 (1-2), 149-156 (1997).
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M107730 Sugano Homo sapiens CDNA library Homo sapiens CDNA clone
HEP01701, mRNA sequence.
                                                           AU107729 50 bp mRNA EST 05-APR-2001
AU107729 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HEP01448, mRNA sequence.
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/db_xref="taxon:9606"
/clone="HEP01448"
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Matches 13; Conserv
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 50)
Suzuki, Y., Tsunda, T., Taira, H., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Nakamura, Y., Morishita, S., Okubo, K., Suyama, A. and Sugano, S.
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AU107736 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
KAT09254, mRNA sequence.
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AU107737 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
REC00765, mRNA sequence.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                   Score 13; DB 107;
Pred. No. 4.9e+04;
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100.0%; Pred. No. 4...
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/db_xref="taxon:9606"
/clone="RAT09254"
/clone_lib="Sugano Homo sa
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AU107737.1 GI:13557258
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Best Local Similarity 100.
Matches 13; Conservative
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                                                      Query Match
Best Local Similarity
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AU107737/c
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                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (Dases 1 to 50)

Suzuki,Y., Tsunoda,T., Talra,H., Mizushima-Sugano,J., Sese,J., Hata, H., Otar,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo,K., Suyama,A. and Sugano,S.

Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries on upublished (2001)

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4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo Makagawa,K., Maruyama,K., Suyama,A. and Sugano
S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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AU107734 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HEP14963, mRNA sequence.
AU107734
GI:13557255
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_cref="taxon:9606"
/clone="HEF13813"
/clone=lib="Sugano Homo sapiens cDNA library"
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m c} 13 q 9 t
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/db_xref="taxon:9606"
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Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
                                                                                                                                                                                                                                                                                                                      Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Bukaryota, Metazoa, Chordata, Catarrhini, Hominidae, Homo.

(bases 1 to 50)
Suzukli,Y. Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isoqai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo,K., Suyama,A. and Sugano,S.
Fine Structural analysis of transcription start sites of human mnNAs using full-length enriched and 5'-end enriched cDNA libraries
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                           AU107739 50 bp mRNA EST 05-APR-2001
AU107739 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
2RV61978, mRNA sequence.
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Contact: Robert B. Weiss
University of Utah Genome Center:
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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/organism="Homo sapiens"
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/clone=lbb="Sugano Homo sapiens cDNA library"
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Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries of npublished (2001)
Contact: Yutaka Suzuki
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1 Medical Science, University of Tokyo
4-6-1, Shrokanedai, Minatoku, Tokyo 108-8639, Japan
Bmail: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
                                                                                    Contact: Yutaka Suzuki
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Institute of Medical Science, University of Tokyo
Suzuki, Mirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
'S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries Unpublished (2001)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/G0 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarcse gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (qi|4732114 qib|AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

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1. (Dasas 1 to 50)

1. Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo,K., Suyama,A. and Sugano,S.

1. Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries on Unpublished (2001)

1. Contact: Yutaka Suzuki

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AU105903 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
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                                                Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0414 row: M column: 23
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 45.
Location/Qualifiers
                                                                                                                                                                                                                                                                         /organism="Mus musculus"
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AU105903.1 GI:13555424
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Tel: 801 585 5606
Fax: 801 585 7177
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Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers
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                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
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1 2 1 c 9 9 17 t
                                                                                                                                                                                                                                                                                                                                                  Score 12.8; DB 107; Length 50;
Pred. No. 6.1e+04;
0; Mismatches 2; Indels 0
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87.5%;
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Matches 14; Conservative
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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       GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                             1344157 seqs, 7733874588 residues
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Maximum Match 100%
Listing first 45 summaries
                                                   OM nucleic - nucleic search, using sw model
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AR038139 Sequence 179867 Sequence 7 A87594 Sequence 2 AR075944 Sequence E10759 PCR primer E10798 PCR primer A97414 Sequence 4 AR022050 Sequence

Description

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NON-COVALENT COMPLEX COMPRISING AT LEAST AN ANTIBODY AND ELEMENT BINDING WITH IMMUNOGLOBULINS ASSOCIATED WITH AN ACTIVE SUBSTANCE, BETHOD OF PREPARING AND APPLICATIONS PACENT: WO 9834956-A 213-AGG-1998; COMMISSARIAT ENERGIE ATOMIQUE (FR); DREVET PASCAL (FR)
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Pred. No. 2.1e+04;
0; Mismatches 4; Indels
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            PAT
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Pred. No. 1.6e+04;
0; Mismatches 2;
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/organism="unidentified"
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a 9 c 10 g 15
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AR075944
AR075944.1 GI:10002690
 1/9867 29 bp DNA
Sequence 7 from patent US 5708140.
179867
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A87694
A87694.1 GI:6736312
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Drevet, P. and Menez, A.
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80.0%;
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ilarity 88.2%;
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A65301 Sequence 24
AR036134 Sequence
AR0669509 Sequence
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AR071481 Sequence
AR080501 Sequence
AR071089 Sequence
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E15443 PCR primer
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AR084169 Sequence
A36486 Sequence 27
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AR028960 Sequence
A23344 Artificial
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AR079838 Sequence
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117561 Sequence 24
I92840 Sequence 14
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65366 Sequence 2
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AR088908 Sequence
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1 (bases 1 to 29)
Martens,G.JullanusMaria, Chaudhuri,B. and Stephan,C.
Recombinant production of proteins using 7B2 protein
Patent: US 5804417-A 9 08-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69.0%; Score 13.8; DB 9; Length 29; 88.2%; Pred. No. 1.6e+04; Live 0; Mismatches 2; Indels
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Sequence 9 from patent US 5804417.
AR038139
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AR038139.1 GI:5956856

RESULT 1 AR038139/c DEFINITION Unknown.

ORGANISM

REFERENCE AUTHORS

ACCESSION VERSION KEYWORDS SOURCE

tgatgcttaaaagctta 19 Conservative

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Similarity

Query Match Best Local Simi Matches 15;

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FEATURES

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Higashida H., Murakami K., Hama Y., Tsukamoto Y., Isoai A., Kumagai H.; "FUSED PROTEIN AND GENE CODING SAID PROTEIN"; Patent number JP1996053500-A/8, 27-FEB-1996. ASAHI GLASS CO LID.
                                                                                                                                                                                                                                                                                                                                                                                                               11-AUG-1994 JP 1994209368
HIGASHIDA HIDEKI, MURAKAMI KIMIKO, HAWA YUKO, TSUKAMOTO YOKO, ISOAI ATSUSHI, KUMAGAI HIROMICHI
COTAISOO, CL2N1/19, Cl2N1/5/09, Cl2P21/02, (Cl2N1/19, Cl2R1:645), Cl2R1:645);
                           Length 20;
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                                              Indels
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                          Score 13.2; DB 45;
Pred. No. 3.2e+04;
0; Mismatches 3;
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83.3%; Pred. No. 3.2e+04;
live 0; Mismatches 3;
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02-SEP-2000 (Rel. 65, Last updated, Version 2)
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/db_xref="taxon:32644"
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Best Local Similarity 83.3%;
Matches 15; Conservative
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20 ATGAAGATCAAAAGCTTA 3
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JP 1996053500-A/8
27-FEB-1996
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                                                                                                                                                                             E10798.1
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E10798
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A97414
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1 (bases 1 to 44)
Thastrup,O., Tullin,S.slashed.ren, Poulsen,L.Kongsbak and Bj.o slashed.rn,S.Petersen.
Method of detecting biologically active substances by using green fluorescent protein
Fluorescent protein
Patent: US 5558713-A 5 28-SEP-1999;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                    Higashida H., Murakami K., Hama Y., Tsukamoto Y., Isoai A., Kumagai H., "MODIFIED GENE CODING HUMAN SERUM ALBUMEN";
Patent number JP1996051982-A/11, 27-FEB-1996.
ASAHI GLASS CO LID.
                                                                                                                                                          Gaps
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                                                                                                                                 Score 13.4; DB 9; Length 44;
Pred. No. 2.6e+04;
0; Mismatches 1; Indels
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/organism="Artificial sequences"
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02-SEP-2000 (Rel. 65, Last updated, Version 2)
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                                                                                                                                                                                                                                                                                                                                            PCR primer for gaining human serum albumin.
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                                                                                                                                                                                                                                                   standard; DNA; UNC; 20 BP.
                                                                                  /organism="unknown"
8 c 11 g
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                                                                                                                                    67.0%;
93.3%;
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Artificial sequences.
JP 1996051982-A/11
27-FEB-1996
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                                                                                                                                    Query Match 67.0
Best Local Similarity 93.3
Matches 14; Conservative
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hypothetical: No;
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unclassified
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E10769/c
ID E10769
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Length 33;

09-MAR-1998

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1 (bases 1 to 25)
Sasaki,K., Mori,T. and Makino,S.
Attenuated measles virus vaccine containing specific nucleotide sequence and a method for its absolute identification patent: US 58247777 A 10 20-OCT-1998;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61.0%; Score 12.2; DB 9; Length 25;
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Pred. No. 3.3e+04;
0; Mismatches 3;
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Pred. No. 6.4e+04;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                      FMR1 RELATED PROTEIN
PATENT: WO 9712969-A 3 10-APR-1997;
DEUTSCHES KREBSFORSCH (DE)
Other publication DE 19534763 970515.
Location/Qualifiers
        Patent: US 5728821-A 14 17-MAR-1998;
Location/Qualifiers
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AR049871
AR049871.1 GI:5971863
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/organism="unidentified"
/db_xref="taxon:32644"
a 7 c 7 g l:
                                                                                                                                                                                                                                                                  A61915 35 bp DNA
Sequence 3 from Patent W09712969.
A61915
A61915.1 GI:3716021
                                                 /organism≂"unknown"
12 a 7 c 7 g
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7 c 6 q
                                                                                                                    66.0%;
83.3%;
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78.9%;
                                                                                                                                                                                                                                                                                                                                                                 unclassified.
1 (bases 1 to 35)
Poustka, A. and Coy, J.
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                                                                                                                                                                          3 tgatgcttaaaagcttac 20
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Best Local Similarity 78.9°
Matches 15; Conservative
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         26-JAN-2000
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                                                                                                                 1 (bases 1 to 33)
Waldmann, H. and Zelenika, D.
TRANSGENIC MOBEL COMPRISING TCR ALPHA AND BETA CHAINS
PATENT: WO 9916867 A 4 08-APR-1999;
COBBOLD STEPHEN P (GB); ISIS INNOVATION (GB)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Telton, D., Glaser, S., Huse, W. and Rosok, M. Joanne. Mutant BR96 antibodies reactive with human carcinomas Patent: US 5792456-A 14 11-AUG-1998; Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 33)
Yelton,D., Glaser,S., Huse,W. and Rosok,M.Joanne.
Mutant BR96 antibodies reactive with human carcinomas
                                                                                                                                                                                                                                                                                             66.0%; Score 13.2; DB 9; Length 33; 83.3%; Pred. No. 3.3e+04; Live 0; Mismatches 3; Indels
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Sequence 14 from patent US 5728821.
192840
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/organism="unidentified"
/db_xref="taxon:32644"
a 5 c 9 9 9
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AR022050
AR022050.1 GI:3976112
A97414 33 bp DNA
Sequence 4 from Patent WO9916867.
A97414
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83.3%;
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                                              A97414.1 GI:6780760
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AR022050/c
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Length 35;

29-SEP-1999

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1 (bases 1 to 29)
Jepson, I., Greenland, A.J., Thomas, D.R. and Philippe.
CYSTEINE PROTEASE PROMOTER FROM OIL SEED RAPE AND A METHOD FOR THE CONTAINMENT OF PLANT GERMPLASM
Patent: WO 9735983-A 24 02-0CT-1997;
ZENECA LTD (GB)
Other publication AU 2033797 19971017.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 29)
Elrod, S.L. and Cherry, J.R.
Aspergillus oryzae 5-aminolevulinic acid synthases and nucleic acids encoding same
Patent: US 5871991-A 4 16-FÉB-1999;
Location/Qualifiers
                                                                                                                                                                                                                                                                                              61.0%; Score 12.2; DB 9; Length 29; 82.4%; Pred. No. 1e+05; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Length 29;
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Pred. No. 1e+05;
0; Mismatches
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/organism="unidentified"
/db_xref="taxon:32644"
/clone="CYSG12CR"
7 a 4 c 8 9 10
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Sequence 4 from patent US 5871991.
AR036134 GI:5952802
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82.4%;
 A65301
A65301.1 GI:4531080
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18 TGCTGCTTAAATGCATA 2
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Best Local Similarity 82.4
Matches 14; Conservative
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                                        unidentified.
unidentified
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Best Local Similarity
Matches 14; Conserv
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AR036134/C
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ORIGIN
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Unknown.
Unclassified.
I (bases I to 25)
Sasaki,K., Mori,T. and Makino,S.
Attenuated measles virus vaccine, containing specific nucleotide sequence and a method for its absolute identification
Patent: US 5654136-A 10 05-AUG-1997;
Location/Qualifiers
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1 (bases 1 to 27)

1 (bases 1 to 27)

Hunan blue-light photoreceptor hCRY2

Patent: US 6114503-A 13 05-SEP-2000;

Location/Qualifiers
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Pred. No. 1e+05;
0; Mismatches 3; Indels
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Pred. No. 1e+05;
0; Mismatches 3;
 Pred. No. 1e+05;
             Mismatches
                                                                                                                                             Sequence 10 from patent US 5654136.
159435
159435.1 GI:2478067
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Sequence 13 from patent US 6114503.
AR110319
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82.4%;
Best Local Similarity 82.4%;
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illarity 82.4%;
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       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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1117. 9p_cst48.*

119. 9p_cst48.*

120. 9p_cst51.*

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127. 9p_cst52.*

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139. 9p_cst62.*

131. 9p_cst62.*

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131. 9p_cst62.*

132. 9p_cst62.*

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144. 9p_cst63.*

148. 9p_cst63.*

149. 9p_cst88.*

140. 9p_cst88.*

141. 9p_cst88.*

142. 9p_cst88.*

143. 9p_cst67.*

144. 9p_cst87.*

145. 9p_cst87.*

146. 9p_cst88.*

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148. 9p_cst103.*

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170. 9p_cst20.*

171. 9p_cst20.*

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170. 9p_cst20.*

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| gb_est110:* gb_est111:* gb_htc:* em_gss_hum:* em_gss_hum2:* em_gss_hum2:* em_gss_hum4:* em_gss_hum6:* em_gss_hum6:* em_gss_hum6:* em_gss_hum6:* em_gss_hum6:* em_gss_hum6:* em_gss_hum6:* em_gss_hum7:* em_gss_hum7:* em_gss_hum9:* | 20-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0- | 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 | 200 200 200 200 200 200 200 200 200 200 |
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts JOURNAL Unpublished (2000) COMMENT Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Fax: 801 585 5006 Fax: 801 585 7177 | Email: adunnagenetics.utah.edu Insert Length: 1000 Plate: 0171 row: I column: 17 Seq primer: CGTTCTAAACGACGGCCAGT Class: plasmid ends High quality sequence stop: 50. FEATURES Location/Qualifiers I. :50 /organism="Mus musculus" /strain="CS7BL/6J" /db_xref="taxon:10090" /clone="UUGCIMO171117" /clone="UUGCIMO171117" /sex="Male" /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resources/documents/dnares/). The DNA | Was hydrogramically sheared by repeated passage Unrougn a was hydrogramically sheared by repeated passage Unrough a constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligomucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarcse gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil4732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XIIO-Gold (Stratagene) cells and selected for ampicillin resistance. "Exatagene) cells ORIGIN | Ouery Match 66.0%; Score 13.2; DB 243; Length 50; Best Local Similarity 83.3%; Pred. No. 1.7e+04; Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0; Qy 3 tgatgcttaaaagcttac 20 | RESULT 2 AZ785639 LOCUS LOCUS DEFINITION 2M0029012R Mouse 10kb plasmid UUCCIM library Mus musculus genomic clone UUGCZM0029012 R, DNA sequence. ACCESSION AZ785639 VERSION AZ785639.1 GI:12922599 KEYWORDS SOURCE Nouse mouse. ORGANISM Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Marmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus. 1 (bases 1 to 27) AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reallly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. |
|---|---|--|--|---|
| Score Match Length DB ID 13.2 66.0 50 243 AZ403428 13.65.0 27 249 AZ78539 13.65.0 39 189 U74031 12.8 64.0 37 258 H37H11P | 2 61.0 37 1250 TAS233003 AL425003 2 61.0 37 15 A102443 A1024143 2 61.0 37 15 A102443 A1024143 2 61.0 37 15 A1024443 A1024143 2 61.0 37 158 H40544 H40544 8 59.0 48 128 TAS180010 A14561199 8 59.0 49 258 TAS180010 A14561199 8 59.0 50 189 T73552 A1478473 6 58.0 32 254 A2487122 A245901 6 58.0 47 242 A2345901 A106753 A245901 6 58.0 50 107 A1010753 A245901 6 58.0 50 107 A1010753 A245901 6 58.0 50 107 A1010753 A245901 6 58.0 50 107 A10105753 A245901 6 58.0 50 107 A10105753 A245901 6 58.0 50 107 A10105753 A245901 7 7 7 0 50 258 TAS48100 A14773287 8 57.0 40 242 A2378207 A2378207 8 56.0 40 8 A266447 A266447 | 11.2 56.0 47 15.2 63.245.39 63 | 10.8 53.0 28 249 AZ775467 10.6 53.0 32 249 AZ780363 10.6 53.0 32 249 AZ775467 | RESULT 1 AZ403428 AZ403428 AZ403428 AZ403428 AZCESSION 100171117 F MOUSC 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0171117 F, DNA sequence. AZCESSION AZ403428 AZ403428 AZ403428 AZ403428 AZ403428 AZ403428 AZ403428 AZAMORNS SOURCE Mus musculus ENERTENCE ADMIN D. Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. AMMMALIA, Dases I to 50) AUTHORS I (bases I to 50) AONAGIA. Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. |

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also expressed in brain, cerebellum, eye, lung, kidney and liver as determined by RT-PCR.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: cochlea; Vector: lambda ZAPII; Site_1: EcoRI; Site_2: XhoI"  
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma bruce! (TREU927/4 GUTAT 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
innert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
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Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hall, M., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S. E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
Rebillard,G., Vago,P., Pujol,R. and Hamel,C.P.
Identification of preferentially expressed cochlear genes by
systematic sequencing of a rat cochlea cDNA library
Brain Res. Mol. Brain Res. 47 (1-2), 1-10 (1997)
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T. brucei sheared genomic DNA clone 37h11, forward sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="pco83"
/clone_lib="rat lambda ZAPII library (C.P.Hamel)"
/dev_stage="postnatal day 24"
/lab_host="Escherichia col!"
                                                                                                                           Contact: Hamel, CP
Laboratoire de Neurobiologie de l'Audition - INSERW U254
Institut National de la Sante et de la Recherche Medicale
C.H.R. St-Charles, 34295 Montpellier cedex, France
Tel: (33) 04 67 33 69 75
Fax: (33) 04 67 52 56 01
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 39;
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100.0%; Pred. No. 2.1e+04;
ive 0; Mismatches 0;
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/organism="Rattus norvegicus"
/strain="Wistar"
/db_xref="taxon:10116"
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                                                                                                                                                                                                                                                                                        Email: biomol@mnet.fr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwBAC (gqli4732114)gblAR129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                    Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained .from the Jackson
Laboratory Mouse DNA Resource
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                        Mouse whole genome scaffolding with paired end reads from 10kb
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Soto-Prior,A., Lavigne-Rebillard,M., Lenoir,M., Ripoll,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
/clone="UUGC2M0029012"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
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                                                                                                                                                                                                                       Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0029 row: 0 column: 12
Seq primer: CACACAGGAAAACAGCTAATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/strain="C57BL/6J"
                                                                        Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 27. Location/Qualifiers
and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U74031.1 GI:1658134
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                                                                                                                                                                                                                                                                                                                                                                                              Class: plasmid ends
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                                                   plasmid inserts
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Length 30;

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project, Sanger Center, The Wellcome Trust Genome Sequenting project, Sanger Center, The Wellcome Trust Genome Sequenting Cambridge CB10 18A, E-mail: barrell@sanger.ac.uk and nhl@sanger.ac.uk and nhl@sanger.ac.uk and constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TRED1927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org

Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TA52H11Q 31 bp DNA GSS 13-DEC-2000
T. brucei sheared genomic DNA clone 52h11, reverse sequence, genomic survey sequence.
AL456059
AL456059.1 GI:11856930
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1 (bases 1 to 31)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
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Bukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                        Score 12.2; DB 250;
Pred. No. 5.2e+04;
0; Mismatches 3; I
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Pred. No. 5.2e+04;
0; Mismatches 3;
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/db_xref="taxon:5691"
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(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.065 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligomicleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarcse gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil47321H4glb/H2129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bunalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
El (bases 1 to 30)
Sun, D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
Engublished (2000)
Coulect: Robert B. Weiss
University of Utah Genome Center
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2M0115J16R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0115J16 R, DNA sequence.
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/db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="uu0Gc2M0115J16"
/clone="lib="Mouse 10kb plasmid UUGCIM library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant,
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Pred. No. 2.7e+04;
); Mismatches 2; Indels 0;
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84112, USA
  /organism="Trypanosoma brucei"
/strain="TRE0927"
/db_xref="taxon:5691"
/clone="37h11"
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Insert Length: 10000 Std Error: 0.00
Plate: 0115 row: J. column: 16
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/organism="Mus musculus"
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ilarity 87.5%;
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Fax: 801 585 7177
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Length 31; Indels 27-AUG-1998

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Entaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Entaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla: Eutheria; Primates; Catarrhini; Hominidae; Homo.
E 1 (bases 1 to 48)
E 1 (bases 1 to 48)
E 1 (bases 1 to 48)
I NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC/DCTD/TPP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAW9760 row: k column: 10
High quality sequence stop: 48.
Location/Qualifiers
                                                                                   Email: cgapbs-remain.nib.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by:Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAMS259 row; g column: 01
High quality sequence stop: 38.
Location/Qualifiers
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Investigator providing samples: Gilbert Smith, NIH"
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  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/strafn="CSECH II"
/db_xref="taxon.10090"
/clone="IMAGE:4014744"
/clone_lib="NCI_CGAP_Lu30"
/tissue_type="tumor, metastatic to mammary"
/lab_host="DH10B"
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0; Mismatches
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/db_xref="taxon:9606"
/clone="IMAGE:3923841"
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Matches 14; Conserv
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Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing Center
information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BF144195 38 bp mRNA EST 24-OCT-2000 601786804F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4014744 5', mRNA sequence.
ov73a08.sl Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1642934
3' similar to gb:Dl3748 EUKARYOTIC INITIATION FACTOR 4A-I (HUMAN);,
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                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 37)

1. (CGAP http://www.ncbl.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 38)
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Pred. No. 5.3e+04;
); Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trace considered overall poor quality
Insert Length: 669 Std Error: 0.00
Seq primer: -40m13 fwd. Er from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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/clone_lib="Soares_testis_NHT"
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/organ1sm="Homo sapiens"
/db_xref="taxon:9606"
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/lab_host="DH10B"
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AI024143.1 GI:3239187
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82.4%;
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                                               mRNA sequence.
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Gaps

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(Pharmacia). Library went through one round of normalization to a Cot = 53. Library constructed by Bento Soares and M.Fatima Bonaldo. The adult brain RNA was provided by Dr. Donald H. Gilden. Tissue was acquired 17-18 hours after death which occurred in consequence of a ruptured aortic aneurysm. RNA was prepared from a pool of tissues representing the following areas of the brain: frontal, parietal, temporal and occipital cortex from the left and right hemispheres, subcortical white matter, basal gangila, thalamus, cerebellum, midbrain, pons and medulla."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TRE927/4 GuTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
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Details of T. Drucel sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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1 (bases 1 to 48)
Hall.N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
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T. brucei sheared genomic DNA clone 78c03, reverse sequence,
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Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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                                                                                                                                                                                                                                                                                                                                                                59.0%; Score 11.8; DB 158; Length 37; 81.2%; Pred. No. 8.4e+04; ive 0; Mismatches 3; Indels 0;
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8.7e+04;
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86.7%; Pred. No. 8.7e+04;
ive 0; Mismatches 2;
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/strain="TREU927"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                         /tissue_type="melanotic melanoma"
/tissue_type="melanotic melanoma"
/hab_bost="bull08 (phage-resistant)"
/note="Organ: Siin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Site_1 insert size 2 kb. Library constructed by Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H40544 31-JUL-1995
yn87h08.rl Soares adult brain N2b5HB55Y Homo sapiens cDNA clone
IMAGE:175455 5' similar to gb:X63526 ELONGATION FACTOR 1-GAMMA.
(HUMAN); mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality Insert Length: 1280 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                               Score 12.2; DB 141; Length 48; Pred. No. 5.5e+04; 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Soares adult brain N2b5HB55y"
/sex="Male"
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/db_xref="GDB:3837490"
/db_xref="taxon:9606"
/clone="IMAGE:175455"
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High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
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Location/Qualifiers
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14 c
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82.4%;
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H40544.1 GI:916596
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                                                                                                                                                                                                                                                                                                                                                              1 catgatgcttaaaagct 17
                                                                                                                                                                                                                                                                 Query Match 61.0
Best Local Similarity 82.4
Matches 14; Conservative
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                                                                                                                                                                     BASE COUNT
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AUTHORS
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KEYWORDS
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High qality sequence starts: 1 High qality sequence stops: 1 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 873 Std Error: 0.00
  Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Goderwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280, 000 human expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nhl@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TRE0927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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T. brucei sheared genomic DNA clone 318d05, forward sequence,
genomic survey sequence.
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1 (bases 1 to 32)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S. E., Rajandream, M.A. and Barrell, B.G.
                                                                                                              Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 873
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Pred. No. 8.7e+04;
0; Mismatches 5; I
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/organism="Homo sapie
/db_xref="GDB:499780'
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72.2%;
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Matches 13; Conserv
                                                                                             97044478
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TA318D05P/c
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                                                                                             MEDLINE
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 50)

Hiller, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,

Chissoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins

M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Mardis, E., Moore, M., Hultman, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,

B., Mortis, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Infleanger ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TRE927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
lnsert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: nelsayed@tigr.org
Details of T. brucel sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                   Trypanosoma.

I (bases 1 to 49)

I (bases 1 to 49)

I (bases 1 to 49)

Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.

Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CBIO 1SA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                              TA213B01Q 49 bp DNA GSS 13-DEC-2000
T. brucei sheared genomic DNA clone 213b01, reverse sequence, genomic survey sequence.
AL478475.1 GI:11844434
                                                                                                                                                                                                                                                                          Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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Pred. No. 8.7e+04;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Trypanosoma brucei"/strain="TREU927"
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/clone="213b01"
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Best Local Similarity 86.7
Matches 13; Conservative
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20 GATGCTTAACAGCCT 34
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                                                                                        TA213B01Q/c
                                                                                                                                   DEFINITION
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DEFINITION
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Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
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Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (http://www.jax.org/resources/documents/dnares/). The DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AZ487122 38 bp DNA GSS 05-OCT-2000
1M0316P22F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0316P22 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
1 (bases 1 to 38)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
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/db_xref="taxon:10090"
/clone="UUGC1M0316P22"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
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                                                                                                                                                                                                                                                                                                                                                                                                                              DB 258; Length 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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Pred. No. 1e+05;
0; Mismatches 4;
                                                                                                                                                                                                                1. .32
/organism="Trypanosoma brucei"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0316 row: P column: 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism-"Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                           /strain="TREU927"
/db_xref="taxon:5691"
/clone="318d05"
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Location/Qualifiers
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AZ487122.1 GI:10654557
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Best Local Similarity 77.8
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Fax: 801 585 7177
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was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide Kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarcse gel electrophoresis. Vector DNA was prepared from a derivative of pWDA2 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance. The shear of 9 g 12 t esistance. The pred. No. 1.1e+05; Match SB.08; Score 11.6; DB 244; Length 38; Match SB.08; Pred. No. 1.1e+05; Match SB.08; Pred. No. 1.1e
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Run on:

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176917 Sequence 25
E26933 Vascular en
AR090736 Sequence
111623 Sequence
854330 V alpha J a
AR080704 Sequence
AR019663 Sequence
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                                                             October 2, 2001, 15:56:52; Search time 3339.34 Seconds (without alignments) 69.480 Million cell updates/sec
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       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                       1344157 seqs, 7733874588 residues
                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                            OM nucleic - nucleic search, using sw model
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Perfect score:
Sequence:
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C12N1/21,C12N5/10,C12P21/02//(C12N1/21,C12R1:19),(C12N5/10, PC
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C12P21/02,C12R1:19),(C12P21/02,C12R1:91),C12N15/00,A61K37/24,
                                                                                           1 (bases 1 to 22)
Roblin, R.O. III, Hu, M., Tang, J.S. and Lee, S.
Mycoplasma polymerase chain reaction testing system using a set of mixed and single sequence primers
Patent: US 5693467-A 25 02-DEC-1997;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A61K37/24, A61K37/24, A61K37/24, C12N5/00, (C12N5/00, C12R1:91) CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HIROSHI MITSUI, SUNIL C KAURU, TAKASHI SUGIHARA, RENU WADAWA, PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HIDEO SUZUKI
PC C12N15/09, A61K38/22, A61K38/22, A61K38/22, A61K38/22, A61K38/22,
           03-APR-1998
                                                                                                                                                                                                                                                                                                                                         07-FEB-2001
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Hiroshi, M.S.C.C., Takashi, S.R.W.W. and Suzuki.
Vascular endothelial cell growth factor
Patent: JP 199169183-A 13 29-JUN-1999;
AGENCY OF IND SCIENCE & TECHNOL, TOAGOSEI CHEM IND CO LTD
                                                                                                                                                                                                                         Length 22;
                                                                                                                                                                                                                                              Indels
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Location/Qualifiers
             PAT
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                                                                                                                                                                                                                      Score 11.4; DB 10;
Pred. No. 4.3e+04;
0; Mismatches 1;
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Vascular endothelial cell growth factor.
E26933
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     1/6917 22 bp DNA
Sequence 25 from patent US 5693467.
176917
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/organism="unidentified"
/db_xref="taxon:32644"
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JP 1999169183-A/13
29-JUN-1999
11-DEC-1997 JP 1997362118
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8 c 4 g
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92.3%;
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C Topology: Linear;
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                                         I76917.1 GI:3013071
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JP 1999169183-A/13
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Matches 12; Conservative
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AR082206 Sequence
778252 Sequence 50
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119530 Sequence 6
119532 Sequence 9
186209 Sequence 6
186210 Sequence 7
                                                   AX092192 Sequence
AX007130 Sequence
E51076 Novel Esche
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X70713 M.musculus
I46492 Sequence 47
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A60222 Sequence 18
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A69911 Sequence 6
AX041988 Sequence
AR017555 Sequence
AR084745 Sequence
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I21731 Sequence 6
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AR095615 Sequence
AR049682 Sequence
AR098915 Sequence
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58772 Sequence 18
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AR017553 Sequence
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AX020004 Sequence
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Cowsert,L.M.
Antisense modulation of RhoG expression
Patent: US 5965370-A 17 12-Ocr-1999;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17 from patent US 5965370.
AR078873
AR078873.1 GI:10005619
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AR090849
I06514
MMTCRAIC7
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AX007130
E51076
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AR082206
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AR095615
AR049682
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6 c 6 g
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Query Match
Best Local S:
Matches 12,
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AR078873/c
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JOURNAL
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VERSION
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SOURCE
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Length 21;

DB 10;

Score 11;

73.38;

Query Match

FEATURES

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Gaps

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 37).

Roth, M. E., Holman, P. O. and Kranz, D. M.

Nonrandom use of J alpha gene segments. Influence of V alpha and J alpha gene location
J. Immunol. 147 (3), 1075-1081 (1991)
                                                                                                                                                                                                           General Staff at the National Library of Medicine created this entry [NCBI gibbsq 45430] from the original journal article. This sequence comes from Figure 2 B. On Nov 21, 1996 this sequence version replaced gi:1619731.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Bennett, C. Frank, Condon, T.P. and Cowsert, L.M.
Antisense inhibition of integrin .alpha.4 expression
Patent: US 5968026.A 9 19-OTT-1999;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  73.3%; Score 11; DB 95; Length 37; ilarity 100.0%; Pred. No. 7.1e+04; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                             /gene="V&agr;J&agr;"
/note="T-cell receptor alpha chain"
10 c 9 g 12 t
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85.7%; Pred. No. 1.1e+05;
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                                                           Mus sp. BALB C adult day-37 thymus.
Mus sp.
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Sequence 9 from patent US 5968826.
AR080704
AR080704.1 GI:10007434
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DEFINITION Sequence 2 from patent US 5783683.
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/organism="Mus sp."
/db_xref="taxon:10095"
/partial
 day-37 thymus, Genomic, 37 nt].
S45430
S45430.1 GI:1679985
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Smith, R.S., Curtiss, L.K., Koduri, K.R., Witztum, J.L. and Young, S.G.
Nonnatural apolipoprotein B-100 peptides and apolipoprotein
B-100-apolipoprotein A-I fusion peptides
Patent: US 5408038-A 8 18-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S45430 37 bp DNA ROD 31-MAR-1995 V alpha J alpha ^{\circ}T-cell receptor alpha chain [mice, BALB C, adult
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               Indels
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                                                                                                                                                                                                                                 Unclassified.

Unclassified.

E 1 (bases 1 to 25)
S. Chenchik, A., Jokhadze, G. and Bibilashvilli, R. Methods of assaying differential expression
AL Patent: US 5994076-A 856 30-NOV-1999;
Location/Qualifiers
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 Pred. No. 7.8e+04;
               Mismatches
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Sequence 856 from patent US 5994076.
AR090736 IG::10017491
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Sequence 8 from Patent US 5408038.
111623
111623.1 GI:909141
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Best Local Similarity 100.
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07-0CT-1997

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Unclassified.
I (bases 1 to 24)
Garner J., Darlymple, M.L., Prunkard, D.E. and Foster, D.C.
Garner J., Darlymple, M.L., Prunkard, D.E. and Foster, D.C.
Production of fibrinogen in transgenic animals
Patent: US 5639940-A 10 17-JUN-1997;
Location/Qualifiers
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                                                                              Score 10.8; DB 9; Length 24;
Pred. No. 1e+05;
0; Mismatches 2; Indels
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Sequence 10 from patent US 5639940.
1147711 G1:2471676
           /organism="unknown"
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a 8 c 6 g
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Garner, I., Cottingham, I.R., Temperley, S.M., Foster, D.C., Sprecher, C.A. and Prunkard, D.E. Protein C production in non-human transgenic mammals Patent: US 5905185-A 9 18-MAY-1999;
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Pred. No. 1e+05;
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Leung,W., Darrow,A. and Andrade-Gordon,P.
PAR2 modified transgenic mice
Patent: US 6077990-A 9 20-JUN-2000;
Location/Qualifiers
                                                                                                                                    Patent: US 5783683-A 2 21-JUL-1998;
Location/Qualifiers
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Sequence 9 from patent US 5905185.
AR070473
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Sequence 9 from patent US 6077990.
AR099765.1 GI:12809531
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/organism="unknown"
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AR019663.1 GI:3974777
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Morrison, R.S.
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Best Local Similarity 85.7
Matches 12; Conservative
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1 (bases 1 to 29)

Draper,K.G., Chowrira,B., McSwiggen,J., Stinchcomb,D.T. and Thompson,J.D.

Thy nef targeted ribozymes
Patent: US 5972704-A 50 26-OCT-1999;

Location/Qualifiers
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85.7%; Pred. No. 9.9e+04;
tive 0; Mismatches 2;
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Sequence 50 from patent US 5972704.
AR082206
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synthetic construct.
synthetic construct
artificial sequence.
1 (bases 1 to 36)
Schantz,C. and Kopetzki,E.
Escherichia coll host/vector system based on antibiotic-free selection by complementation of an auxotrophy Patent: EP 0972838-A 16 19-JAN-2000;
ROCHE DIAGNOSTICS GMBH (DE)
                                                                                                                                                                                                                                                                        Score 10.8; DB 9; Length 3
Pred. No. 9.5e+04;
0; Mismatches 2; Indels
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/db_xref="taxon:32630"
/note="primer"
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 AX007130.1 GI:9995021
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Tandon,N., Sun,B., Nakamura,T. and Yamamoto,N.
Platelet membrane glycoprotein vi (gpvi) dna and protein sequences, and uses thereof
Patent: WO 0116321-A 8 08-MAR-2001;
OTSUKA PHARMACEUTICAL CO., LTD. (JP)
Location/Qualifiers
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                                                                                                                                         Unknown.
Unclassified.
1 (bases 1 to 29)
1 (bases 1 to 29)
Draper, K.G., Chowrira, B., McSwiggen, J., Stinchcomb, D.T. and Thompson, J.D.
HIV targeted ribozymes
Patent: US 5693535-A 50 02-DEC-1997;
Location/Qualifiers
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    /organism="synthetic construct"
/db_xref="taxon:32630"

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(without alignments)
13.131 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

4

| TITLE Mouse whole genome scaffolding with paired end reads from 10kb Damand Inseries (2000) COMMENT CONTACT. Robert B. Weiss to Contact: Robert B. Weiss and Contact: Robert B. Weiss Robert B. Weiss and Contact: Robert B. Weiss Robert B. Weiss and | AZ834614 C AZ834614 50 bp DNA GSS 20-FEB-2001 LOCUS AZ834614 |
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| Score Auth Length DB ID Description 11.8 78.7 40 244 AA453043 AZ453043 1M0254A13 11.1 73.3 50 107 AU103235 AU105258 AU102352 11.7 73.3 50 107 AU103235 AU102352 AU | 1) A2453043 40 bp DNA GSS 04-OCT-2000 LM0254Al3F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0254Al3 F, DNA sequence. A2453043 1 GI:10610442 S A2453043 |
| A 8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 | RESULT 1 AZ453043/C LOCUS DECTINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS |

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Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries (Unpublished (2001)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y. yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
Suzuki, Y., Tsunoda, T., Taira, H., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Nakamura, Y., Morishita, S., Okubo, K., Suyama, A. and Sugano, S.
Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries
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Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Suzuki, Mirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers
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AU102352 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HRC01304, mRNA sequence.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RAT00883"
/clone_lib="Sugano Homo sapiens cDNA library"
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Pred. No. 3.3e+04;
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iive 0; Mismatches 0;
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/note-"Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/G1 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pwD42 (qi|473211qip)AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (stratagene) cells
and selected for ampicialin resistance."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo
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AU106328 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
KAT00883, mRNA sequence.
                                                                                                                                                                                         SIC,
                             Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                         Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., 84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone="UUGC2M0117121"
/clone_llb="Mouse 10kb plasmid UUGC1M library"
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                                                                                                                                                                                                                                                                                   Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0117 row: I column: 21
                                                                                                                                                                                                                                                                                                                                                             Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/strain="C57BL/6J"
                                                    plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                  Class: plasmid ends
High quality sequence stop: 50.
Location/Qualifiers
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AU106328.1 GI:13555849
       and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="Male"
                                                                                                                                                                                                                              Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@qenet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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/ctune_nouse into present cooten interests
/lab_host="E. Coli strain XIIO-Gold, Tl-resistant, F-"
/lab_host="E. Coli strain XIIO-Gold, Tl-resistant, F-"
/note="Westor: pW042nv; Purified genomic DNA from M.
musculus C57BL/GJ (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligomucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AR129072.1), a copy-number
inducible derivative of plasmid RI. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
chemically-competent E. coli XIIO-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 38)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AZ591206 38 bp DNA GSS 13-DEC-2000 1M0401K03F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC1M0401K03 F, DNA sequence.
     S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/db_chone="UGC1M0258R21"
/clone_lib="Mouse 10kb plasmid UGGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 10.8; DB 244; Length 27;
Pred. No. 6.9e+04;
0; Mismatches 2; Indels 0;
        308, Biomedical Polymers Research Bldg., 20
  Rm. 308, Biomedical Polymers Research Bld 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0258 row: K column: 21
Seq primer: CGTYGTAAAACGACGGCCAGT
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Ontpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
                                                                                                                                                                                                                                                    High quality sequence stop: 27. Location/Qualifiers
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AZ591206.1 GI:11713312
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Matches 12
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Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Email: Suzuki@Ims.u-tokyo.ac.jp
Suzuki,Y.. Yoshitomo.Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
S. Construction and characterization of a full length-enriched and 5'-end-enriched cDNa library. Gene 200 (1-2), 149-156 (1997).
                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota, Mactazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 50)
Suzukli, Y., Tsunoda, T., Taira, H., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isoqai, T., Tanaka, T., Nakamura, Y., Morishita, S., Okubo, K., Suyama, A. and Sugano, S.
Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
1 (Jases 1 to 27)
Dunn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
A., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
Musce whole genome scaffolding with paired end reads from 10kb
plasmid inserts
                                                                                                                                                             AU102356 50 bp mRNA EST 05-APR-2001
AU102356 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ADSH00944, mRNA sequence.
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0
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16 c 20 g 6 t
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73.3%; Score 11; DB 107; Length 50;
Best Local Similarity 100.0%; Pred. No. 5.6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels
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/db_xref="taxon:9606"
/clone="ADSH00944"
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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19 GCGGGCTCACA 9
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Gaps

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FEATURES

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3/); double-stranded CDNA was ligated to Eco RI adaptors [AATTCGGATCCTTG], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library constructed by Bob Barstead. "
12 c 12 g 6 t
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Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTAt 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + 1 method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
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1 (bases 1 to 44)

Hall, M., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,

Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,

Chillingworth, C., Sanondream, M.A. and Barrell, B.G.

Direct Submission

Submitted (10-DEC-2000) Trypanosoma brucel genome sequencing

project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,

Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:592524
Trace considered overall poor quality
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:1078228"
/clone_lib="Barstead mouse proximal colon MPLRB6"
/dev_stage="7 day juvenile"
/lab_host="DH108"
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Eukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae;
                     WashU-HHMI Mouse EST Project Washington University School of MedicineP 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 10.8; DB 12;
Pred. No. 7.2e+04;
); Mismatches 2;
  Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="FVB/N"
/db_xref="taxon:10090"
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AL481198
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85.7%;
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Trypanosoma brucei
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the Dunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (qil4732114 qib]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10.Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Dases I to 41)
Marra,M., Hiller,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host="E. Coli strain Xil0-Gold, Ti-resistant, F-"/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                     Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 84112, USA
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                                                                                                                                                    Std Error: 0.00
                                                                                                                                                                            Plate: 0401 row: K column: 03
Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                      /organism-"Mus musculus"
                                                                                                                                                                                                                                                                                                                                                            /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0401K03"
                                                                                                                                                                                                                                                            High quality sequence stop: 38. Location/Qualifiers
                                                                                                                           Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
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85.7%;
University of Utah
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Best Local Similarity 85.7
Matches 12; Conservative
                                                                    Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genet
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Mus musculus
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RESULT

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SOURCE

ORIGIN

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Gaps

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Length 41; Indels 13-DEC-2000

Gaps

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 50)

Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo,K., Suyama,A. and Sugano,S.
Fine Structural analysis of transcription start sites of human mnNAs using full-length enriched and 5'-end enriched cDNA libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Suzukitute of Medical Science, University of Tokyo
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers
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                                                                                                                                                                                                             AU107932 50 bp mRNA EST 05-APR-2001
AU107932 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ZRV62008, mRNA sequence.
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T. brucei sheared genomic DNA clone 140a04, forward sequence,
genomic survey sequence.
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Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
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Pred. No. 7.3e+04;
0; Mismatches 2; Indels 0
       Indels
     5
     Mismatches
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/db_xref="taxon:9606"
/clone="ZRV62008"
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Trypanosoma brucei
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Turnor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NOI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/Dbrp/Image/image.html
Seq primer: -40ml3 fwd. ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      //note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 wector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."
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                      Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA934014 48 bp mRNA EST 27-APR-1998 om58e11.s1 NCI_CGAP_GC4 Homo sapiens CDNA clone IMAGE:1551404 3' similar to 9b:X01683 ALPHA-1-ANTITRYPSIN PRECURSOR (HUMAN);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 48) NCI-OGAP http://www.ncbi.nlm.nih.gov/ncicgap. NCI-OGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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                                                                                                                                                                                                                                                                                                          Score 10.8; DB 258; Length 44; Pred. No. 7.2e+04; 0; Mismatches 2; Indels 0
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/db_xref="taxon:9606"
/clone="IMAGE:1551404"
/clone="Ib="NCI_CGAP_GC4"
/tissue_type="pooled germ cell tumors"
/lab_host="DH108"
                                                                                       1. .44
/organism="frypanosoma brucei"
/strain="freugy7"
/db_xref="taxon:5691"
/clone="233a12"
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Email: nelsayed@tigr.org
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85.7%;
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LOCUS RESULT 10 AA934014/c

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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AUTHORS TITLE

REFERENCE

JOURNAL COMMENT

BASE COUNT ORIGIN

FEATURES

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Gaps

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FEATURES

BASE COUNT

ORIGIN

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31 bp
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AZ345566/c
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               Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.corg
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
France Contact
University of Utah
Head Contact
University of Utah
B41112, USA
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Eukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 25)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islan, H., Longarce, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
'M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1M0572G03F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0572G03 F, DNA sequence.
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/clone="UGC1M0572603"
/clone_11b="Mouse 10kb plasmid UGC1M library"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69.3%; Score 10.4; DB 258; Length 22; 91.7%; Pred. No. 1.1e+05; ive 0; Mismatches 1; Indels 0.
                                                                                                                                                                                                                                                                                                                         /organism≂"Trypanosoma brucei"
/strain="TREU927"
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Insert Length: 10000 Std Error: 0.00
Plate: 0572 row: G column: 03
Seg primer: CGTTGTAAAACGACGGCCAGT
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/organism="Mus musculus".
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Fax: 801 585 7177
nhl@sanger.ac.uk
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high monar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114) HgblARL29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rose, M., Rose, M., Rose, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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Unpublished (2000)
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/strain="057BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0080114"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 10.4; DB 249; Length 25;
Pred. No. 1.1e+05;
); Mismatches 1; Indels 0;
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Fax: 801 585 7177
Email: ddun@qenetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: I column: 14
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Class: plasmid ends
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University of Utah Genome Center
University of Utah
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Best Local Similarity 91.7%;
Matches 11; Conservative
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                                                                                                         (http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4. polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil47321Hqfb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Welss, R., Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts.
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/lab_host-"E. Coli strain XLIO-Gold, Tl-resistant, F-" /note-"Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/63 (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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Insert Length: 10000 Std Error: 0.00
Plate: 0333 row: G column: 22
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Seq primer: CACACAGGAAACAGCTATGACC
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University of Utah
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Location/Qualifiers
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Contact: Robert B. Weiss
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Fax: 801 585 7177
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114)fplAh129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the linsert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
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                                                                                                                                                                              Laboratory Mouse DNA Resource
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Matches 11; Conservative
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                             October 2, 2001, 15:56:53 ; Search time 3339.34 Seconds (without alignments) 69.480 Million cell updates/sec
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      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                       1344157 seqs, 7733874588 residues
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Maximum Match 100%
Listing first 45 summaries
                                           OM nucleic - nucleic search, using sw model
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Database

152125 Sequence 45 AR032874 Sequence 129614 Sequence 129615 Sequence 48 129615 Sequence 48 191288 Sequence 48 191289 Sequence 48

144719 Sequence 45

144719 152125 AR032874 AR032875

Description

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SUMMARIES

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Unclassity.

Walsh, T.A., Hey, T.D. and Morgan, A.E.R.
Walsh, T.A., Hey, T.D. and Morgan, A.E.R.
Ribosome-inactivating proteins, inactive precursor forms thereof, process for making and a method of using Patent: US 5646026-A 45 08-JUL-1997;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                l (bases 1 to 50)
Edwards, C.A., Cantor, C.R., Andrews, B.W., Turin, L.M. and Fry, K.E.
Method of determining DNA sequence preference of a DNA-binding
molecule
                                                                                                                                                                                                                                                     Gaps
                     07-OCT-1997
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Pred. No. 1.4e+04;
); Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                          AR032874 50 bp DNA
Sequence 486 from patent US 5869241.
AR032874
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Sequence 487 from patent US 5869241.
AR032875.1 GI:5948480
                 Sequence 45 from patent US 5646026. 152125 GI:2473376
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Best Local Similarity 93.3%;
Matches 14; Conservative (
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86.78;
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Best Local Similarity 86.7
Matches 13; Conservative
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AR015530 Sequence
AX019566 Sequence
E04774 Synthetic D
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AR07892 Sequence
AR080603 Sequence
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A803874 Sequence
AR026168 Sequence
AR02629 Sequence
AR026248 Sequence
E61327 Probe for d
I82910 Sequence 64
I82956 Sequence 64
I82976 Sequence 78
I82976 Sequence 78
I82996 Sequence 78
I82996 Sequence 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 18)
Walsh,T.A., Hey,T.D. and Morgan,A.E.R.
Ribosome-inactivating proteins, inactive precursor forms thereof, a
process for making and a method of using
Patent: US 5635384-A 45 03-JUN-1997;
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A57638 Sequence 13
AR088301 Sequence
AR032336 Sequence
AX049383 Sequence
AX05134 Sequence
AX05164 Sequence
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106269 Sequence 27
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Pred. No. 1.1e+03;
); Mismatches 1;
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                   AX022755
AR016058
AR075530
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AR026168
AR026220
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Best Local Similarity 93.3
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                      Unknown.
Unknown.
Unknown.
Unclassified.
1 (bases 1 to 50)
Edwards,C.A., Cantor,C.R., Andrews,B.M. and Turin,L.M.
Edwards,C.B., Cantor,C.R., Andrews,B.M. and Turin,L.M.
Edwards,C.B., Canton,C.B., Canto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 50)
Edwards, C.A., Cantor, C.R., Andrews, B.M. and Turin, L.M.
Screening assay for the detection of DNA-binding molecules
Patent: US 5726014-A 487 10-MAR-1998;
Location/Qualifiers
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86.7%; Pred. No. 1.4e+04;
ive 0; Mismatches 2;
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86.7%; Pred. No. 1.4e+04;
ive 0; Mismatches 2;
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191289
191289.1 GI:3918785
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Sequence 486 from patent US 5726014.
191288 191388.1 GI:3935758
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Sequence 23 from Patent W00118250.
AX094845 GI:13511048
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1 (Bases I to 50)
Edwards,C.A., Cantor,C.R., Andrews,B.M., Turin,L.M. and Fry,K.E. Sequence-directed DNA-binding molecules compositions and methods Patent: US 5578444-A 487 26-NOV-1996;
Location/Qualifiers
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Edwards, C.A., Cantor, C.R., Andrews, B.M., Turin, L.M. and Fry, K.E. Sequence-directed DNA-binding molecules compositions and methods Patent: US 5578444-A 486 26 NOV-1996;
Location/Qualifiers
Edwards,C.A., Cantor,C.R., Andrews,B.M., Turin,L.M. and Fry,K.E. Method of determining DNA sequence preference of a DNA-binding molecule
Patent: US 5869241-A 487 09-FEB-1999;
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REFERENCE AUTHORS source

FEATURES

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Tucker,W., Huttner,E., Ignart,F. and Vermeulen,A.
Ribozymes capable of conferring resistance to potyvirus infection, and plants expressing said ribozymes
Patent: Wo 9928485-A 46 10-JUN-1999;
Gene Shears PTY LTD (401); TUCKER WILLIAM (AU); HUTTNER ERIC (FR);
IGNART FREDERIC (FR); VERMEULEN AGNES (FR)
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1 (bases 1 to 25)

1 (labonteau, B., Feng, J., Funk, W. and Andrews, W.H. Assays for the DNA component of human telomerase Patent: US 5776679-A 26 07-JUL-1998;
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Valleponteau, B., Feng, J., Funk, W. and Andrews, W.H. Mammalian telomerase
Patent: US 5958680-A 27 28-SEP-1999;
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Sequence 26 from patent US 5776679.
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Sequence 27 from patent US 5958680.
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                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 21)
Lander, E.S., Gargill, M., Ireland, J.S., Bolk, S., Daley, G.Q. and Mccarthy, J.J.
Single nucleotide polymorphisms in genes Patent: WO 0118250-A 23 15-WAR-2001; WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US); Millennium Pharmaceuticals, Inc. (US)
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Matches 12; Conservative
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E04774 I E1993091876-A 13 16-APR-1993;
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C C12N9/54,C11D3/386,C12N1/21,C12N15/57,(C12N9/54,C12R1:07), PC
(C12N1/21,
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Synthetic DNA for site directed mutagenesis of protease derived
from Bacillus NKS-21.
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Artifical sequence: Genes.
Bacillus NKS-21
JP 1993091876-A/13
16-ARP-1993
02-OCT 1991 JP 1991280313
TAKINISHI EIKO, KAKINUMA SHINJI, TAKEMOTO AYANO, PI
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KEITH WILLIAM NICOL (GB); CANCER RES CAMPAIGN TECH (GB)
Location/Qualifiers
                                        Score 11.4; DB 9; Length 25;
Pred. No. 2.5e+04;
0; Mismatches 1; Indels
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/organism="synthetic construct" /
/db_xref="taxon:32630" /
/note="primer" 9 9 3 t
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Sequence 20 from Patent WO9938964.
AX019566
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92.3%;
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synthetic construct
artificial sequence.
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Keith, W. N.
                                 Query Match
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1. 26
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3 5 c 5 9 t
strandedness: Single;
              topology: Linear;
hypothetical: No;
anti-sense: No;.
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Best Local Similarity 92.3%;
Matches 12; Conservative
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
                                                                                     OM nucleic - nucleic search, using sw model
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| JOURNAL Unpublished (1997) COMMENT Contact: Robert Strausberg, Ph.D. Email: cgapbs-rémail.nih.gov Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R. Emmert-Buck, M.D., Ph.D. | CDNA Library Preparation: Stratagene, Inc. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html | Trace considered overall poor quality Insert Length: 660 Std Error: 0.00 Seq primer: -40m13 fwd. ET from Amersham High quality sequence stop: Location/Qualifiers | color de la color | t SK-; Site_1: y. Primer: Oli quence: 5' | 1.2 KB. | Query Match 78.7%; Score 11.8; DB 12; Length 41; Best Local Similarity 86.7%; Pred. No. 3.2e+04; Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0; | Oy 1 taagcagctgccatt 15 | RESULT 2 AA662608 LOCUS AA662608 LOCUS AA662108 AA662608 AA662608 BET 12-NOV-1997 LOCUS DEFINITION nr16a12.s1 NCI_CGAP_EW1 Homo sapiens CDNA clone IMAGE:1168126 Similar to SW:RIJ4 HIMAN P38663 608 RIROSWAR, PROFEN 1.24 MRNA | GI:2615457 | NISM | REFERENCE 1 (bases 1 to 50) AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), TUMOR Gene Index JOURNAL Unpublished (1997) COMMENT Contact: Robert Strausberg, Ph.D. | Email: cgapps-remail.nin.gov Tissue Procurement: Lee Helman, M.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: David B. Krizman, Ph.D. | CDNA LIDITARY ATRAYED DY: Greg Lennon, FN.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CEAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Seq primer: -40ml3 fwd. ET from Amersham. FEATURES Location/Qualifiers |
|---|---|--|---|--|--|--|--|--|--|------------|--|--|---|
| SUMMARIES Result Query No. Score Match Length DB ID | 11.8 78.7 41 12 AA829551 11.8 78.7 50 10 AA662608 11.4 76.0 45 12 AA794942 11.4 76.0 47 143 BF036568 11 73.3 47 158 H59245 11 73.3 50 107 AU103473 | 7 11 73.3 50 107 AUT04774 AUT04774 AUT04774 B 10.4 77.2 19 244 AZ481008 AZ481008 AZ481008 AZ481008 AZ481008 AZ481008 AZ481008 P 10.8 72.0 28 258 TAX355F03Q AZ487027 AZ487070 AZ487027 AZ487070 AZ487027 AZ487027 AZ487027 AZ487027 AZ48702427 AZ487024027 AZ4870267 AZ487024027 AZ487024027 AZ48702670 AZ487024027 AZ48702677 AZ48702670 AZ48702677 AZ487077 AZ48702677 AZ48702677 AZ48702677 AZ48702677 AZ48702677 AZ4870277 AZ4877 AZ4870277 AZ4877 AZ4877 AZ4870277 AZ4877 AZ48 | 13 10.8 72.0 44 9 AA553766 AA553766 14 10.8 72.0 44 9 AA600013 AA600013 ag 15 10.8 72.0 44 11 AA713885 AA713885 AA713885 n 16 10.8 72.0 44 14 AA989114 AA989114 AA989114 17 10.8 72.0 50 20 A1476044 A1476044 A1476044 18 10.8 72.0 50 107 AU102666 AU102666 | 10.8 72.0 50 107 A0103462 - A0103462 10.8 72.0 50 107 A0104066 A0104066 10.8 72.0 50 107 A0107071 A0107071 10.4 69.3 20 243 A2435787 A2435787 10.4 69.3 21 242 A2337498 A2337498 | 10.4 69.3 22 249 AZ805989 10.4 69.3 26 247 AZ632821 10.4 69.3 31 15 AX1032592 10.4 69.3 31 15 AX1032592 10.4 69.3 31 2244 AZ448456 | 29 10.4 69.3 32 258 TA371C10P AL495613 30 10.4 69.3 34 4 AA282064 AA282064 zt 31 10.4 69.3 34 429 AZ7585014 AZ75913 AZ759713 AZ759713 | 33 10.4 69.3 41 241 A2327077 A2327077 34 10.4 69.3 41 247 A2634745 A2634745 35 10.4 69.3 42 4275762286 A2760286 36 10.4 69.3 42 188 T17561 T17561 R | 37 10.4 69.3 48 249 AZ787799 AZ787799 38 10.4 69.3 49 1 AA047951 AA047951 mJ 39 10.4 69.3 49 13 AA914273 AA914273 AA014273 v 40 10.4 69.3 50 107 AU102448 AU102448 AU102448 41 10.4 69.3 50 107 AU103390 AU1033167 AU1033167 | 10.4 69.3 50 1 10.4 69.3 50 1 10.4 69.3 50 1 | ALIGNMENTS | 10 0 4 10 11 | , | REFERENCE : (bases 1 to 41) AUTHORS NOT. CGAP. Include: Craniata: Vertebrata; Euteleostomi; Mammalia: Eutheria: Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 41) AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), TUMOR Gene Index |

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/clone_lib="NIH_MGC_66"
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/lab_host="DH10B (phage-resistant)"
/note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LiAM9604 row: d column: 09
High quality sequence stop: 47.
Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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/db_xref="taxon:9606"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
I (Dasas 1 to 45)
Marral M. Hiller, L. Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Gelsel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Theising, B., Wilser, Esptce, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wilse, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

The WashU-HHMI Mouse EST Project
Upublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashU-HHMI Mouse EST Project
WashU-HMI Mouse EST Project
WashU-HMI Mouse EST Project
Fax: 314 286 1810
1. .50
/organism="Homo sapiens"
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/db_aref="taxon:9606"
/clone="Inb="NoI_CGAP_Ew1"
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/lab_host="Nector: pAMP10; mRNA made from Ewing's sarcoma,
/note="Vector: pAMP10; mRNA made from Ewing's sarcoma,
/cDNA made by oligo-dT priming. Non-directionally cloned.
Size-selected on agarose gel, average insert size 600 bp.
Reference: Rizman et al. (1996) Cancer Research
56:5380-5383."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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/clone="IMAGE:1110964"
/clone="IMAGE:1110964"
/clone_lib="Knowles Solter mouse blastocyst B3"
/tissue_type="blastocyst"
/dev_stage="embryo (pre-implantation)"
/lab_host="bH10B"
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Pred. No. 3.3e+04;
0; Mismatches 2;
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/strain="B6D2 F1/J"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 50)

Suzuki,Y., Taunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata.

K., Suyama,A. and Sugano,S.

Fine Structural analysis of transcription start sites of human
mRNAs using full-length enriched and 5'-end enriched cDNA libraries

Unpublished (2001)

Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
1 Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitome-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
                                                                                                                                                                                   Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Entitute of Medical Science, University of Tokyo
Banali: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y. Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo,K., Suyama,A. and Sugano,S.
Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries Unpublished (2001)
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AU104774 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HRC05287, mRNA sequence.
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21 c 15 q 9 t
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12 c 11 g 1
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/clone="HRC05287"
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Best Local Similarity 100.
Matches 11; Conservative
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1419
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (Info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 1419 Std Error: 0.00
Seq primer: Promega -21m13
High quality sequence stop: 1.
Location/Qualifiers
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                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 47)

1 (lases 1 to 47)

1 (lases 1 to 47)

N. Jubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M.; Lennon, G., Marra, M., Parsons, J., Rifkln, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.

Unpublished (1995)
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AU103473 Sugano Homo sapiens CDNA library Homo sapiens CDNA clone
HEP17451, mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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/db_xref="taxon:9606"
/clone="IMAGE:204269"
/clone_lib="Soares fetal liver spleen lNFLS"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 47;
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    .47
    /organism="Homo sapiens"

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Best Local Similarity 91.7%;
Matches 11; Conservative (
                           GI:1012077
                                                                                                                                                                                                                                                                                                                                      Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 aagcagctgcca 13
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Gaps

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Indels

RESULT 8 AZ481008/c

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SOURCE

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

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Trypanosound.

Trypanosound.

Trypanosound.

Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,

Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,

Melville,S.E., Rajandream,M.A. and Barrell,B.G.

Direct Submission

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing

project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,

Cambridge CBIO iSA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nhi@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTAT 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: nelsayedetigr.org

Email: nelsayedetigr.org

Details of T. brucel sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA806226 40 bp mRNA EST 12-FEB-1998 oe29f12.s1 NCL_CGAP_Pr25 Homo sapiens cDNA clone IMAGE:140999 3's similar to 9b:M33552 LYMPHOCYTE-SPECIFIC PROTEIN LSP1 (HUMAN);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
                                                                                                                                                                                                                                                                                                                 TA355F03Q 28 bp DNA GSS 13-DEC-2000
T. brucei sheared genomic DNA clone 355f03, reverse sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 10.8; DB 258; Length 28; Pred. No. 1e+05;
                     Score 10.8; DB 244; Length 19; Pred. No. 9.8e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5;
                                                   Pred. No. 9.8e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:5691"
/clone="355f03"
5 c 4 q
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                                                                                                                                                                                                                                                                                                                                                                 genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                  AL497072.1 GI:11872664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA806226.1 GI:2874976
                        72.0%;
85.7%;
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85.7%;
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Matches 12; Conservative
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                                                                                                                            2 aagcagctgccatt 15
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                                                                                                                                                            14 AAGCAGCTACCGTT 1
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                                        Best Local Similarity
Matches 12; Conserv
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                        Query Match
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TA355F03Q/c
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AA806226/c
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DEFINITION
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil4732114[gb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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                                                                                                                                                                                                                                                                             AZ481008 19 bp DNA GSS 04-OCT-2000 1M0302N15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic Clone UUGC1M0302N15 R, DNA sequence. AZ481008 GI:10641989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse whole genome scaffolding with paired end reads from 10kb
                                                   Gaps
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/clone="UUGCIM0302N15"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
                                                0; Indels
                        9e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0302 row: N column: 15
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"/strain="C57BL/6J"
                        Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 19.
Location/Qualifiers
100.08; Pic
                        Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genet
                                                                                                 2 aagcagctgcc 12
                                                                                                                                                    36 AAGCAGCTGCC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                             house mouse
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source

FEATURES

In

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Gaps

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Indels

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

BASE COUNT ORIGIN

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Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: DCTD/DTP CDNA Library Preparation: Ling

Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.

Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing

project Clone distribution: MGC clone distribution information can

be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality

Scores: PRRED from University of Washingtion Genome Center. PRRAP suite. Poly-T Identification: patMatch.pl from Berkeley

Drosophila Genome Project. University of Washingtion Genome Center.

http://www.genome.washington.edu Low Quality Sequence: 10

contiguous PRRED high quality bases following vector sequence. Very

Low Quality Sequence: Trace file contained 42 contiguous distinct

peaks following vector sequence. Polyadenylation: Based upon the

presence of a Xhol site followed by a run of 14 or more T residues
described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Emarell, Oxford University Press, 1999).

Email: nelsayed@tigr.org
Details of T. brucel sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucel/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AW249855 42 bp mRNA EST 07-JAN-2000 BEST 07-JAN-2000 MRNA sequence.
AW249855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                Score 10.8; DB 258;
Pred. No. 1.1e+05;
); Mismatches 2; 1
                                                                                                                                                                                                                 /organism="Trypanosoma brucei"
/strain="TREU927"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                         /db_xref="taxon:5691"
/clone="126907"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
Other_ESTs: 2821534.5prime
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85.7%;
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Best Local Similarity
Matches 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
Gound through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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1 (bases 1 to 41)
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Hall,N., Bowman,S.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nhl@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
                            1 (bases 1 to 40)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Suzanne L. Topalian, M.D., Robert K. Bright,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T. brucel sheared genomic DNA clone 126g07, reverse sequence, AL463426
       Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Pred. No. 1.1e+05;
); Mismatches 2;
                                                                                                                                                                                                                                    CDNA Library Preparation: Stratagene, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                Trace considered overall poor quality
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                            Contact: Robert Strausberg, Ph.D.
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85.7%;
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Trypanosoma brucei
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Best Local Similarity 85.7
Matches 12; Conservative
                                                                                                 Tumor Gene Index
Unpublished (1997
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2 aagcagctgccatt 15
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                                 21 AAGCAGCTCCCAAT
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Best Local Similarity
Matches 12; Conserv
                                                                                                                                                       AA600013
                                                                                                                                                                                                                                                                                                           human.
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AA600013/c
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AA713885/c
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Inpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Elias Campo,
M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Stratagene, Inc.
CDNA Library Preparation: Stratagene, Inc.
CDNA Library Arrayed by: Greg Leanon, Ph.D.
DNA Sequencing by: Mashington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LiNIx at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 865 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
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/note="Organ: lung; Vector: poTB7; Site_1: Xho1; Site_2: ECORI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/Xho1 sites using the following 5' adaptor: GGCAGCAGGGG. Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Butheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 44)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA553766 44 bp mRNA EST 08-SEP-1997 nk29h01.s1 NCI_CGAP_CO11 Homo sapiens cDNA clone IMAGE:1014961 3' similar to gb:M33552 LYMPHOCYTE-SPECIFIC PROTEIN LSP1 (HUMAN);
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/clone_11b="NCI_CGAP_Col1"
/tissue_type="tumor"
/lab_host="SOLR (kanamycin resistant)"
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/db_xref="taxon:9606"
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AA553766.1 GI:2324305
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85.7%;
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Best Local Similarity 85.7
Matches 12; Conservative
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/Lissue_type="bone marrow stroma"
/dev_stage="mixed"
/lab_host="XLI-Blue MRF'/SOLR"
/lab_host="XLI-Blue MRF'/SOLR"
/note="Vector: pBluescript; Site_1: EcoRI; Site_2: XhoI; mRNA made from human bone marrow stroma, CDNA made by oligo-dT priming. Directionally cloned. Size-selected for average insert size >0.5 kb. Library supplied by Dr. Libin Jia (NHGRI)."
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Jia, L., Robey, P., Young, M., Schuler, G., Powell, J., Yang, L., Lennon, G., Hillier, L., Allen, M., Bowles, L., Geisel, S., Kucaba, T., Marra, M., Martin, J., Steptoe, M., Tan, F., Theising, B., Bowers, Y., Wylle, T., Waterston, R., Wilson, R. and Francomano, C.

T., Waterston, R., Wilson, R. and Francomano, C.

Onpublished (1997)

Contact: Wilson RK / Jia L

MashU-MGB/NHGRI EST Project
                          ag29h11.s1 Jia bone marrow stroma Homo sapiens cDNA clone
IMAGE:1091013 3' similar to gb:M33552 LYMPHOCYTE-SPECIFIC PROTEIN
                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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AA713885.1 GI:2726159
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/organism="Homo sapiens"
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                                                                          LSP1 (HUMAN);, mRNA sequence.
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85.7%;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 44)

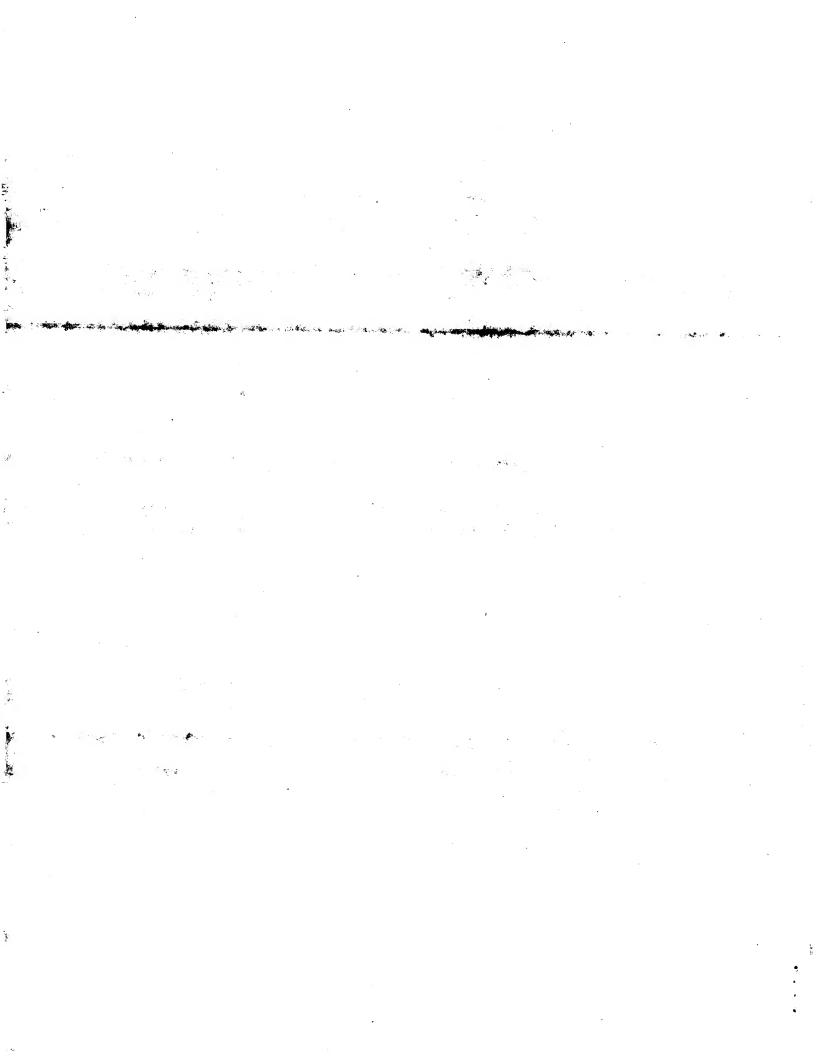
NOI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

Tumor Gene Index

Ontact: Robert Strausberg, Ph.D.
Email: capabs-rfmail.nih.gov

Tissue Procurement: Ilan Kirsch, M.D., Kristina A. Cole, M.D.,
Ph.D. student, Rodrigo F. Chuaqui, M.D., Michael R. Emmert-Buck,
Ph.D. student, Rodrigo F. Chuaqui, M.D., Michael R. Emmert-Buck,
Dh.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CONE distribution: NCI-CGAP Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Trace considered overall poor quality Insert Length: 521 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 1. Location/Qualifiers
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130544 Sequence 7
AR057320 Sequence
AR091705 Sequence
E3480 HSV probe.
136150 Sequence 34
AR060552 Sequence 34
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       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                1344157 seqs, 7733874588 residues
                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                               OM nucleic - nucleic search, using sw model
                                                                                                                                                  IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                              1 tacccaggtgagtct 15
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em_htg_rod:*
em_hum1:*
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em_htgo_hum:*
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em_htg_hum5:*
em_htg_hum6:*
                                                                                                      US-09-757-100B-31
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gb_in1:*
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em_hum7:*
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em_hum5:;
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em_hum3:
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Maximum DB seq length: 50
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Sequence:
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Database

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1 (bases 1 to 22)
Evans,G.A. and Smith,M.W.
Evans,G.A. and Smith,M.W.
Method for generation of sequence sampled maps of complex genomes
Patent: US 5851760-A 668 22-DEC-1998;
Location/Qualifiers
          29-SEP-1999
                                                                                                                                                                                                                                                                                                   07-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 48), Madeau, J.G., Pitner, J.L. Madeau, J.G., Pitner, J.Bruce, Linn, C.Preston and Schram, J.L. Detection of nucleic acids by fluorescence quenching Patent: US 5958700-A 6 28-SEP-1999;
                                                                                                                                                                                                               ;
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Ting,J.Pan-Yung and Chin,K.
Forms of class II MHC transactivator (CIITA)
Patent: US 5994505-A 15 30-NOV-1999;
Location/Qualifiers
            PAT
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Pred. No. 5.4e+03;
); Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 11.8; DB 9;
Pred. No. 1.3e+04;
); Mismatches 2;
          AR067320 22 bp DNA
Sequence 668 from patent US 5851760.
AR067320
                                                                                                                                                                                                                                                                                               Sequence 15 from patent US 5994505. AR091705.1 GI:10018459
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Sequence 6 from patent US 5958700.
AR075823
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5 c 4 g
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11 c 10 g
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                                      AR067320.1 GI:5998542
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92.9%;
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86.7%;
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Best Local Similarity 92.9
Matches 13; Conservative
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Best Local Similarity 86.7
Matches 13; Conservative
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16 TACCCAGCTGTGTCT 30
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AR075823/c
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AR043842 Sequence
AR042502 Sequence
AR088382 Sequence
AR088208 Sequence
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M12881 Mouse Ig re
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AR013900 Sequence
AR013914 Sequence
AR042514 Sequence
AR058394 Sequence
AR013872 Sequence
AR013872 Sequence
AR013876 Sequence
AR01386 Sequence
AR013826 Sequence
AR013732 Sequence
AR013732 Sequence
AR013732 Sequence
        AR003365 Sequence
AR04398 Sequence
AR04398 Sequence
AR073521 Sequence
AR073521 Sequence
AX022131 Sequence
AX022131 Sequence
                                                                                     Sequence 78
Sequence 79
AX069241 Sequence
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143338 Sequence 6
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AX015626 Sequence
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Hoke,G.D., Bradley,M.O., Williams,T.J. and Lee,C.
Antisense oligonucleotides directed against human ICAM-I RNA
Patent: US 5580969-A 7 03-DEC-1996;
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Pred. No. 5.4e+03;
); Mismatches 1;
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AX022132
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AR013888
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AR042502
AR058382
AR088208
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AR058394
AR088220
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AR013872
AR033826
AR042486
AR058366
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AR088192
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AX015626
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9 c 5 g
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130544
130544.1 GI:1821335
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82.7%;
92.9%;
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| TTCCCAGGTGAGTC 5
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Gaps

Query Match

BASE COUNT ORIGIN

SOURCE ORGANISM

AUTHORS TITLE JOURNAL

FEATURES

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RESULT

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Recombinant polypeptides of the haemorrhagical septicemia virus in
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Wadsworth, S., Snyder, B., Reddy, V.B. and Wei, C.
CDNA-genomic DNA hybrid sequence encoding APP770 containing a
genomic DNA insert of the KI and Ox-2 regions
Patent: US 5604131-A 34 18-FEB-1997;
Location/Qualifiers
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                                                                                                                                                            Score 11.4; DB 9; Length 18;
Pred. No. 2.6e+04;
0; Mismatches 1; Indels
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Eriksson, U., Olofsson, B., Alitalo, K. and Pajusola, K. Vascular endothelial growth factor-B
Patent: US 5840693-A 53 24-NOV-1998;
Location/Qualifiers
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                                                                1. .18
/organism="synthetic construct"
/db_xref="taxon:32630"
4 c 7 g 2 t
                           Patent: EP 0377349-A 20 11-JUL-1990;
EUROGENTEC S.A
Location/Qualifiers
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AR060552
AR060552.1 GI:5987002
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Sequence 34 from patent US 5604131.
136150
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/organism="unknown"
a 9 c 5 g
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Best Local Similarity 92.3%;
Matches 12; Conservative (
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PF 29-MAY-1998 JP 1998166141
PR 30-MAY-1997 US 08/865.675
PI JAMES G NADEAU.J BLUCE PITONA,C PRESTON RIN,JAMES L SHURAMU PC C12N15/09.C12N15/00 CC Strandedness: Single, CC Topology: Linear;
FR Key
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unclassified.
1 (bases 1 to 48)
James,G.N.J.J., Pitona,C.P.R.R. and L,S.
Method for detecting target nucleic acid sequence and
Patent: JP 1999056380-A 6 02-MAR-1999;
                                                                                                                                                                                                                                      E30456 48 bp DNA PAT 07-1
Method for detecting target nucleic acid sequence and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 48;
                                                                                         78.7%; Score 11.8; DB 9; Length 48; 86.7%; Pred. No. 1.3e+04; ive 0; Mismatches 2; Indels
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Pred. No. 1.3e+04;
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                          /organism="unknown"
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1 (bases 1 to 18)
Renard,A. and Thiry,M.
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E30456
E30456.1 GI:13025613
JP 1999056380-A/6.
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HSV probe.
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29-SEP-1999

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Unclassified.

1 (bases 1 to 21)
Bazin, H. and Latinne, D.
Methods of inhibiting T-cell medicated immune responses with
LO-CD2a-specific antibodies
Patent: US 5817311-A 78 06-OCT-1998;
Location/Qualifiers
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Bazin, H. and Latinne, D.
Methods of inhibiting T-cell medicated immune responses with
                                                                                                                                                          Inflammation-induced expression of a recombinant gene Patent: US 5851822-A 4 22-DEC-1998; Location/Qualifiers
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AR043988
AR043988.1 GI:5965453
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Sequence 4 from patent US 5851822.
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 20)
Greaves, D.R., Thomsen, L., Catchpole, I.R. and Ford, M.J.
Dna constructs based on the eif4a gene promoter
Patent: WO 0102594-A 52 11-JAN-2001;
GLAXO GROUP LIMITED (GB)
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73.3%; Score 11; DB 9; Length 20; 100.0%; Pred. No. 4.7e+04; Live 0; Mismatches 0; Indels
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Sequence 52 from Patent WO0102594.
AX069241
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AR003365
AR003365.1 GI:3964624
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/db_xref="taxon:9606"
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1 (bases 1 to 21)
Bazin H., Latinne, D., Kaplan, R., Kieber-Emmons, T., Postema, C.E. and White-Schaff, M.E.
Methods of inhibiting T cell mediated immune responses with humanized LO-CD2A-specific antibodies
Patent: US 5951983-A 78 14-SEP-1999;
Location/Qualifiers
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Bazin, H., Latinne, D., Kaplan, R., Kieber-Emmons, T., Postema, C.E. and White-Schaff, M.E.
Methods of inhibiting T cell mediated immune responses with humanized LO-CD2A-specific antibodies
Patent: US 5951983-A 79 14-SEP-1999;
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LO-CD2a-specific antibodies
Patent: US 5817311-A 79 06-OCT-1998;
Location/Qualifiers
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Sequence 79 from patent US 5951983.
AR073522.1 GI:10000286
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Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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| TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts JOURNAL Unpublished (2000) COMMENT Contact: Robert B. Weiss University of Utah Genome Center | University of Octan Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA 101 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0347 row: C column: 11 Seq primer: CGTTGTAAAACGACGCCAGT Class: plasmid ends High quality sequence stop: 25 | FEATURES | (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymoutectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil4732114)gp[AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into | SE COUNT IGIN Duery Match 3est Local Simil Aatches 12; (1 | |
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| SUMMARIES Query Score Match Length DB ID Score Tength DB ID | 11.4 76.0 25 245 A2506197 11 73.3 32 241 A2303920 0.8 72.0 27 244 A2495501 0.8 72.0 43 249 A2785625 0.4 69.3 33 242 A2382781 0.4 69.3 34 103 A1873935 0.4 69.3 42 243 A2438946 0.4 69.3 46 190 W47560 0.4 69.3 47 249 A279556 | 69.3 48 250 AZ819513 AZ819513 69.3 49 17 AI188352 AI188352 69.3 50 107 AU105506 AU105506 69.3 50 107 AU105506 AU105506 68.0 24 241 AZ303688 AZ303688 68.0 43 244 AZ480568 AZ480568 AZ480568 68.0 47 156 D38689 D38689 BF740568 68.0 49 168 BF740213 BF740213 68.0 50 15 AI024893 AI024893 AI024893 66.7 26 250 AZ827167 AZ827167 AZ827167 | 10 66.7 34 250 A2827876 A2827876 A2827876 ZM0104M01 10 66.7 41 246 A2580746 A2580746 IM0369111 10 66.7 48 188 T17575 IM0865111 10 86.3 28 242 A234567 A24367 IM0080801 10 86.3 34 242 A2345677 A2349201 IM0086808 10 86.3 37 102 A1862676 A2349201 IM0086808 10 86.3 42 243 A2427649 A3626733 A366273 Eala8403.s 10 86.3 44 13 A893614 A2495842 IM0331123 10 86.3 45 250 A2828142 A365338 U966603.x 10 86.3 46 23 A1663836 A365338 U966603.x 10 86.3 46 23 A1663836 A36531 A3653114 | 65.3 49 246 AZ607150 AZ607150 65.3 50 107 AU102408 65.3 50 107 AU102658 AU102408 65.3 50 107 AU102658 AU102658 65.3 50 107 AU102658 AU102658 65.3 50 107 AU102658 AU106203 65.3 50 108 R88739 R88739 Ye 62.7 24 246 AZ588336 AZ588336 62.7 25 241 AZ380576 AZ588336 AZ588336 AZ588336 62.7 25 241 AZ380576 | AZ506197 25 bp DNA GSS 05-OCT-2000 N 1M0347C11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0347C11 F, DNA sequence. AZ506197 AZ506197.1 G1:10687513 GSS. House mouse. M Mus musculus M Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus. I (Dasses 1 to 25) Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A:, von Niederhausern, A. and Wright, D., Weiss, R. |
| Result | 00000 0 104400 | 11 13 13 13 14 16 17 10 20 21 22 | 0 0 0 22222 24222 2628 2638 2638 2638 2638 2638 2638 2 | 0 000 0 | RESULT 1 AZ506197 LOCUS DEFINITION ACCESSION VERSION KEYWORS SOURCE ORGANISM REFERENCE AUTHORS |

us-09-757-100b-31.szlim50.rst

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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
//note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/G0 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonicleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil47321141gblAR129072.1), a copy number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the linsert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
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Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
                                                                                                                                                                                              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
                                               Mouse whole genome scaffolding with paired end reads from 10kb
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Pred. No. 6.8e+04;
); Mismatches 2; Indels 0:
                                                                                                                                                                                                                                                                                                                      Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0331 row: P column: 21
Seg primer: CGTTGTAAAACGACGCCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"/strain="C57BL/6J"
                                                                                                                                Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
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                            and Wright, D., Weiss, R.
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Best Local Similarity 85.7
Matches 12; Conservative
                                                                                                                                                                                                                                                                 Tel: 801 585 5606
Fax: 801 585 7177
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25 TACCCATGTGATTC 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pmO2 (gill47321141gblA712972.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll XLLO-Gold (Stratagene) cells and selected for ampicillin resistance."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 27)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
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kb plasmid UUGC1M library Mus musculus genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="E. Coli strain XLIO-Gold, Ti-resistant, F-" /note="Weetcn: PWD42Ivy: Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
     Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
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/sex="Male"
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                                                                                                                                                                                                                                                                                        Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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1M0331P21F Mouse 10kb plasmid UUGC1M
clone UUGC1M0331P21 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                         Insert Length: 10000 Std Error: (Paper) 19 Insert Column: 19 Seg primer: CACACGGAAACAGCTATGACCCCTASS: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
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Location/Qualifiers
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AZ495501.1 GI:10670983
and Wright, D., Weiss, R.
                                                                                                                                                                                                                                        Tel: 801 585 5606
Fax: 801 585 7177
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gilq732114 [gb]ARL29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                          plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 B., SLC, UT
84112, USA
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similar to TR:070396 070396 SIK SIMILAR PROTEIN. ;, mRNA sequence.
AI873935
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., Mongo, T., Welss, R.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="C57BL/6J"
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0140 row: N column: 08
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
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91.7%; Pred
0; }
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Best Local Similarity 91.7
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (http://www.lax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymerase are the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (q1|4732114|q19|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 33)
                       ISlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                  S. 2030 E., SLC,
                                       ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern, and Wright,D.,Welss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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/db_xref="taxon:10090"
/clone="UUGC2M0029L08"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
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                                                                                                                                                                                                                                                                                         Tel: 801 585 5006
Fax: 801 585 7177
Email: ddunnégenetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0029 row: L column: 08
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 43.
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Pred. No. 7e+04;
0; Mismatches
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                                                                                                                                            Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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                                                      Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly M., Rose, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="serous papillary carcinoma, high grade, 2 pooled tumors"
1 (bases 1 to 34)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
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91.7%; Pred. No. 1...
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/clone="IMAGE:2438799"
/clone_lib="NCI_CGAP_Ut4"
                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Best Local Similarity 91.7
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
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1M0132111F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
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/clone="UUGCIM0229L15"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
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Pred. No. 1.2e+05;
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Plate: 0229 row: L column: 15
Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                             /organism="Mus musculus"
                                                        High quality sequence stop: 35.
Location/Qualifiers
                                                                                                                               /strain="C57BL/6J
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91.7%;
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/clone_lib="Soares_senescent_fibroblasts_NbHSF"
/tissue_type="senescent fibroblast"
/lab_host="DH10B (ampicillin resistant)*
/note="Vector: pT77B) (Pharmacia) with a modified
polylinker V_TYPE: phagemid; Site_1: Not I; Site_2: Eco RI
: 1st strand cDNA was primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2000)
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Fm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2M0051F07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Unun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality Possible reversed clone: similarity on wrong strand Insert Length: 2909 Std Error: 0.00 Seq primer: mob.REGA+ET High quality sequence stop: 1. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 10.4; DB 190; Length 46; Pred. No. 1.2e+05; 0; Mismatches 1; Indels 0;
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                                                                                                                                                                                                1. 46
/organism="Homo sapiens"
/db_xref="GDB:1255776"
/db_xref="taxon:9606"
/clone="IMAGE:324264"
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Insert Length: 10000 Std Erro
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AZ795746.1 GI:12943089
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Best Local Similarity 91.7%;
Matches 11; Conservative
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Fax: 801 585 7177
Email: ddunn@genet
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                                                                                                                                                                                                                                                                                                                                                           //ducingle-E. Coll Sitel Air Air Cold, Trieslatur, F. // Antote="Vector: PWAZINY; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwDA2 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 46)
1 Hillier,L., Clark,N., Duque,T., Elliston,K., Hawkins,M., Holman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
The WashU-warck EST Project
Contact: Wilson RK
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clone IMAGE:324264 5' similar to PIR:S43417 S43417 RNA/DNA-binding
protein - mouse ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                              /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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0
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/clone_lib="Mouse lOkb plasmid UUGC1M library"
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                           Std Error: 0.00
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0132 row: I column: 11
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
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/organism="Mus musculus"
                                                                                                                       High quality sequence stop: 42. Location/Qualifiers
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91.7%;
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W47560.1 GI:1332239
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Best Local Similarity 91.7
Matches 11; Conservative
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
WR. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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2M0091L11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0091L11 F, DNA sequence.
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                 /note-"Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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                                                                                                                                         /clone_lib-"Mouse 10kb plasmid UUGC1M library"
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Insert Length: 10000 Std Error: 0.00
                                                /organism="Mus musculus"
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Class: plasmid ends
                                                                                           /db_xref-"taxon:10090"
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Location/Qualifiers
                                                                       /strain="C57BL/6J
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                                                                                                                                                                   /sex="Male'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 69.3
Best Local Similarity 91.7
Matches 11; Conservative
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Fax: 801 585 7177
Email: ddunn@qenet
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114) applyant129072.1), a copy number inducible derivative of plasmid Rl. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for amplitilin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                             /lab_host="E. Coli strain XLIO-Gold, T1-resistant, F-"/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/61 (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (infe@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 1262 Std Error: 0.00
Seg primer: -400P from Gibco
High quality sequence stop: 1.
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                                                                                                                           /db_xref="taxon:10090"
/clone="UUGC2M0091L11"
/clone_lib="Mouse 10kb plasmid UUGClM library"
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Pred. No. 1.2e+05;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                Laboratory Mouse DNA Resource
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/db_xref="taxon:9606"
/clone="IMAGE:1723091"
                                                                    /organism="Mus musculus"
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Location/Qualifiers
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                                                                                               /strain="C57BL/6J"
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                                                                                                                                                                                                                                 /sex="Male"
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Unpublished (1997)
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Best Local Similarity 91.7
Matches 11; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (basca 1 to 50)

2. Suzuki, Y., Tsunoda, T., Taira, H., Mizushima -Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Taira, H., Mizushima -Sugano, J., Sese, J., Hata, K., Syyama, A. and Sugano, S.

Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries Contact: Yutaka Suzuki

Department of Virology
Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus.
1 (bases 1 to 24)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
.M., Rose, M., Rose, R.,
and Wright, D., Walss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
                          AU105507 50 bp mRNA EST 05-APR-2001
M105507 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HRC12884, mRNA sequence.
AU105507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A2303688 24 bp DNA GSS 29-SEP-2000 1M00003M11F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0003M11 F, DNA sequence.
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14 c 17 g 8 t
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Pred. No. 1.2e+05;
0; Mismatches 1;
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/db_xref="taxon:9606"
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AZ303688.1 GI:10339066
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Unpublished (2000)
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Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ins.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers
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Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata
.H., Ota,T., Isogal,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo
.K., Suyama,A. and Sugano,S.
Fine Structural analysis of transcription start sites of human
mNAs using full-length enriched and 5'-end enriched cDNA libraries
Unpublished (2001)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 1.2e+05;
0; Mismatches 1; Indels 0
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Pred. No. 1.2e+05;
0; Mismatches 1;
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/db_xref="taxon:9606"
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91.7%;
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91.78;
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Best Local Similarity 91.7
Matches 11; Conservative
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Matches 11; Conservative
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AUTHORS
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1; Indels

Email: ddunn@genetics.utah.edu

14

RESULT

δ g

Length 50;

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/Jab host-"E. Coli strain XL10-Gold, T1-resistant, F-"
// note-"Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114(gb)AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib-"Mouse 10kb plasmid UUGCIM library"
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       Std Error: 0.00
                                                                                                                                                                                                                          1. .24
/organism="Mus musculus"
/strain="C57BL/6J"
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/clone="UUGC1M0003M11"
Insert Length: 10000 Std Error:
Plate: 0003 row: M column: 11
Seq primer: CGTYGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
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ö Gaps ; 0 68.0%; Score 10.2; DB 241; Length 24; 80.0%; Pred. No. 1.5e+05; 1ve 0; Mismatches 3; Indels 0; Query Match
Best Local Similarity 80.0
Matches 12; Conservative

1 tacccaggtgagtct 15

ö

17 TATCCAGATAAGTCT 3

Search completed: October 2, 2001, 15:01:13 Job time: 10842 sec

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Run on:

Searched:

Database

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2000 Compugen Ltd.
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AR042372 AR052280 AX095001 AX002270 E28251 AR012670 I25036 I30498

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Description

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SUMMARIES

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (2021) (
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Huang, S.
Retinoblastoma protein-interacting zinc finger proteins
Patent: US 5831008-A 11 03-NOV-1998;
Location/Qualifiers
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Sequence 11 from patent US 5831008.
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Sequence 179 from Patent W00118250.
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Nucleic acid molecules encoding retinoblastoma protein-interacting
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Patent: US 5811304-A 11 22-SEP-1998;
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                  E28251 21 bp DNA PAT 07-FEB-2(Purification of higher transcription complex from nonhuman transgenic animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 21)
Bernd, K.E.B.B. and Meisterernst, G.P.
Purification of higher transcription complex from nonhuman
           unclassified.

1 (bases 1 to 21)

Berglund, E.D. and Kirschbaum, B.D.

Purification of higher order transcription complexes from transgenic non-human animals

Patent: EP 0881288-A 7 02-DEC-1998;

HOBCHST AG (DE)
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Pred. No. 3.4e+04;
0; Mismatches 2; Indels
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/organism="unidentified"
//db_xref="taxon:32644"
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26-MAY-1997 DE
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C12R1:91), PC C12N15/00,
PC Strandedness: Single;
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location
FT exon 1...21.
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86.78;
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Best Local Similarity 86.7
Matches 13; Conservative
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                                                                                                                    1 (bases 1 to 30)
Godowski,P.J.
Receptor activation with hepatocyte growth factor agonists
Patent: US 576384-A 9 '09-UUN-1998;
Location/Qualifiers
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Pred. No. 3.3e+04;
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Godowski,P.J., Lokker,N.A. and Mark,M.R.
Hepatocyte growth factor variants
Patent: US 5547856.A 10 20-AUG-1996;
Location/Qualifiers
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Unclassified.
1 (bases 1 to 30)
Godowski,P.J., Lókker,N.A. and Mark,M.R.
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Sequence 10 from patent US 5547856.
125036 125036.1 GI:1604906
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Sequence 10 from patent US 5580963.
130498
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AR012670 30 bp DNA
AR012670 9 from patent US 5763584.
AR012670.1 GI:3970988
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/organism="unknown"
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86.7%;
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Sequence 50 from Patent WO0118198.
AX093520
                                                                                     Sequence 7 from patent US 5550020.
125220
125220.1 GI:1605090
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1 2 c 6 g
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92.3%;
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Best Local Similarity 92.3
Matches 12; Conservative
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AR040915
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Unclassified.
I (bases 1 to 21)
Stevens, J. K. and Dunn, J. M.
Method for testing for mutations in DNA from a patient sample Patent: US 5545527-A 7 13-AUG-1996;
Location/Qualifiers
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Godowski.P.J.
Chimeric hepatocyte growth factor (HGF) ligand variants
Patent: US 5684136-A 9 04-NOV-1997;
Location/Qualifiers
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Pred. No. 3.3e+04;
0; Mismatches 2; Indels
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Single-chain hepatocyte growth factor variants Patent: US 5580963-A 10 03-DEC-1996;
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Pred. No. 3.3e+04;
0; Mismatches 2;
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Sequence 7 from patent US 5545527.
124623
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Sequence 9 from patent US 5684136.
172560
                    Location/Qualifiers
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86.7%;
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Best Local Similarity 86:7
Matches 13; Conservative
                                                                                                                         13; Conservative
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Best Local Similarity
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124623
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Gallie,B.L., Dunn,J.M. and Stevens,J.K.
Mathod, reagents and kit for diagnosis and targeted screening for retinoblastoma
Patent: US 5550020-A 7 27-AUG-1996;
Location/Qualifiers
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07-OCT-1996
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1 (bases 1 to 21)
Weissenbach, J. and Hazan, J.
Cloning, expression and characterisation of the spg4 gene responsible for the most frequent form of autosomal spastic
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paraplegia
Patent: WO 0118198-A 50 15-MAR-2001;
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
Location/Qualifiers
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Pred. No. 5.8e+04;
0; Mismatches 1;
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/db_xref="taxon:32630"
/note="Amorce"
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73.3%; Score 11; DB 10; Length 24; 100.0%; Pred. No. 1e+05; tive 0; Mismatches 0; Indels

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Location/Qualifiers
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/organism="unknown"
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11; Conservative
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Job time: 14179 sec
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Best Local Similarity
Matches 11; Conserv
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                                                                                                                    1 (bases 1 to 24)
Stemmer, W.P.C. and Crameri, A.
Methods for generating polynucleotides having desired
Characteristics by iterative selection and recombination
Patent: US 5811238-A 14 22-SEP-1998;
Location/Qualifiers
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Unknown.
Unclassified.
Unclassified.
I (bases 1 to 24)
Stemmer, W.P.C. and Crameri, A.
Stemmer, W.P.C. and Trandom fragmentation and reassembly
DNA mutagenesis by random fragmentation and reassembly
Patent: US 5830721-A 14 03-NOV-1998;
Location/Qualifiers
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1 (bases 1 to 24)
Stemmer,W.P.C.
Methods for in vitro recombination
Patent: US 5605793-A 14 25-FEB-1997;
акичи915 24 bp DNA
Sequence 14 from patent US 5811238.
AR040915
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Sequence 14 from patent US 5830721.
AR051822 GI:5975186
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Sequence 14 from patent US 5605793.
136212
136212.1 GI:2086725
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts JOURNAL Unpublished (2000) COMMENT Contact: Robert B. Weiss University of Utah Genome Center | Annual of the control | Oy 1 tggcttatctcagt 15 | RESULT 2 AZ830358 AZ8 |
|---|--|------------------------|--|
| SUMMARIES Result Query No. Score Match Length DB ID Description | 11.8 78.7 21 249 AZ787920 AZ787920 ZA0034409 2 11.8 76.0 23 240 AZ787920 AZ787920 ZA0034409 3 10.4 69.3 37 340406910 AA9466910 AA946891 Oylobad 4 10.4 69.3 37 340406910 AA9466910 AA946891 Oylobad 5 10.4 69.3 37 340406910 AA9466910 Oylobad 6 10.4 69.3 37 340406910 AA9466910 Oylobad 8 10.4 69.3 37 37 37 340406910 AA9466910 Oylobad 9 10.4 69.3 37 37 37 37 37 37 10.4 69.3 42 42 42 42 42 42 10.4 69.3 42 42 42 42 42 10.4 69.3 42 42 42 42 10.4 69.3 42 42 42 42 10.4 69.3 42 42 42 10.4 69.3 42 42 10.5 68.0 37 23 42 10.6 69.0 42 42 10.7 68.0 42 42 10.7 68.0 42 42 10.7 68.0 42 42 10.8 68.0 42 42 10.8 68.0 42 42 10.1 68.0 42 42 10.2 68.0 44 42 10.3 68.0 44 42 10.4 69.3 42 10.5 68.0 44 42 10.5 68.0 44 42 10.5 68.0 44 42 10.5 68.0 44 42 10.6 7 42 10.6 7 42 10.7 68.0 44 10.8 68.0 44 10.9 68.0 69.0 10.9 69.0 69.0 10.9 69.0 69.0 10.9 69.0 10.9 69.0 69.0 10.9 69.0 69.0 10.9 69.0 69.0 10.9 69.0 69.0 10.9 69.0 69.0 10.9 69.0 69.0 10.9 69.0 69.0 10.9 69.0 69.0 10.9 69.0 69.0 10.9 69.0 69.0 10.9 69. | ALIGNMENTS | AZ787920,C LOCUS AZ787920 AZ787920 |

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114 (pilAR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                          Unpublished (2000)
Contact: Robert B. Weiss
Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 84112, USA
Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="E. Coli strain XLIO-Gold, T1-resistant, F-" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/63 (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                      Mouse whole genome scaffolding with paired end reads from 10kb
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T. Drucel sheared genomic DNA clone 187a02, reverse sequence,
genomic survey sequence.
AL476274
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/clone="UGGCIMO519NO9"
/clone_lib="Mouse 10kb plasmid UGGIM library"
/sex="Male"
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
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Insert Length: 10000 Std Error: 0.00
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Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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/strain="C57BL/6J"
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   ,M., Rose,M., Rose,R.,
and Wright,D.,Weiss,R.
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Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pway2 (gil47321141gblAF129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XiliO-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                               plasmid inserts
Unpublished (2000)
Unpublished (2000)
University of Utah Genome Center
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A2649569 23 bp DNA GSS 14-DEC-2000 UN519W09F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0519N09 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Westor: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                           Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                                                                                                           Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0109 row: M column: 04
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism-"Mus musculus"
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/clone="UUGC2M0109M04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: 43.
Location/Qualifiers
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Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Class: plasmid ends
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AA906910 37 bp mRNA EST 09-JUN-1998 oj70b12.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1503647 3' similar to TR:Q33565 Q33565 EATRO 164 KINETOPLAST
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 37)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Pred. No. 1.3e+05;
0; Mismatches 1; Indels
                                                                                               /db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="IXAGE:1398085"
/clone_lib="Soares_mammary_gland_NDMMG"
/sex="male"
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/lab_host="DH108"
                                                                                                                                                                                                    /tissue_type="mammary gland"
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t
                                                             /organism="Mus musculus"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                              /dev_stage="4 weeks"
/lab_host="DH10B"
              Location/Qualifiers
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Best Local Similarity 91.7
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Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
cambridge CBIO 15A, E-mail: barrell@sanger.ac.uk and
nhl@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TRED9274 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
Trypanosoma brucei (TRED9274 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
to give a tight size distribution (
the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barzell, Oxford University Press, 1999)
Bemail: nelsayed@tigr.org
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
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Bukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 28)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AII18907 28 bp mrna EST 02-SEP-1998 uc15f07.r1 Soares_mammary_gland_NbAmG Mus musculus cDNA clone IMAGE:1388085 5' similar to TR:Q13825 Q13825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE. ; mrna sequence.
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Contact: Marra M/Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 10.8; DB 258; Length 40;
Pred. No. 8e+04;
0; Mismatches 2; Indels 0
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Sossible reversed clone: similarity on wrong strand
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="TREU927"
/db_xref="taxon:5691"
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85.7%;
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D45802 38 bp mRNA EST 20-FEB-1995
HUMGS03019 Human adult lung 3' directed Mbol cDNA Homo sapiens cDNA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Human adult lung 3' directed MboI cDNA"
/note="Adult human lung, 3' directed MboI"
4 c 5 g 17 t
                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 38)
Itoh.K., Okubo,K., Yosii,J., Yokouchi,H. and Matsubara,K.
An expression profile of active genes in human lung
DNA Research 1, 279-287 (1994)
95236275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 10.4; DB 156; Length 38;
Pred. No. 1.3e+05;
0; Mismatches 1; Indels 0
    91.7%; Pred. No. 1.3e+05;
iive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Institute for Molecular and Cellular Biology
Osaka University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3-1, Yamadaoka, Suita, Osaka, 565, Japan
Tel: 06-877-5111 x3910
Fax: 06-877-1922.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
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Best Local Similarity 91.7%;
Matches 11; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Kohichi Itoh
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                                                                                                                                                                                                                                                                            GI:662756
                                                                                                                                                                                                                                      3', mRNA sequence.
D45802
D45802.1 GI:66275
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                          11; Conservative
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                                                                                  11 CTTATCTTCATT 22
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      Best Local Similarity
Matches 11; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.

Email: capaba-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmart-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 1106 Std Error: 0.00
Seq primer: -40ml3 fwd. Er from Amersham
High quality sequence stop: 1.

Location/Qualifiers
vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of 1.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
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                                                                                                                                                                                                                                                                                                                                                                                                                              AA946896 37 bp mRNA EST 23-JUL-1998 oq53f01.sl NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1590073 3' similar to TR:007708 007708 HYPOTHETICAL 23.7 KD PROTEIN. ;, mRNA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bummalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 37)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NATIONAL Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Unpublished (1997)
                                                                                                                                                                                                                                                            Gaps
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/db_xref="taxon:9606"
/clone="IMAGE:1590073"
/clone=lib="NCI_CGAP_Kid5"
/tisus=Iype="2 pooled tumors (clear cell type)"
/lab_host="DH108"
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                                                                                                                                                                                                                    Length 37;
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Pred. No. 1.3e+05;
0; Mismatches 1;
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AA946896
AA946896.1 GI:3110291
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91.7%;
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Best Local Similarity
Matches 11; Conserv
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Gaps

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1 (bases 1 to 42)
Morimyo,M. and Mita,K.
Identification of expressed sequence tags of Schizosaccharomyces
AU010757 Schizosaccharomyces pombe late log phase cDNA Schizosaccharomyces pombe cDNA clone spc10335, mRNA sequence. AU010757 GI:3347437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome Research Group Astronomes National Institute of Radiological Sciences 9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan Email: morimyoënirs.go.jp.
                                                                                                                                                                                                                                                              Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
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DB 14; Length 37;

Score 10.4;

69.38;

Query Match

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was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 bNA polynmerase and 74 polynuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil4732114|gb|RF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for amplicillin resistance."
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Blan, H., Aoyai, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.; Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AZ324419 46 bp DNA GSS 29-SEP-2000
1M0046B20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0046B20 F, DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 10.4; DB 249; Length 45; Pred. No. 1.4e+05; 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

    .46
    /organism="Mus musculus"

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/clone="UUGC1M0046B20"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 69.3%;
Best Local Similarity 91.7%;
Matches 11; Conservative
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USA
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                                                                                                                                                                                                           /note="Vector: Mi3mp19; The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA into the Smal site of Mi3mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, http://www.nirs.go.jp)"
                                                                     /strain="972" consequence pomper / strain="972" db_xref="taxon:4896" / db_xref="taxon:4896" / dclone="spc10335" / dclone="spc10335" / dclone=lib="Schizosaccharomyces pombe late log phase cDNA" / sex="h minus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rm.\ 308,\ \mbox{\sc Blomedical Polymers Research Bldg.,}\ 20 S. 2030 E., SLC, UT 84112, USA
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 45)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Slam,H., Longacres,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AZ772066 45 bp DNA GSS 16-FEB-2001
1M0574L08R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0574L08 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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/db_xref="taxon:10090"
/clone="UUGC1M0574L08"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 10.4; DB 106; Length 42;
Pred. No. 1.3e+05;
0; Mismatches 1; Indels 0,

    .42
    /organism="Schizosaccharomyces pombe"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0574 row: L column: 08
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
        Location/Qualifiers
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Best Local Similarity 91.7
Matches 11; Conservative
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Fax: 801 585 7177
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RESULT 13
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            was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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(http://www.jax.org/resources/documents/dnares/). The DNA
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longarere, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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/clone="UGGC2M0046D07"
/clone_lib="Mouse 10kb plasmid UUGClM library"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69.3%; Score 10.4; DB 241; Length 46; 91.7%; Pred. No. 1.4e+05; 1ve 0; Mismatches 1; Indels 0;
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Insert Length: 10000 Std Error: 0.6
Plate: 0046 row: D column: 07
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 46.
Location/Qualifiers
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Matches 11; Conservative
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Fax: 801 585 7177
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114 [gb]AR129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLLO-Gold (Stratagene) cells and selected for ampicillin resistance.
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Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael

R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NOT-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL, send email to:

info@image.llnl.gov

Seq primer: -40RP from Gibco.
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Site_2: NotI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 0.8 kb."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/db_xref="taxon:9606"
/clone="IMAGE:2692497"
/clone="IMAGE:2692497"
/clone=Lib="NCI_CGAP_Li5"
/tissue_type="hepatic adenoma"
/lab_host="DH108"
Laboratory Mouse DNA Resource
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Search completed: October 2, 2001, 15:01:15 Job time: 10844 sec
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Pine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries Unpublished (2001)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Emali sysuskitelma. u-tokyo.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
, S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers
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AU103710 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HEP14727, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
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T. brucel sheared genomic DNA clone 288e04, forward sequence, acrovey sequence.
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(bases 1 to 22)

Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,

Hallingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,

Melville, S. E., Rajandream, M. A. and Barrell, B.G.

Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
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Pred. No. 1.4e+05;
0; Mismatches 1; Indels 0
Score 10.4; DB 120; Length 49;
Pred. No. 1.4e+05;
0; Mismatches 1; Indels 0
                                         0; Mismatches
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/db_xref="taxon:9606"
/clone="HEP14727"
/clone_lib="sugano Homo sa
a 12 c 20 q 9
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  69.3%;
91.7%;
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91.7%;
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                  Best Local Similarity 91.7
Matches 11; Conservative
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Best Local Similarity 91.7
Matches 11; Conservative
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                                                                                                    9 GCCTTATCTTCA 20
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    Query Match
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TA288E04P
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nhidsanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, WD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU9274 GUTA 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shockun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
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project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
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Pred. No. 1.6e+05;
0; Mismatches 3; Indels
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Best Local Similarity
Matches 12; Conserv
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11908, A 2, Appli 7807, Ap 7807, Ap 10084, A

13218, A 13218, A 7, Appli 1511, Ap

Sequence Seq

US-09-818-875-2710 US-09-818-875-2714 US-09-818-875-2714 US-09-818-11908 US-09-75-216-2 US-09-77-18-2 US-09-371-7728-7807 US-09-371-7728-7807 US-09-371-7728-7807 US-09-371-7728-7807 US-09-371-7728-7807 US-09-371-7728-7807 US-09-371-7728-7807 US-09-371-7728-7807 US-09-25-592-13218 US-09-921-1511 US-09-921-515-13 US-09-921-515-13 US-09-921-515-18 US-09-921-515-18

13, Appl 15, Appl 18, Appl 2269, Ap

US-09-877-804-10

ALIGNMENTS

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GRUERAL INTORNARYIN:

APPLICANT: 01, YOOGGANG
APPLICANT: 01, YOOGGANG
APPLICANT: 01, YOOGGANG
APPLICANT: HANEL, David K.

APPLICANT: CHEN, WARKE: US/09/866,108

CORRENT FILING DATE: 2001-05-25

FRIOR APPLICANTION NUMBER: US 60/236,359

FRIOR APPLICANTION NUMBER: BCT/US01/0066

FRIOR APPLICANTION NUMBER: PCT/US01/0066

FRIOR FILING DATE: 2001-01-30

FRIOR FILING DATE: 2001-01-30

FRIOR FILING DATE: 2001-01-30

FRIOR FILING DATE: 2001-01-30

FRIOR FILING DATE: 2011-30

FRIOR 
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    US-09-866-108-7017/c
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                                                                                                                                 Search time 2173.58 Seconds (without alignments)
19.290 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*

2: /cgn2_6/ptodata/2/pna/USO6_NEW_COMB.seq:*

3: /cgn2_6/ptodata/2/pna/USO8_NEW_COMB.seq:*

4: /cgn2_6/ptodata/2/pna/USO8_NEW_COMB.seq:*

5: /cgn2_6/ptodata/2/pna/USO9_NEW_COMB.seq:*

6: /cgn2_6/ptodata/2/pna/USO9_NEW_COMB.seq:*

7: /cgn2_6/ptodata/2/pna/USO9_NEW_COMB.seq:*

8: /cgn2_6/ptodata/2/pna/USO9_NEW_COMB.seq2:*
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APPLICANT: GIVERALI LINGUAGE
APPLICANT: BANGE, David K
APPLICANT: HANGEL, David K
APPLICANT: PRIM, SHALTON G
APPLICANT: PRIM, SHALTON G
APPLICANT: PRIM, SHALTON G
APPLICANT: PRIM, SHALTON G
APPLICANT: RAKE, David K
APPLICANT: SHANNON, WAIX
TITLE OF INVERTION: WIGHER: US/09/866,108
TITLE OF INVERTION: MYGHER: US 60/20/356
FILE REPRENCE: ADDICA-TON NUMBER: US 60/20/456
FILE REPRENCE: ADDICA-TON NUMBER: US 60/20/356
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Pred. No. 3.2e+03;
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US-09-866.108-11910/c
Sequence 11910, Application US/09866108
GENERAL INFORMATION:
REPLICANT: GU, Yizhong
                                                                                                                                                                                                                            ; Sequence 11909, Application US/09866108; GENERAL INFORMATION:
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87.5%;
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Best Local Similarity 87.5
Matches 14; Conservative
      4 aagcagctgccattat 19
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                                        16 AAGCAGCTGCCACCAT 1
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US-09-866-108-11909/c
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; ORGANISM: HOMO :
US-09-866-108-11909
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LENGTH: 25
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APPLICANT: GU, YIZHONG

APPLICANT: GU, YOUNG

APPLICANT: GU, YOUNG

APPLICANT: GU, YOUNG

CURRENT FILING DATE: 2001-05-25

PRIOR FILING DATE: 2001-05-25

PRIOR FILING DATE: 2001-06-25

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/0066

PRIOR APPLICANTON NUMBER: PCT/US01/0067

PRIOR APPLICANTON NU
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Pred. No. 3e+03;
0; Mismatches 2; Indels
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87.5%;
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                          TYPE: DNA
CORGANISM: Homo sapiens
US-09-866-108-7017
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ORGANISM: Homo sapiens
US-09-866-108-7018
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Best Local Similarity
Matches 14; Conserva
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Best Local Similarity
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-09-866-108-7018/c
LENGTH: 17
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APPLICANT: JI, Yonggang
APPLICANT: GU, Yizhong
APPLICANT: GU, Yizhong
APPLICANT: Hanzel, David K.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: ADMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT APPLICATION NUMBER: US 60/207,456
PRIOR PRILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: CT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR PILING DATE: 2001-01-30
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PRIOR APLILOGATION NUMBER: GB 24263.6
PRIOR FILLING DATE: 2000-10-04
PRIOR FILLING DATE: 2000-10-04
PRIOR FILLING DATE: 2000-10-05-27
PRIOR FILLING DATE: 2000-09-27
PRIOR FILLING DATE: 2001-01-30
PRIOR PILLING DATE: 2001-01-30
PRIOR FILLING DATE: 2001-01-30
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PRIOR FILLING DATE: 2
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Best Local Similarity 87.5
Matches 14; Conservative
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US-09-866-108-11912/c
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SEQ ID NO 11911
LENGTH: 25
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                                                                 APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYCSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AECMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT PILING DATE: 2001-05-25
PRIOR PELICATION NUMBER: US 60/207,456
PRIOR PELICATION NUMBER: US 60/236
PRIOR PELICATION NUMBER: US 60/236, 359
PRIOR PELICATION NUMBER: DC7/US01/0066
PRIOR PELICATION NUMBER: PC7/US01/0066
PRIOR PELICATION NUMBER: PC7/US01/00667
PRIOR PELICATION NUMBER: PC7/US01/00667
PRIOR PLILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
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GENERAL INFORMATION:
APPLICANT: GI, YIZHONG
APPLICANT: JI, YONGGANG
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, MAIK
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AFOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
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Pred. No. 3.2e+03;
0; Mismatches 2; Indels
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SOFTWARE: Acomica Sequence Listing Engine
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PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR PLICATION NUMBER: US 60/266,860
PRIOR FILING DATE: 2001-02-05
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Matches 14; Conservative
                                                RANK, David R.
CHEN, Wensheng
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; ORGANISM: Homo sapiens
US-09-866-108-11910
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Gaps

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APPLICANT: GIV, Yizhong
APPLICANT: BANKE, David K.
APPLICANT: RANKE, David R.
APPLICANT: RANKE, David R.
APPLICANT: RANK David R.
APPLICANT: RANK David R.
APPLICANT: RANK David R.
APPLICANT: SHANNON, Mark
APPLICANTON: WORSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
ITITLE OF INVENTION: MOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE ERFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT APPLICATION NUMBER: US 60/236,359
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-13
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
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Pred. No. 3.2e+03;
); Mismatches 2;
                            PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR APLICATION NUMBER: PCT/US01/00661
PRIOR APLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2001-02-05
NUMBER: OF SEQ ID NOS: 15752
SEQ ID NOS: 15752
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APPLICATION NUMBER: PCT/US01/00662
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APPLICATION NUMBER: PCT/US01/00661
FILING DATE: 2001-01-30
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APPLICATION NUMBER: US 60/234,687
FILING DATE: 2000-09-21
APPLICATION NUMBER: US 60/266,860
FILING DATE: 2001-02-05
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87.5%;
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Best Local Similarity 87.5
Matches 14; Conservative
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; ORGANISM: Homo sapiens
US-09-866-108-11913
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APPLICANT: GU, YLLANOG
APPLICANT: GU, YLLANOG
APPLICANT: GU, YLLANOG
APPLICANT: HANZEL, DAVIG K.
APPLICANT: HANZEL, DAVIG K.
APPLICANT: HANZEL, DAVIG K.
APPLICANT: RANK, DAVIG R.
APPLICANT: RANK, DAVIG R.
APPLICANT: SHANK, DAVIG R.
TILE REFERENCE: ACOMICA-7
CURRENT APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2001-01-30
PRIOR PLICATION NUMBER: PCT/USO1/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
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Pred. No. 3.2e+03;
0; Mismatches 2; Indels
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                                                 PRIOR FILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PELICATION NUMBER: PCT/US01/00661
PRIOR PELING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/256,860
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR PILING DATE: 2001-02-05
NUMBER OF SECUID NOS: 15752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO 11912
LENGTH: 25
APPLICATION NUMBER: PCI/US01/00664
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87.5%;
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Best Local Similarity 87.5
Matches 14; Conservative
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; ORGANISM: Homo sapiens
US-09-866-108-11912
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Pred. No. 3.2e+03;); Mismatches 2;

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Best Local Similarity 87.5
Matches 14; Conservative
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APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, MISSIN LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
TITLE OF INVENTION: ABOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05.25
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Pred. No. 3.2e+03;
0; Mismatches 2;
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PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-05-26
PRIOR PLILING DATE: 2000-10-04
PRIOR FILLING DATE: 2000-10-04
PRIOR PLILING DATE: 2000-10-04
PRIOR PELLING DATE: 2000-09-27
PRIOR PELLING DATE: 2001-03-27
PRIOR PELLING DATE: 2001-01-30
PRIOR PELLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR PLILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR PELLING DATE: 2001-01-30
PRIOR PELLING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
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NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Acomica Sequence Listing Engine
SEQ ID NO 11915
LENGTH: 25
                          SOFTWARE: Acomica Sequence Listing Engine SEQ ID NO 11914
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 11915,
Sequence 11915, Application US/09866108
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/266,860
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Best Local Similarity 87.5%;
Matches 14; Conservative
  NUMBER OF SEQ ID NOS: 15752
                                                                                                                                                                                                                                                                                                                                                                  4 aagcagctgccattat 19
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; ORGANISM: Homo sapiens
US-09-866-108-11915
                                                                                                                                       ; ORGANISM: Homo sapiens US-09-866-108-11914
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Length 25;

64.0%; Score 12.8; DB 6;

Query Match

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APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AGOMICAN.
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
CURRENT FILING DATE: 2001-05-25
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Pred. No. 3.2e+03;
0; Mismatches 2;
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PRIOR APPLICATION NUMBER: 05 02/20/420
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR PELICATION NUMBER: US 60/236,359
PRIOR PELING DATE: 2000-09-27
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
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SOFTWARE: Aeomica Sequence Listing Engine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
                                                                                                                                                                                                                ; Sequence 11916, Application US/09866108; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                             APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David K.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
Query Match 64.(
Best Local Similarity 87.5
Matches 14; Conservative
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; ORGANISM: Homo sapiens
US-09-866-108-11916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
US-09-866-108-11917/c
                                                                                                                                                         RESULT 10
US-09-866-108-11916/C
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Sequence 10, Application US/09930251

GENERAL INFORMATION:
APPLICANT: Matsuo, Masafumi; Kamei, Shoichiro
TITLE OF INFORMON: Pharmaceutical Composition for Treatment of Duchenne Muscular
FILE REFERENCE: P21360
CURRENT APPLICATION NUMBER: US/09/930,251
CURRENT FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: JP2000-256547
PRIOR PILING DATE: 2000-08-25
NUMBER OF SEQ ID NOS: 19
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Pred. No. 7.1e+03;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                     CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PLILING DATE: 2000-09-47
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
                       CURRENT APPLICATION NUMBER: US/09/866,108 CURRENT FILING DATE: 2001-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Aeomica Sequence Listing Engine SEQ ID NO 11918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64.0%;
87.5%;
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llarity 82.4%;
Conservative
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nes 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-11918
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US-09-930-251-10
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Best Local Similarity
Matches 14; Conserv
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                                                                                                                                                                       APPLICANY: HANZEL, DAVIG K.
APPLICANY: HANZEL, DAVIG K.
APPLICANY: CHEN, Wensheng
APPLICANY: CHEN, Wensheng
APPLICANY: CHEN, Wensheng
APPLICANY: CHEN, Wensheng
APPLICANY: SHANNON, MAIK
TILLE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US 60/207, 456
PRIOR PELICATION NUMBER: US 60/207, 456
PRIOR APPLICATION NUMBER: US 60/207, 456
PRIOR APPLICATION NUMBER: US 60/207, 456
PRIOR PELING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207, 30
PRIOR PELING DATE: 2000-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELICATION NUMBER: PCT/USO1/00663
PRIOR PELICATION NUMBER: PCT/USO1/00663
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR PELICATION NUMBER: PCT/USO1/00664
PRIOR PELICATION NUMBER: PCT/USO1/00667
PRIOR APPLICATION NUMBER: PCT/USO1/00667
PRIOR APPLICATION NUMBER: PCT/USO1/00667
PRIOR APPLICATION NUMBER: PCT/USO1/00670
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GENERAL INFORMATION:
APPLICANT: 01, Yougang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: RANK, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Pred. No. 3.2e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Aeomica Sequence Listing Engine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR FILING DATE: 2001-02-05
Sequence 11917, Application US/09866108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64.0%;
87.5%;
                                                            APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 87.5
Matches 14; Conservative
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; ORGANISM: Homo sapiens
US-09-866-108-11917
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US-09-866-108-11918/c
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Gaps

49 GTAAGCCGAAGCCATTA 33

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Search completed: October 2, 2001, 16:55:02 Job time: 17665 sec
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                                                                                                                              Sequence 6257, Application US/60278561
GENERAL INFORMATION:
APPLICANT: Morris, MacDonald
APPLICANT: Lal, Preeti
APPLICANT: Lal, Preeti
APPLICANT: Diep, Dinh
TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
TITLE OF INVENTION: Polymorphisms Identified Thereby
TITLE OF INVENTION: Polymorphisms Identified Thereby
CURRENT APPLICATION NUMBER: US/60/278,561
CURRENT APPLICATION NUMBER: US/60/278,561
KINBER OF SEQ ID NOS: 15598
SOFTWARE: PERL PROGram
SEQ ID NO 6257
LENGTH: 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09681508
GENERAL INFORMATION:
APPLICANT: Lin, Yun
APPLICANT: Lin, Yun
APPLICANT: Jayasena, Sumedha D
TITLE OF INVENTION: Aptamer Based Two-Site Binding Assay
FILE REFERENCE: US/09/681,508
CURRENT FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 60/198,016
PRIOR PILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 12.2; DB 8;
Pred. No. 7.5e+03;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: SNP00060057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: snp

: LCCATION: 26

: OTHER INFORMATION: 229652.27, 1901, A->G

US-60-278-561-6257
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82.4%;
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Query Match
Best Local Similarity 82.49
Matches 14; Conservative
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Best Local Similarity 82.45
Matches 14; Conservative
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                                                                                              RESULT 14
US-60-278-561-6257/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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12.6
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                                                                                                                                            Search time 17695.9 Seconds (without alignments) 16.701 Million cell updates/sec
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**Can2_6/ptodata/1/pna/USO8_COMB.seq:**

**Can2_6/ptodata/1/pna/USO9_COMB.seq:**

**Can2_6/ptodata/1/pna/USO9_COMB.seq:
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/cgn2_6/ptodata/1/pna/US6011_COMB.seq:
                  GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pending_Patents_NA_Main:*
    /cgn2_6/ptodata/1/pna/PCTUS_COMB.seq:*
    /cgn2_6/ptodata/1/pna/US06_COMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                         14155048 segs, 7388405095 residues
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                                                                                                                                            2, 2001, 21:50:11;
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Maximum Match 100%
Listing first 45 summaries
                                                                                                    OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                            1 ttttgctagatgctaggtat 20
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20
                                                                                                                                                 October
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Sequence:
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44: /cgn2_6/ptodata/1/pna/US6012_COMB.seq:*
45: /cgn2_6/ptodata/1/pna/US6013_COMB.seq:*
46: /cgn2_6/ptodata/1/pna/US6013_COMB.seq:*
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48: /cgn2_6/ptodata/1/pna/US6016_COMB.seq:*
49: /cgn2_6/ptodata/1/pna/US6016_COMB.seq:*
50: /cgn2_6/ptodata/1/pna/US6019_COMB.seq:*
51: /cgn2_6/ptodata/1/pna/US6019_COMB.seq:*
52: /cgn2_6/ptodata/1/pna/US6021_COMB.seq:*
53: /cgn2_6/ptodata/1/pna/US6022_COMB.seq:*
54: /cgn2_6/ptodata/1/pna/US6022_COMB.seq:*
55: /cgn2_6/ptodata/1/pna/US6022_COMB.seq:*
56: /cgn2_6/ptodata/1/pna/US6022_COMB.seq:*
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50: /cgn2_6/ptodata/1/pna/US6022_COMB.seq:*
50: /cgn2_6/ptodata/1/pna/US6022_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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                                                                                                                                     APPLICANT: Monia, Brett P.
APPLICANT: Gaarde, William A.
APPLICANT: Nero, Pamela S.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0476
CURRENT PILING DATE: 2000-07-13
PRIOR APPLICATION NUMBER: 09/377,310
PRIOR FILING DATE: 1999-08-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Monia, Brett P.
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0389
CURRENT APPLICATION NUMBER: US/09/377,310A
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 9
LENGTH: 20
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ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 20; 100.0%; Pred. No.
                                                                                     Sequence 9, Application PC/TUS0018999
GENERAL INFORMATION:
APPLICANT: Isis Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: antisense sequence PCT-US00-18999-9
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SOFTWARE: PatentIn Ver. 2.0
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Best Local Similarity 100.
Matches 20; Conservative
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Best Local Similarity
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US-09-757-100B-9
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SEQ ID NO 9
LENGTH: 20
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Sequence 9, Application US/09757100B

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APPLICANT: Monia, Brett P.
APPLICANT: Gaarde, William A.
APPLICANT: Nero, Pamela S.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
TITLE OF INVENTION: Expression
TITLE OF INVENTION: 2001-03-15
CURRENT APPLICATION NUMBER: US/09/757,100B
CURRENT FILING DATE: 2001-03-15
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/US00/18999
PRIOR FILING DATE: 2000-07-13
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn Ver. 2.0
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APPLICANT: Gaarde, William A.
APPLICANT: Gaarde, William A.
APPLICANT: Gaarde, William A.
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
FILE REFRENCE: ISPH-0476
CURRENT APPLICATION NUMBER: PCT/USO0/18999
CURRENT FILING DATE: 2000-07-13
PRIOR APPLICATION NUMBER: 09/377,310
NUMBER OF SEQ ID NOS: 43
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Pred. No.
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100.0%;
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Best Local Similarity 100.
Matches 15; Conservative
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Matches 20; Conserv
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APPLICANT: Monia, Brett P.
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase; TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0389; CURRENT APPLICATION NUMBER: US/09/377,310A; CURRENT FILING DATE: 1999-08-19; NUMBER OF SEQ ID NOS: 43; SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8; SEQ ID NO 9; SEQ ID N
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APPLICANT: Monia, Brett P.
APPLICANT: Garde, William A.
APPLICANT: Nero, Pamela S.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase FITLE OF INVENTION: Expression
FITLE OF INVENTION: Expression
FITLE REFERENCE: ISPH-0533
CURRENT APPLICATION NUMBER: US/09/757,100B
PRIOR APPLICATION NUMBER: 09/377,310
PRIOR FILING DATE: 1999-08-19
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         CURRENT APPLICATION NUMBER: PCT/US00/18999 CURRENT FILING DATE: 2000-07-13
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Pred. No.
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PRIOR FILING DATE: 2000-07-13
                                      1999-08-19
S: 42
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; OTHER INFORMATION: antisense sequence
US-09-377-310-8
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100.0%; Pre
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ORGANISM: Artificial Sequence
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                                   CURRENT FILING DATE: 2000-C
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1999-08-
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.(
SEQ ID NO 8
LENGTH: 20
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SOFTWARE: PatentIn Ver. 2.0
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Best Local Similarity 100.
Matches 15; Conservative
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Matches 15; Conservative
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US-09-757-100B-8
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APPLICANT: Gaarde, William A.
APPLICANT: Gaarde, William A.
APPLICANT: Gaarde, William A.
APPLICANT: Mero, Pamela S.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase;
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0533
CURRENT FILING DATE: 2001-03-15
PRIOR FILING DATE: 2001-03-15
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 2000-07-13
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 29
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APPLICANT: Gaarde, William A.
APPLICANT: Garde, William A.
APPLICANT: Nero, Pamela S.
ATTLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0476
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-03189
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
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GENERAL INFORMATION:
APPLICANT: Isis Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                        CTHER INFORMATION: antisense sequence US-09-377-310-29
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Best Local Similarity 100.
Matches 15; Conservative
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US-09-757-100B-29
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LENGTH: 15
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; DATABASE ACCESSION NUMBER: SGD YERO50C US-60-232-638-58459
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US-60-233-620-16838
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Sequence 407, Application US/09422978

GENERAL INFORMATION:
APPLICANT: Chen, Daniel
APPLICANT: Chumakov, IJsa
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET.020C1
CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT PAPLICATION NUMBER: US 09/298,850
EARLIER APPLICATION NUMBER: US 09/298,850
EARLIER FILLING DATE: 1999-10-20
EARLIER FILLING DATE: 1998-11-23
EARLIER RPLICATION NUMBER: US 60/109,732
EARLIER RPLICATION NUMBER: US 60/082,614
EARLIER RPLING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796

SEQ ID NO 477

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GENERAL INFORMATION:
APPLICANT: Mittmann
TITLE OF INVENTION: Methods of Genetic Analysis of Yeast
TITLE OF INVENTION: Methods of Genetic Analysis of Yeast
FILE REFERENCE: 3110
CURRENT APPLICATION NUMBER: US/60/232,638
CURRENT FILING DATE: 2000-09-14
NUMBER OF SEQ ID NOS: 138410
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 58459
                                                                                                                                                                        Length 20;
                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTHER INFORMATION: 99-14678-75 : polymorphic base G or US-09-422-978-407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 14.8; DB 18;
Pred. No. 2.3e+03;
0; Mismatches 2;
                                                                                                                                                                      75.0%; Score 15; DB 29; 100.0%; Pred. No. 1.6e+03; tive 0; Mismatches 0;
                                                                         FEATURE:

COTHER INFORMATION: antisense sequence
US-09-757-100B-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Saccaromyces cerevisiae PUBLICATION INFORMATION:
                                     TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74.0%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 75.0
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 74.0
Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
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LOCATION: 24
                                                                                                                                                                                                                                                                                                                                                                US-09-422-978-407
SEQ ID NO 8
LENGTH: 20
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 Length 25;
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Sequence 209206, Application US/60234017

GENERAL INFORMATION:

APPLICANT: Mittmann, M

TITLE OF INVENTION: Methods of Genetic Analysis of Mus

FILLE REFERENCE: 3115

CURRENT APPLICANTON: Musculus

FILLE REFERENCE: 3115

CURRENT FILING DATE: 2000-09-20

NUMBER OF SEQ ID NOS: 605887

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 209206

LENGTH: 25
                                       Indels
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                                                                                                                                                                                                                                         APPLICANT: Mittmann
APPLICANT: Mittmann
APPLICANT: Mittmann
TITLE OF INVENTION: Methods of Genetic Analysis of
TITLE OF INVENTION: Methods of Genetic Analysis of
TITLE OF INVENTION: Machinopsis thaliana
FILE REFERENCE: 3116
CURRENT APPLICATION NUMBER: US/60/233,620
CURRENT FILING DATE: 2000-110-24
NUMBER OF SEQ ID NOS: 131820
SOFTWARR: FastSEQ for Windows Version 4.0
SEQ ID NO 16838
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 14.4; DB 55;
Pred. No. 3.4e+03;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 14.2; DB 55;
Pred. No. 4.3e+03;
0; Mismatches 3;
Score 14.4; DB 55
Pred. No. 3.4e+03;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AC005499
US-60-233-620-16838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
CREANISM: MUS MUSCULUS
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: GenBank AI504141
US-60-234-017-209206
                                                                                                                                                                                                           ; Sequence 16838, Application US/60233620; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Arabidopsis thaliana
72.0%;
93.8%;
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93.8%;
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84.2%;
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Query Match 72.0
Best Local Similarity 93.8
Matches 15; Conservative
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Best Local Similarity 93.8
Matches 15; Conservative
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Best Local Similarity
Matches 16; Conserva
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Search completed: October 2, 2001, 21:50:12
Job time: 24525 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 20;
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GENERAL INFORMATION:
APPLICANT: Mittmann
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis of Yeast
FILE REFERENCE: 3110
CURRENT APPLICATION NUMBER: US/60/232,638
CURRENT PILING DATE: 2000-09-14
NUMBER OF SEQ ID NOS: 138410
SOUTHWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 50420
LENGTH: 25
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Pred. No. 6.6e+03;
0; Mismatches 2;
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; ORGANISM: Other nucleic acid, synthetic DNA
US-09-486-816-26
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PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: SGD YDR240C
US-60-232-638-50420
                                                                                                            Sequence 26, Application US/09486816 GENERAL INFORMATION:
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Best Local Similarity 88.2%;
Matches 15; Conservative
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3 tttgataaatgctaggt 19
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Best Local Similarity 88.29
Matches 15; Conservative
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2052, Ap 116945, A 117300, A 117300, A 118915, A 26816, A 6194, Ap 6484, Ap 6683, Ap 7183, Ap

24, Appl 6, Appli 3901, Ap 13773, A

7502, A 8470, A 25152,

seduence Sequence Seq

OM nucleic

Run on:

Searched:

Sequence:

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US-60-278-258-6107/c
Sequence 6107, Application US/60278258
Sequence 6107, Application US/60278258
SERINGAL INFORMATION:
APPLICANT: Morris, MacDonald
APPLICANT: Diep, Dinh
TITLE OF INVENTION: Polymorphisms Identification of Sequence Polymorphisms Using:
TITLE OF INVENTION: Polymorphisms Identified Thereby
CURRENT APPLICATION NUMBER: US/60/278,258
CURRENT FILING DATE: 2001-03-23
SUFFMERE: PELL PROGRAM
SOFTWARE: PERL PROGRAM
SOFTWARE: PERL PROGRAM
SOFTWARE: PERL PROGRAM
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GENERAL INFORMATION:
APPLICANT: Warrington, Janet
APPLICANT: Shah, Nila
APPLICANT: Shah, Nila
APPLICANT: Gingeras, Thomas Raymond
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Human Lymphoblast Polymorphisms
FILE REFERENCE: 3229.2
CURRENT APPLICATION NUMBER: US/09/574,376B
Score 13.8; DB 8;
Pred. No. 8.8e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: SNP00057112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: 350403.1, 20, G->A US-60-278-258-6107
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Best Local Similarity 88.2
Matches 15; Conservative
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US-09-574-376B-1127/c
    NAME/KEY: snp
LOCATION: 20
  FEATURE
    δ
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Sequence 4811, Ap
Sequence 5557, Ap
Sequence 6920, Ap
Sequence 11076, A
Sequence 16613, A
Sequence 16613, A
Sequence 20, Appl
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Sequence 1127, Ap
Sequence 1141, Ap
Sequence 1801, Ap
Sequence 5496, Ap
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1751, Ap
12658, A
12658, A
96, Appl
2124, Appl
2124, Appl
2431, Ap
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8122, Ap
                                                                                                                                                               Search time 2173.58 Seconds (without alignments) 19.290 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 1
Sequence 1
Sequence 2
Sequence 9
Sequence 9
Sequence 2
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Sequence 1
Sequence 4
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1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*

2: /cgn2_6/ptodata/2/pna/USOG_NEW_COMB.seq:*

3: /cgn2_6/ptodata/2/pna/USOB_NEW_COMB.seq:*

4: /cgn2_6/ptodata/2/pna/USOB_NEW_COMB.seq:*

5: /cgn2_6/ptodata/2/pna/USOB_NEW_COMB.seq:*

6: /cgn2_6/ptodata/2/pna/USOB_NEW_COMB.seq:*

7: /cgn2_6/ptodata/2/pna/USOB_NEW_COMB.seq:*

8: /cgn2_6/ptodata/2/pna/USOB_NEW_COMB.seq2:*

8: /cgn2_6/ptodata/2/pna/USOB_NEW_COMB.seq2:*
                        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-801-274-1141

US-09-817-879-5496

US-09-445-283B-47

US-09-817-879-4811

US-09-817-879-6811

US-09-817-879-6920

US-09-817-879-9024

US-09-817-879-9024

US-09-817-879-9024

US-09-801-1076

US-09-801-1076

US-09-801-274-1731

US-09-801-274-1751

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-09-817-879-2431
-09-827-383-1410
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US-60-278-232-4276
US-60-253-457-8122
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                                                                                                                                                     October 2, 2001, 16:55:01;
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Maximum Match 100%
Listing first 45 summaries

    nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 50
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Match 1
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664.0
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Sequence 5496, Application US/09817879
GEMERAL INFORMATION:
APPLICANT: Ribozyme bharmaceuticals Inc.
ATTLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Rel
TITLE OF INVENTION: Hepatitis C Virus Infection
FILE REPRENCE: MBH800-801-F
CURRENT APLICATION NUMBER: US/09/817,879
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9703
SOFTWARE: Patentin version 3.0
SEQ ID NO 5496
LENGTH: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 47, Application US/09445283B
GENERAL INFORMATION:
APPLICANT: Maliga, Pal
APPLICANT: Silhavy, Daniel
APPLICANT: Siraman, Priya
TITLE OF INVENTION: Plastid Promoters for Transgene
TITLE OF INVENTION: Expression in the Plastids of Higher Plants
FILE REFERENCE: Rut 97-0097
CURRENT APPLICATION NUMBER: US/09/445,283B
CURRENT FILING DATE: 1998-06-03
PRIOR FILING DATE: 1998-06-03
PRIOR FILING DATE: 1998-06-03
PRIOR FILING DATE: 1997-09-12
PRIOR FILING DATE: 1997-06-03
SOFTWARR: FASTSEQ for Windows Version 3.0
SEQ ID NOS: 62
LENGTH: 27
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Pred. No. 2.8e+03;
1; Mismatches 3;
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Pred. No. 2.8e+03;
0; Mismatches 2;
                                                                                                                          1; Mismatches
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87.5%;
                                                                                 Query Match
Best Local Similarity 77.8%;
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                                                                                                                            14; Conservative
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Best Local Similarity 87.5
Matches 14; Conservative
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US-09-801-274-1801
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US-09-817-879-5496
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GENERAL INFORMATION:
APPLICANT: Cargill, Michele
APPLICANT: Leander, Eric S.
APPLICANT: Lander, Eric S.
TITLE OF INFORMATION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
FILE REFERENCE: 225.2009-001
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 60/187,510
PRIOR APPLICATION NUMBER: US 60/187,510
PRIOR PILING DATE: 2000-03-07
PRIOR PILING DATE: 2000-05-02
NUMBER OF SEQ ID NOSS: 1802
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1801
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1141, Application US/09801274
GENERAL INFORMATION:
APPLICANT: Cargill, Michele
APPLICANT: Lander, James S.
TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS;
FILE REFERENCE: 2825.2009-001;
CURRENT APPLICATION NUMBER: US/09/801,274
CURRENT FILING DATE: 2001-03-07
PRIOR PPLICATION NUMBER: US 60/187,510
PRIOR FILING DATE: 2000-03-07;
PRIOR PLICATION NUMBER: US 60/206,129
PRIOR FILING DATE: 2000-03-07;
PRIOR FILING DATE: 2000-05-22
NUMBER OF SEQ ID NOS: 1802
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1141
LENGER HANDER OF SEQ.
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Pred. No. 2.8e+03;
1; Mismatches 3
                   NUMBER OF SEQ ID NOS: 1330
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1127
LENGTH: 31
2000-05-19
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77.8%;
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Best Local Similarity 75.0
Matches 15; Conservative
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Best Local Similarity 77.8
Matches 14; Conservative
                                                                                                                        ORGANISM: Homo sapiens; PUBLICATION INFORMATION:
US-09-574-376B-1127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-09-801-274-1141
CURRENT FILING DATE:
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US-09-801-274-1141
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US-09-801-274-1801
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APPLICANT: Ribozyme Pharmaceuticals Inc.
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Rel
TITLE OF INVENTION: Hepatitis C Virus Infection
FILE REFERENCE: MBHB00-801-F
CURRENT APPLICATION NUMBER: US/09/817,879
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9703
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6920
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TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Rel
TITLE OF INVENTION: Hepatitis C Virus Infection
FILE REFERENCE: MHBB00-801-F
CURRENT APPLICATION NUMBER: US/09/817,879
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9703
SSFTWARE: PatentIn version 3.0
SEQ ID NO 9954
LENGTH: 31
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GENERAL INFORMATION:
APPLICANT: Havukkala, 11kka J
TITLE OF INVENTION: Polynucleotides isolated from plants; TITLE OF INVENTION: and methods for their use.
FILE REFERENCE: 1054P3
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Pred. No. 5.8e+03;
0; Mismatches 3;
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Pred. No. 5.8e+03;
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                                           ; Sequence 6920, Application US/09817879 ; GENERAL INFORMATION:
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ORGANISM: artificial sequence
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82.4%;
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82.4%;
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Best Local Similarity 82.4
Matches 14; Conservative
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Best Local Similarity
Matches 14; Conserva
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                                                                                                                                                                                                               Sequence 4811. Application US/09817879
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals Inc.
APPLICANT: Ribozyme Pharmaceuticals Inc.
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
TITLE OF INVENTION: Hepatitis C Virus Infection
FILE REFERENCE: MBHB00-801-F
CURRENT APPLICATION NUMBER: US/09/817,879
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9703
SOFTWARE PATENT OF SEQ ID NOS: 9703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ribozyme Pharmaceuticals Inc.
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
TITLE OF INVENTION: Hepatitis C Virus Infection
FILE REFERENCE: MBHB00-801-F
CURRENT APPLICATION NUMBER: US/09/817,879
UNRBER FILING BATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9703
SOFTWARE: Patentin version 3.0
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    Score 12.4; DB 6;
Pred. No. 4.5e+03;
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Pred. No. 5.8e+03;
                                           Mismatches
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82.4%;
    62.0%;
92.9%;
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82.4%;
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Best Local Similarity 92.9
Matches 13; Conservative
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Best Local Similarity 82.4
Matches 14; Conservative
                                                                                3 ttgctagatgctag 16
                                                                                                                      17 TIGCTAGATICTAG 4
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Best Local Similarity
Matches 14; Conserv
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LENGTH: 31
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APPLICANT: Poque, Gregory P.
TITLE OF INVENTION: METHOD OF DETERMINING THE FUNCTION OF
TITLE OF INVENTION: METHOD OF DETERMINING THE FUNCTION OF
TITLE OF INVENTION: TRANSFECTING THE SAME INTO A HOST
FILLE REPERENCE: 080101371051
CURRENT APPLICATION NUMBER: U5/09/232,170
CURRENT FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 49
SEQ ID NO 20
LENGTH: 36
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5 Gedence 773, Application US/09840424

5 GENERAL INFORMATION:

APPLICANT: Gearing, David P.

5 APPLICANT: MCGARTHY, Sean A.

TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A

TITLE OF INVENTION: NUMBER: US/09/840,424

CURRENT FILING DATE: 1090.1010-002

FRIOR REPLICATION NUMBER: US 60/084,098

PRIOR APPLICATION NUMBER: US 60/123,523

PRIOR APPLICATION NUMBER: US 60/123,523

PRIOR FILING DATE: 1999-03-08

PRIOR FILING DATE: 1999-03-08

PRIOR FILING DATE: 1999-03-30

PRIOR FILING DATE: 1999-03-30

PRIOR FILING DATE: 1999-05-04

PRIOR PRICE DATE: 1999-05-04

PRIOR PRICE DATE: 1999-05-04
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Pred. No. 9.6e+03;
); Mismatches 2;
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; OTHER INFORMATION: n = A,T,C or G
US-09-840-424-773
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86.7%;
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Best Local Similarity 86.7
Matches 13; Conservative
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Best Local Similarity 86.7
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: VIRAL
US-09-232-170-20
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US-09-801-274-1751
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US-09-840-424-773
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; Sequence 16613, Application US/09708690
; GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Bavco, pam
APPLICANT: Bavco, pam
APPLICANT: Baccobcdo, Jaim
APPLICANT: Escobcdo, Jaim
APPLICANT: Levels of Vascular Endothelial Growth Factor Receptor
ITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHBDO, 976-L (400/002)
CURRENT APPLICATION NUMBER: US 60/708,690
PRIOR APPLICATION NUMBER: US 60/205,974
PRIOR APPLICATION NUMBER: US 09/371,772
PRIOR PILING DATE: 1996-01-08
PRIOR FILING DATE: 1996-01-08
PRIOR FILING DATE: 1996-01-08
PRIOR FILING DATE: 1996-01-08
PRIOR PILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 20828
SOFTWARE: PatentIn version 3.0
SEQ ID NO 16613
LENGTH: 31
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US-09-708-690-16613
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CURRENT APPLICATION NUMBER: US/60/253,378
CURRENT FILING DATE: 2000-11-27
NUMBER OF SEQ ID NOS: 40367
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11076
LENGTH: 36
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US-09-232-170-20/C
; Sequence 20, Application US/09232170
; GENERAL INFORMATION:
; APPLICANT: Erwin, Robert L.;
; APPLICANT: Erwin, Robert L.;
; APPLICANT: Hanley, Kathleen M.;
APPLICANT: Hanley, Kathleen M.;
; APPLICANT: Lindbo, John A.;
; APPLICANT: Lindbo, John A.;
; APPLICANT: MGGee, David R.
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86.7%;
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Best Local Similarity 75.0
Matches 15; Conservative
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Best Local Similarity 86.7
Matches 13; Conservative
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                                                                                                                                                ; TYPE: DNA
; ORGANISM: Pinus radiata
US-60-253-378-11076
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US-09-708-690-16613
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## APPLICANT: Lander, Eric S.
### TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
### FILLE REPERENCE: 2825.2009-00.0
### CURRENT APPLICATION NUMBER: US 60/187,510
### PRIOR APPLICATION NUMBER: US 60/206,129
### PRIOR PILING DATE: 2000-05-22
### SEQ ID NOS: 1802
### SEQ ID NOS: 1803
### SEQ ID NOS: 1804
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(without alignments)
16.701 Million cell updates/sec
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(cgn2_6/ptodata/1/pna/uS06_COMB.seq:*
(cgn2_6/ptodata/1/pna/uS06_COMB.seq:*
(cgn2_6/ptodata/1/pna/uS08_COMB.seq:*
(cgn2_6/ptodata/1/pna/uS08_COMB.s
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/cgn2_6/ptodata/1/pna/US6011_COMB.seq:*
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/cgn2_6/ptodata/1/pna/US6008_COMB.seq:
/cgn2_6/ptodata/1/pna/US6009_COMB.seq:
                             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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                                                                                Sequence 8, Application PC/TUS0018999
GENERAL INFORMATION:
APPLICANT: IS1S Pharmaceuticals, Inc.
APPLICANT: Baret P.
APPLICANT: Gaarde, William A.
APPLICANT: Garde, William A.
APPLICANT: Nero, Pamela S.
ITILE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
ITILE OF INVENTION: Expression
FILE REFERENCE: ISPH-0476
CURRENT APPLICATION NUMBER: PCT/US00/18999
CURRENT FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-08-19
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 8
LENGTH: 20
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Sequence 8, Application US/09377310A

Sequence 8, Application US/09377310A

GENERAL INFORMATION:

APPLICANT: Gearde, William A.

TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase

TITLE OF INVENTION: Expression

TITLE OF INVENTION: Expression

TITLE OF INVENTION: Expression

CURRENT APPLICATION NUMBER: US/09/377,310A

CURRENT FILING DATE: 1999-08-19

NUMBER OF SEO ID NOS: 43

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 8

LENGTH: 20
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100.0%; Pred. No. 1.6
Live 0; Mismatches
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ALIGNMENTS
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US-09-757-100B-8
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ORGANISM: Artificial Sequence
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Matches 20; Conserva
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APPLICANT: Monia, Brett P.
APPLICANT: Garde, William A.
APPLICANT: Garde, William A.
APPLICANT: Nero, Pamela S.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase;
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0533
CURRENT APPLICATION NUMBER: US/09/757,100B
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: 09/377,310
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 2000-07-13
NUMBER: OF SEQ ID NOS: 44
SOFTWARE: PATENTING Ver. 2.0
SEQ ID NO 8
LENGTH: 20
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GENERAL INFORMATION:
APPLICANT: Mittmann
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis of
TITLE OF INVENTION: Arabidopsis thaliana
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APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis of
TITLE OF INVENTION: Arabidopsis thaliana
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Pred. No. 3.2e+02;
0; Mismatches 2;
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Pred. No. 1.6;
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; DATABASE ACCESSION NUMBER: Genbank AC003672
US-60-233-620-73486
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CURRENT APPLICATION NUMBER: US/60/233,620
CURRENT FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 131820
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 73486
LENGTH: 25
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ORGANISM: Arabidopsis thaliana
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Best Local Similarity 100.0%;
Matches 20; Conservative 0
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Best Local Similarity 89.5
Matches 17; Conservative
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| GENERAL INFORMATION:
| APPLICAMT: Isis Pharmaceuticals, Inc.
| APPLICAMT: Monia, Brett P. .
| APPLICAMT: Mero, Pamela S. | TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase | TITLE OF INVENTION: APPLICAMT: APPLICAMT: Nero, Pamela S. | TITLE OF INVENTION: APPLICAMT: APPLICAMT: NERO | TITLE OF INVENTION: APPLICAMT: ISPH-0476
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APPLICANT: Gaarde, William A.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0389
CURRENT FILINO NUMBER: US/09/377,310A
CURRENT FILINO DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 28
LENGTH: 15
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                                                                                                                       76.0%; Score 15.2; DB 55;
85.0%; Pred. No. 6.9e+02;
tive 0; Mismatches 3;
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100.0%; Pred. No. 8.2e+02;
iive 0; Mismatches 0;
  ; ORGANISM: Arabidopsis thaliana
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank AF096373
US-60-233-620-101590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: PCT/US00/18999
CURRENT FILING DATE: 2000-07-13
PRIOR APPLICATION NUMBER: 09/377,310
PRIOR FILING DATE: 1999-08-19
SOFTWARE: PATENTIN VET. 2.0
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ORGANISM: Artificial Sequence
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Best Local Similarity 85.0°
Matches 17; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
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PCT-US00-18999-28
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SOFTWARE: Par
SEQ ID NO 28
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US-09-377-310-28
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APPLICANT: Cohen, Daniel
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Abderrahim, Hadi
APPLICANT: Abderrahim, Hadi
APPLICANT: BIALLELIC MARKER MAPS FOR USE IN CONSTRUCTING A HIGH DENSITY...
FILE OF INVENTION: BIALLELIC MARKER MAPS FOR USE IN CONSTRUCTING A HIGH DENSITY...
FILE REPRENCE: 84.051.PRO
CURRENT FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 13665
SOOTWARE: Patent.nm
SEO IT NO.
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GENERAL INFORMATION:
APPLICANT: Mittmann
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis of
TITLE OF INVENTION: Arabidopsis thaliana
FILE REFERENCE: 3116
CURRENT APPLICATION NUMBER: US/60/233,620
CURRENT FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 131820
                                                                                                                                                                                                                                                          Score 15.8; DB 55;
Pred. No. 3.2e+02;
0; Mismatches 2;
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Pred. No. 5.9e+02;
1; Mismatches 2;
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DATABASE ACCESSION NUMBER: GenBank AC003672
US-60-233-620-73499
CURRENT APPLICATION NUMBER: US/60/233,620
CURRENT FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 131820
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 73499
LENGTH: 25
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                                                                                                                       TYPE: DNA ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                            79.0%;
89.5%;
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84.2%;
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Best Local Similarity 89.55
Matches 17; Conservative
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Best Local Similarity 84.25
Matches 16; Conservative
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ORGANISM: Homo Sapiens
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SEQ ID NO 101590
LENGTH: 25
TYPE: DNA
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APPLICANT: Monia, Brett P.
APPLICANT: Gaarde, William A.
APPLICANT: Gaarde, William A.
APPLICANT: Brook Bamela S.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase;
TITLE OF INVENTION: Expression
FILE REPERENCE: ISPH-0533
CURRENT APPLICATION NUMBER: US/09/757,100B
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: 09/377,310
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 2000-07-13
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 9
LENGTH: 20
                                                                                                                                                                                                                                         GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Monda, Brett P.
APPLICANT: Garde, William A.
TITLE OF INVENTION: Expression
TITLE OF INVENTION
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Pred. No. 8.6e+02;
0; Mismatches 0;
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100.0%; Pred. No. 8.6e+02;
Live 0; Mismatches 0;
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COTHER INFORMATION: antisense sequence
US-09-377-310-9
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100.08; Pre-
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ORGANISM: Artificial Sequence
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Matches 15; Conservative
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Matches 15; Conservative
                                                     1 ctagatgctaggtat 15
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| ctagatgctaggtat 20
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US-09-757-100B-28
US-09-757-100B-28
Sequence 28, Application US/09757100B
GENERAL INFORMATION:
APPLICANT: Gaarde, William A.
APPLICANT: Garde, William A.
TITLE OF INVENTION: Expression
FILE REPRENCE: ISPH-053
CURRENT APPLICATION NUMBER: US/09/757,100B
CURRENT APPLICATION NUMBER: US/09/757,100B
CURRENT APPLICATION NUMBER: US/09/757,100B
FRIOR APPLICATION NUMBER: POIT-03-15
PRIOR APPLICATION NUMBER: POIT-03-15
PRIOR FILING DATE: 2000-07-13
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 28
LENGTH: 15
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APPLICANT: Gaarde, William A.
APPLICANT: Nero, Pamela S.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
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                                                     Indels
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                          Pred. No. 8.2e+02;
Mismatches 0;
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CURRENT APPLICATION NUMBER: PCT/USOO/18999
CURRENT FILING DATE: 2000-07-13
FRIOR APPLICATION NUMBER: 09/377,310
FRIOR FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTIN Ver. 2.0
SOFTWARE: PATENTIN Ver. 2.0
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9, Application PC/TUS0018999
GENERAL INFORMATION:
APPLICANT: Isis Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: antisense sequence US-09-757-1008-28
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100.08; Pie
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ORGANISM: Artificial Sequence
FEATURE:
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                       Best Local Similarity 100.
Matches 15; Conservative
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Matches 15; Conservative
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Matches 15; Conserva
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; Sequence 48863, Application US/09660220
; GENERAL INFORMATION:
; APPLICANT: Mitthann et al.; APPLICANT: Mitthann et al.; APPLICANT: Mitthann et al.; TITLE OF INVENTION: Methods of Genetic Analysis of Human FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/660,220
; PRIOR FILING DATE: 2000-09-12
; PRIOR PLICATION NUMBER: 60/164,973
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SED ID NOS: 140981
; SOFUMARE: RastSEQ for Windows Version 4.0
; SEQ ID NO 48663
             Genemic 11883, Application US/09660220
GENEMATION:
APPLICANT: Mittmann et al.
APPLICANT: Affymation.
TITLE OF INVENTION:
FILE REFERENCE: 3102.1
CURRENT FILING DATE: 2000-09-12
PRIOR APPLICATION NUMBER: 60/164,973
PRIOR PLILING DATE: 1999-11-11
NUMBER OF SEQ ID NOS: 140981
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11883
LENTH: 25
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84.2%; Pred. No. 2.4e+03;
tive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 71.0%; Score 14.2; DB 26; Best Local Similarity 84.2%; Pred. No. 2.4e+03; Matches 16; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : TYPE: DNA
: ORGANISM: Homo Sapiens
: PUBLICATION INFORMATION:
DATABABSE ACCESSION NUMBER: GenBank M14338
US-09-660-220-48863
                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank D63881
US-09-660-220-11883
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Best Local Similarity 84.29
Matches 16; Conservative
US-09-660-220-11883
                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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Search completed: October 2, 2001, 21:50:11 Job time: 24524 sec

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Sequence 6107, Application US/60278258; GENERAL INFORMATION:
APPLICANT: Worris, MacDonald
APPLICANT: Lal, Preeti
APPLICANT: Diep, Dinh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
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Matches 14; Conserv
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Sequence 3191, Ap
Sequence 3191, Ap
Sequence 31, Appli
Sequence 4320, Ap
Sequence 4320, Ap
Sequence 2606, Ap
Sequence 2606, Ap
Sequence 5533, Ap
Sequence 5533, Ap
Sequence 5534, Ap
Sequence 5534, Ap
Sequence 5536, Ap
Sequence 5537, Ap
Sequence 5540, Ap
Sequence 5541, Ap
Sequence 5443, Ap
                                                                                      ; Search time 2173.58 Seconds
(without alignments)
19.290 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*

2: /cgn2_6/ptodata/2/pna/USOG_NEW_COMB.seq:*

3: /cgn2_6/ptodata/2/pna/USOB_NEW_COMB.seq:*

4: /cgn2_6/ptodata/2/pna/USOB_NEW_COMB.seq:*

5: /cgn2_6/ptodata/2/pna/USOB_NEW_COMB.seq:*

6: /cgn2_6/ptodata/2/pna/USOB_NEW_COMB.seq:*

7: /cgn2_6/ptodata/2/pna/USOB_NEW_COMB.seq:*

8: /cgn2_6/ptodata/2/pna/USOB_NEW_COMB.seq2:*

8: /cgn2_6/ptodata/2/pna/USOB_NEW_COMB.seq2:*
            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-048-473-3

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US-09-086-108-2604

US-09-866-108-2605

US-09-866-108-5533

US-09-866-108-5534

US-09-866-108-5534

US-09-866-108-5536

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Maximum DB seq length: 50
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Match I
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235, App
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191, App
22107, A
16933, A
17980, A
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26932, A
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Sequence Seq
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Sequence
                              US-09-708-690-8033
US-09-546-745A-3189
US-09-801-274-32
US-09-801-274-32
US-09-801-274-32
US-09-17-255-81
US-09-17-255-81
US-09-17-255-81
US-09-17-25-87
US-09-708-690-16933
US-09-708-690-16933
US-09-708-690-1693
US-09-708-690-1802
US-09-708-690-1802
US-09-708-690-1802
US-09-708-690-1802
US-09-708-690-1802
US-09-74-671-235
US-09-74-671-235
US-09-78-561-3466
US-09-635-251-100
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ALIGNMENTS

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Sequence 773, Application US/09840424

Sequence 773, Application US/09840424

Sequence 773, Application US/09840424

Sequence 774, Application US/09840424

PAPLICANT: Gearing, David P.

PAPLICANT: MCGATCHY, Sean A.

TITLE OF INVENTION: HUMAN MICROVASCULAR ENDOTHELIAL LIBRARY

TITLE OF INVENTION: HUMAN MICROVASCULAR ENDOTHELIAL LIBRARY

FILE REFERENCE: 1600.1010-002

CURRENT APPLICATION: NUMBER: US 60/9840,424

CURRENT FILING DATE: 1098-05-04

PRIOR FILING DATE: 1998-05-04

PRIOR APPLICATION NUMBER: US 60/123,523

PRIOR APPLICATION NUMBER: US 60/126,974

PRIOR APPLICATION NUMBER: US 60/126,974

PRIOR PILING DATE: 1999-03-30

PRIOR FILING DATE: 1999-05-04

PRIOR PILING DATE: 1999-05-131

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 773
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Pred. No. 1.5e+03;
0; Mismatches 2;
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87.5%;
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US-09-048-473-3
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TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using TITLE OF INVENTION: Polymorphisms Gequence Databases, and Single Nucleotide FILE OF INVENTION: Polymorphisms Identified Thereby
TITLE OF INVENTION: POLYMORPHISMS IDENTIFIED THEREBY THE COLOR NUMBER: US/60/278,258
CURRENT PEPLICATION NUMBER: US/60/278,258
CURRENT FILING DATE: 2001-03-23
NUMBER OF SEQ ID NOS: 1730
SOFTWARE: PERL PROGRAM
SEQ ID NO 6107
LENGTH: 45
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APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Blatt, Larry
APPLICANT: Batt, Larry
APPLICANT: Pavco, Pam
APPLICANT: Pavco, Pam
APPLICANT: Machael
APPLICANT: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
TITLE OF INVENTION: Regulation of Repressor Genes using Nucleic Acid Molecules
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58.3%; Pred. No. 3.8e+03;
ive 5; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: SNP00057112
NAME/KEY: SNP
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GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: 350403.1, 20, G->A US-60-278-258-6107
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Best Local Similarity 58.3
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Matches 14; Conservative
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Zwick, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
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US-09-546-745A-3190
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US-09-546-745A-3191
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LOCATION: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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Gaps
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** OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-546-7458-3191
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                                                                                                                                                                                                                                                                                               Score 12; DB 6; Length 17;
Pred. No. 3.8e+03;
5; Mismatches 0; Indels
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CORRUTER: IBM Compatible
COERATING SYSTEM: DOS
SOFTWARE: FASEEGO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/048,473
FILING DATE: 26-Mar-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/214,237
FILING DATE: 01-JUL-1992
APPLICATION NUMBER: 07/931,123
FILING DATE: 17-AUG-1992
APPLICATION NUMBER: 08/345,018
FILING DATE: 23-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSE: Genencor International, Inc.
STREET: 925 Page Mill Road
CITY: Palo Alto
STATE: CA
CURRENT APPLICATION NUMBER: US/09/546,745A CURRENT FILING DATE: 2000-04-11 NUMBER OF SEQ ID NOS: 7043 SEQ TWARE: Patentin version 3.0 SEQ ID NO 3191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: ASPARTIC PROTEINP FILAMENTOUS FUNGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: GC45-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Glaister, Debra J.
REGISTRATION NUMBER: 33,888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hayenga, Kirk J.
Lawlis, Virgil B.
Ward, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/09048473 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: US
ZIP: 94304-1013
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Berka, Randy M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 650-845-6504
INFORMATION FOR SEQ ID NO: 3:
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LENGTH: 36 base pairs
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                 60.0%;
58.3%;
                                                                                                                                           TYPE: RNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                      Best Local Similarity 58.3
Matches 7; Conservative
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US-09-048-473-3/C
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Gaps

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APPLICANT: SHANNON, MARK
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
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                                                                                                                                                                                                                                                                                                                                                                                                                               5; Indels
                       TITLE OF INVENTION: Polynucleotides, isolated from plants TITLE OF INVENTION: and methods for their use.
                                                                                                                                                                                                                                                                                                                                                                           60.0%; Score 12; DB 8; 75.0%; Pred. No. 4.4e+03; iive 0; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
PRIOR PELLING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: DCT/US01/00665
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR APPLICATION NUMBER: PCT/US01/00661
                                                                 FILE REFERENCE: 1054P2
CURRENT APPLICATION NUMBER: US/60/253,457
CURRENT FILING DATE: 2000-11-27
NUMBER OF SEQ ID NOS: 48893
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 43320
LENGTH: 39
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SOFTWARE: Acomica Sequence Listing Engine
SEQ ID NO 2604
LENGTH: 17
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APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                               15; Conservative
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                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Pinus radiata
US-60-253-457-43320
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Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRACERC for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/048,473
FILING DATE: 26-Mar-1998
PRIOR APPLICATION DATA:
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International, Inc.
STREET: 925 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 07/214,237
FILING DATE: 01-JUL-1992
APPLICATION NUMBER: 07/931,123
FILING DATE: 17-AUG-1992
APPLICATION NUMBER: 08/345,018
FILING DATE: 23-NOV-1994
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NAME: Glaister, Debra J.
RAGISTRALION NUMBER: 33,888
REFERENCE/DOCKET NUMBER: GC45-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
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; Sequence 43320, Application US/60253457
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                               Sequence 7, Application US/09048473
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
Hayenga, Kirk J.
Lawlis, Virgil B.
Ward, Michael
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ZIP: 94304-1013
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 75.0%;
Matches 15; Conservative C
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                                                                         Conservative
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                                       Best Local Similarity
Matches 15; Conserv
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                       Query Match
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GENERAL INFORMATION:
APPLICANT: 01, Yizhong
APPLICANT: 01, Yizhong
APPLICANT: 01, Yizhong
APPLICANT: 01, Yizhong
APPLICANT: PENN, Sharron G.
APPLICANT: RANK, David R.
APPLICANT: RANK, David R.
APPLICANT: RANK, David R.
APLICANT: CHEN, Wark
ITLE OF INVENTION: WASH-ITE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT APPLICATION NUMBER: US 60/207,456
PRIOR FILING DAVE: 2000-09-24
PRIOR PLING DAVE: 2000-09-24
PRIOR PLING DAVE: 2000-09-30
PRIOR PLING DAVE: 2001-01-30
PRIOR PLING DAVE: 2001-01-30
PRIOR PRIOR PLING DAVE: 2001-01-30
PRIOR PLING DAVE: 2001-01-30
PRIOR PLING DAVE: 2001-01-30
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Pred. No. 4.9e+03;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aeomica Sequence Listing Engine
                                                                                            Sequence 2606, Application US/09866108 GENERAL INFORMATION:
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; GENERAL INFORMATION:
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86.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 59.0
Best Local Similarity 86.7
Matches 13; Conservative
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APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron
 2 agatgctgggcatct 16
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SEQ ID NO 2606
LENGTH: 17
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                                                                            Length 17;
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                                                                                                               Indels
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Pred. No. 4.9e+03;
0; Mismatches 2;
                                                                        Score 11.8; DB 6;
Pred. No. 4.9e+03;
0; Mismatches 2;
                                                                      Query Match 59.0
Best Local Similarity 86.7
Matches 13; Conservative
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Best Local Similarity 86.7
Matches 13; Conservative
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; ORGANISM: Homo sapiens US-09-866-108-2604
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GRGANISM: Homo sapiens
US-09-866-108-2605
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APPLICANT: 11. Yonggang
APPLICANT: 31, Yonggang
APPLICANT: 31, Yonggang
APPLICANT: 11, Yonggang
APPLICANT: BENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: ADONICA-7
CURRENT APPLICATION NUMBER: US 60/207, 456
PRIOR APPLICATION NUMBER: US 60/207, 456
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR PRIOR APPLICATION NUMBER: US 60/236, 359
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: CT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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PRIOR PILING DATE: 2001-01-30
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Pred. No. 5.3e+03;
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                        PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR PELICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-31
PRIOR PELING DATE: 2001-01-31
PRIOR RELING DATE: 2001-01-31
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FILING DATE: 2001-01-30
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; ORGANISM: Homo sapiens
US-09-866-108-5534
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Best Local Similarity
Matches 13; Conserv
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                                                             APPLICANT: SHANNON, MAIK
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
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TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
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Pred. No. 5.3e+
0; Mismatches
                                                                                                                 CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-27
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PELICATION NUMBER: PCT/USO1/00663
PRIOR PELICATION NUMBER: PCT/USO1/00663
PRIOR PELICATION NUMBER: PCT/USO1/00663
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR PELICATION NUMBER: PCT/USO1/00667
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR PELING DATE: 2001-01-30
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CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
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APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Aeomica Sequence
RANK, David R. CHEN, Wensheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 59.0
Best Local Similarity 86.7
Matches 13; Conservative
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APPLICANT:
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A PAPLICANY: CHENN WASTANDAMY

A PAPLICANY: SHANNON, MAZK

TITLE COF INVENTION: MOSSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REPERBACE: AEOMICA-7

CURRENT APPLICATION NUMBER: US/09/866,108

CURRENT FILING DATE: 2001-05-25

PRIOR FILING DATE: 2000-10-04

PRIOR FILING DATE: 2000-10-04

PRIOR FILING DATE: 2000-10-04

PRIOR FILING DATE: 2000-10-04

PRIOR FILING DATE: 2001-01-30

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Pred. No. 5.3e+03;
Mismatches 2; Indels
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO 5536
LENGTH: 25
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Best Local Similarity 86.7
Matches 13; Conservative
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; ORGANISM: Homo sapiens
US-09-866-108-5536
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APPLICANT: HANZEL, DAVIG K.
APPLICANT: RANK, DAVIG K.
APPLICANT: RANK, DAVIG R.
APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, WENSHENG
APPLICANT: SHANNON, MAIK
TITLE OF INYENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
TILE REFERENCE: ADONICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-32
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR PILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: PCI/USOL/UDGOS)
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCI/USOL/00663
PRIOR FILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: PCI/USOL/00661
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PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-09-21
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PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-02-05
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SEQ ID NO 5535
LENGTH: 25
            APPLICATION NUMBER: PCT/US01/00669
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00662
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| | σ. | 14. | 74.0 | 25 | 5 | US-60-233-166-23007 | Sequence 23007, A |
| | 10 | 14. | 74.0 | 25 | 55 | US-60-234-017-131414 | 13141 |
| | 11 | 14. | 71.0 | 25 | 55 | US-60-233-166-280120 | 28012 |
| | c 12 | 13. | 69.0 | 20 | 25 | US-09-657-481A-39 | 39, A |
| | | 13. | 0.69 | 25 | 55 | US-60-233-166-108604 | 10860 |
| ٠, | 14 | 13. | 69.0 | 25 | 55 | US-60-233-166-167371 | |
| | c 15 | 13. | 69.0 | 25 | 22 | US-60-234-017-425796 | 42579 |
| | | 13. | 0.69 | 25 | 55 | US-60-234-017-425802 | |
| | 17 | 13. | 0.69 | 33 | 14 | US-09-016-061-83 | |
| | 18 | 13. | 0.69 | 33 | 17 | US-09-339-922A-83 | |
| | 19 | 13. | 68.0 | 25 | 55 | US-60-232-638-106175 | |
| | 20 | 13. | 68.0 | 25 | 55 | US-60-233-166-168611 | |
| | | 13. | 68.0 | 25 | 55 | US-60-233-166-330256 | edneuce |
| | | 13. | 68.0 | 20 | 12 | US-08-899-858-2789 | |
| | c 23 | 13. | 68.0 | 20 | 34 | US-60-023-277-2789 | |
| | | 13. | 67.0 | 25 | 55 | US-60-233-620-25074 | |
| | 25 | 13. | 99 | 18 | 23 | US-60-216-745-6364 | 6364, |
| | c 26 | 13. | 0.99 | 20 | 18 | US-09-422-978-8164 | 8164, |
| | | 13. | 0.99 | 21 | 53 | US-60-216-745-5644 | Seguence |
| | 28 | 13. | 0.99 | 24 | ٦ | PCT-US00-24784-163 | |
| | 29 | 13. | 0.99 | 25 | 56 | US-09-660-220-87881 | 8788 |
| | 30 | 13. | 99 | 25 | 52 | US-60-232-638-66944 | |
| | c 31 | 13. | 0.0 | 25 | 5 | US-60-232-638-70508 | |
| | | 13. | 0.99 | 72 | ر د ا | T6658-859-757-09-S0 | |
| | | 13. | 0.99 | 25 | 52 | US-60-233-166-26780 | e 26780 |
| | 34 | 13. | 0.99 | 25 | 22 | US-60-233-166-205876 | equence 20587 |
| | 35 | 13. | 0.99 | 25 | 52 | US-60-233-166-236573 | |
| | 36 | 13. | 0.99 | 25 | 55 | US-60-233-166-333957 | 33395 |
| | 37 | 13. | 0.99 | 25 | 55 | US-60-233-166-420026 | |
| | | 13. | 0.99 | 25 | 52 | US-60-233-620-41759 | _` |
| | c 39 | 13. | 99.0 | 25 | 22 | US-60-234-017-43611 | 4361 |
| | | 13. | 0.99 | 25 | 55 | US-60-234-017-43612 | ٠. |
| | 41 | 13. | 99 | 25 | 22 | US-60-234-017-287051 | edneuce |
| | c 42 | 13. | 0.99 | 25 | വ | US-60-234-017-297294 | equence 2972 |
| | 43 | 13.2 | 0.99 | 25 | 22 | 0 - 234 - 017 | 3306 |
| | 44 | 13. | 0.99 | 25 | 22 | 60-234-017-5282 | Sequence 528222, |
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Sequence 129873,

US-60-234-049-129873

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                                                                                                                                     APPLICANT: Monia, Brett P.

APPLICANT: Gaarde, William A.

APPLICANT: Gaarde, William A.

APPLICANT: Garde, William A.

APPLICANT: Garde, William A.

TITLE OF INVENTION: Expression

FILE REFERENCE: ISPH-0476

CURRENT APPLICATION NUMBER: PCT/US00/18999

CURRENT FILING DATE: 2000-07-13

PRIOR PFLLING DATE: 1999-08-19

NUMBER OF SEQ ID NOS: 43

SOFTWARE: Patentin Ver. 2.0

LENGTH: 20
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APPLICANT: Gaarde, William A.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0389
CURRENT APPLICATION NUMBER: US/09/377,310A
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
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15;
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100.0%; Pred. No. 15;
Live 0; Mismatches
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ALIGNMENTS
                                                                                                                        Isis Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: antisense sequence PCT-US00-18999-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: antisense sequence US-09-377-310-7
                                                                                     Sequence 7, Application PC/TUS0018999 GENERAL INFORMATION:
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US-09-757-100B-7
: Sequence 7, Application US/09757100B
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Best Local Similarity 100.
Matches 20; Conservative
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Best Local Similarity 100.
Matches 20; Conservative
                                                                  PCT-US00-18999-7
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US-09-377-310-7
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LENGTH: 20
                                                                                                                        APPLICANT:
APPLICANT:
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TITLE OF INVENTION: RICIN-LIKE TOXIN VARIANTS FOR TREATMENT OF CANCER,
TITLE OF INVENTION: VIRAL OR PARASITIC INFECTIONS
APPLICANT: Monia, Brett P.
APPLICANT: Monia, Brett P.
APPLICANT: Monia, Brett P.
APPLICANT: Monia, Pamela S.
TITLE OF INVENTION: Expression
FILE REPERENCE: ISPH-0533
CURRENT APPLICATION NUMBER: US/09/757,100B
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: 09/377,310
PRIOR APPLICATION NUMBER: PCT/US00/18999
PRIOR FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/US00/18999
PRIOR SED ID NOS: 44
SOFTWARE: Patentin Ver. 2.0
SEC ID NO 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 486, Application US/09310298
; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: PRIMER SEQUENCES FOR SINGLE NUCLEOTIDE; TITLE OF INVENTION: POLYMORPHISMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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Pred. No. 2.7e+03;
0; Mismatches 1;
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Pred. No. 15;
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CURRENT APPLICATION NUMBER: US/09/310,298
CURRENT FILICATION NUMBER: 055-12
EARLIER PEPLICATION NUMBER: 60/085,152
SARLIER FILING DATE: 1998-05-12
NUMBER OF SEQ ID NOS: 5968
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 486
LENGTH: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Oligonucleotide primer US-09-310-298-486
                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: antisense sequence US-09-757-1008-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 115, Application US/09403752A; GENERAL INFORMATION:
APPLICANT: Borgford, Thor
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Best Local Similarity 100.0%;
Matches 20; Conservative 0
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94.18;
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Best Local Similarity
Matches 16; Conserv
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US-09-310-298-486/c
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US-09-403-752A-115
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Gaps

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Length 15;

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APPLICANT: Gaarde, William A.

APPLICANT: Garde, William A.

APPLICANT: Garde, William A.

TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase

TITLE OF INVENTION: Expression

TITLE OF INVENTION: Expression

TITLE OF INVENTION: Expression

CURRENT APPLICATION NUMBER: US/09/757,100B

CURRENT FILING DATE: 2001-03-15

PRIOR APPLICATION NUMBER: 09/377,310

PRIOR APPLICATION NUMBER: 09/377,310

PRIOR FILING DATE: 1999-08-19

PRIOR FILING DATE: 2000-07-13

NUMBER OF SEQ ID NOS: 44

SOFTWARE: PatentIn Ver: 2.0

SEQ ID NO 27
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TITLE OF INVENTION: Methods of Genetic Analysis of the Rat TITLE OF INVENTION: Genome
FILE REFERENCE: 3112
CURRENT APPLICATION NUMBER: US/60/233,166
CURRENT FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 420907
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 25
                                                                                                                                                                                             75.0%; Score 15; DB 17; I
100.0%; Pred. No. 3.5e+03;
Live 0; Mismatches 0;
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                                                                                                     ; OTHER INFORMATION: antisense sequence US-09-377-310-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: antisense sequence US-09-757-100B-27
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APPLICANT: Monia, Brett P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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Best Local Similarity 100.
Matches 15; Conservative
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                                          TYPE: DNA ORGANISM: Artificial
                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 15; Conserv
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  SEQ ID NO 27
LENGTH: 15
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; ORGANISM: Human Prostate-Specific Antigen linker region of pAP-290
US-09-403-752A-115
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TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
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GENERAL INFORMATION:
APPLICANT: Monia, Brett P.
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0389
CURRENT APPLICATION NUMBER: US/09/377,310A
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
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76.0%; Score 15.2; DB 18;
Best Local Similarity 85.0%; Pred. No. 3.3e+03;
Matches 17; Conservative 0; Mismatches 3;
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               CURRENT APPLICATION NUMBER: US/09/403,752A
CURRENT FILING DATE: 1999-10-29
FRIOR APPLICATION NUMBER: U.S. 60/045,148
FRIOR FILING DATE: 1997-04-30
FRIOR FILING DATE: 1997-04-30
FRIOR FILING DATE: 1997-10-29
NUMBER OF SEQ ID NOS: 142
SOFTWARE: Patentin Ver: 2.0
SOFTWARE: Patentin Ver: 2.0
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CURRENT APPLICATION NUMBER: PCT/US00/18999
CURRENT FILING DATE: 2000-07-13
PRIOR APPLICATION NUMBER: 09/377,310
PRIOR FILING DATE: 1999-08-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isis Pharmaceuticals, Inc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 27, Application PC/TUS0018999 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Monia, Brett P.
APPLICANT: Gaarde, William A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 27
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10447-005
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Best Local Similarity
Matches 15; Conserv
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Gaps

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Length 15;

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APPLICANT: Brett P. Monia
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF UBIQUITIN PROTEIN LIGASE WWP1 AND
TITLE OF INVENTION: EXPRESSION
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GENERAL INFORMATION:
APPLICANT: Mittmann
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Genome
TITLE OF INVENTION: Genome
FILE REPERBERS.
CURRENT APPLICATION NUMBER: US/60/233,166
CURRENT FILING DATE: 2000-10-24
NUMBER OF SED ID NOS: 420907
SOFTWARE: FastSEQ for Windows Version 4.0
SED ID NO 108604
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                     Length 20;
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GENERAL INFORMATION:
APPLICANT: Mittmann:
APPLICANT: Affametrix, Inc.
TITLE OF INVENTION: Genome
TITLE OF INVENTION: Genome
FILLE REFERENCE: 3112
CURRENT APPLICATION NUMBER: US/60/233,166
CURRENT FILING DATE: 2000-10-24
                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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Pred. No. 1.4e+04;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                   Score 13.8; DB 25;
Pred. No. 1.4e+04;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Antisense Oligonucleotide US-09-657-481A-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank AA860043
US-60-233-166-108604
                                                                                                                                                             FILE REFERENCE: RTS-0087
CURRENT APPLICATION NUMBER: US/09/657,481A
CURRENT FILING DATE: 2000-09-07
NUMBER OF SEQ ID NOS: 93
                                US-09-657-481A-39/c
; Sequence 39, Application US/09657481A
; GENERAL INFORMATION:
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88.2%;
                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
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88.2%;
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Best Local Similarity 88.2
Matches 15; Conservative
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Best Local Similarity
Matches 15; Conserv
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US-60-233-166-108604/c
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                                                                                                                                                                                                                                     SEQ ID NO 39
LENGTH: 20
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; GENERAL INFORMATION:
; APPLICANT: Mittmann
; APPLICANT: Mittmann
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; TITLE OF INVENTION: Genome
; TITLE OF INVENTION: Genome
; FILE REFERENCE: 3112
; CURRENT APPLICATION UNDBER: US/60/233,166
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 280120
; LENGTH: 25
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                                                     Length 25;
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US-60-234-017-131414
Sequence 131414, Application US/60234017
GENERAL INFORMATION:
APPLICANT: Mittmann, M
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis of Mus
FILE REPERENCE: 3115
CURRENT APPLICATION NUMBER: US/60/234,017
CURRENT FILING DATE: 2000-09-20
NUMBER OF SEQ ID NOS: 605887
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 131414
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                                                   Score 14.8; DB 55;
Pred. No. 4.8e+03;
); Mismatches 2;
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Pred. No. 4.8e+03;
0; Mismatches 2;
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84.2%; Pred. No. 9.2e+03;
ive 0; Mismatches 3;
                                                                                       0; Mismatches
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PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank AA600645
SC-0234-017-131414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
US-60-233-166-280120
                                                 74.0%;
88.9%;
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88.9%;
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                                                 Query Match
Best Local Similarity 88.9
Matches 16; Conservative
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Best Local Similarity 88.9
Matches 16; Conservative
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Best Local Similarity 84.2
Matches 16; Conservative
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US-60-233-166-280120
US-60-233-166-23007
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 425796, Application US/60234017
; Sequence 425796, Application US/60234017
; GENERAL INFORMATION:
; APPLICANT: Mittmann, M
; APPLICANT: Affymetrix, Inc.; TITLE OF INVENTION: Methods of Genetic Analysis of Mus; TITLE OF INVENTION: musculus
; TITLE OF INVENTION: Musculus
; FILE REFRENCE: 3115
; CURRENT APPLICATION UNDBER: US/60/234,017
; CURRENT APPLICATION UNDBER: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 425796
                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                Score 13.8; DB 55;
Pred. No. 1.4e+04;
0; Mismatches 2;
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 167371
; TEMETH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank AA926247
US-60-233-166-167371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
CRGANISM: Mus musculus
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank AV102460
US-60-234-017-425796
                                                                                                                                                                                                                                  Query Match 69.0%;
Best Local Similarity 88.2%;
Matches 15; Conservative
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Best Local Similarity 88.2°
Matches 15; Conservative
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Search completed: October 2, 2001, 21:50:10 Job time: 24523 sec

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22, Appl 247, App 13, Appl

1880, Ap

18674, 18740,

Sequence Sequence Sequence Sequence

App

10876,

Sequence Seq

Run on:

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; OTHER INFORMATION: Human Prostate-Specific Antigen linker region of pAP-290 US-09-551-151-115
                                                                                                                                                                                                                                                                                                                                    APPLICANT: Borgford, Thor
TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
TITLE OF INVENTION: Viral or Parasitic Infections
FILE REPERENCE: 10447-011
CURRENT APPLICATION NUMBER: US/09/551,151
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: US 09/403,752
PRIOR FILING DATE: 1999-10-29
NUMBER OF SEQ ID NOS: 142
SOFTWARE: Patentin Ver. 2.0
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVERTION: Composition
TITLE OF INVERTION: Composition
TITLE OF INVERTION: Composition
TITLE OF INVERTION: Composition
GURRENT APPLICATION NUMBER: US/09/726,774
CURRENT FILING DATE: 2000-11-29
FRIOR FULING DATE: 1999-11-29
NUMBER OF SEQ ID NOS: 139
SEQ ID NO 70
SEQ ID NO 70
LENGTH: 21
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US-09-343-1268-50
US-09-801-274-736
US-09-801-274-734
US-09-801-274-1470
US-09-56-7458-5238
US-09-56-63-10876
US-09-699-011A-293
US-09-851-271A-13
US-09-851-271A-13
US-09-708-690-1822
US-09-708-690-18422
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Pred. No. 4.9e+02;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
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85.0%;
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Best Local Similarity 85.0%
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US-09-551-151-115
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US-09-726-774-70
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LENGTH: 36
FEATURE:
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Sequence 18891, A
Sequence 18891, A
Sequence 1781, Ap
Sequence 616, App
Sequence 22, A
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32245, A
Appl
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35, Appl
36, Appl
74, Appl
75, Appl
9824, Ap
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7, Appli
                                                                             Search time 2173.58 Seconds (without alignments) 19.290 Million cell updates/sec
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Sequence 90, Appl
Sequence 1240, Ap
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Sequence 75,
Sequence 982
Sequence 140
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1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*

2: /cgn2_6/ptodata/2/pna/USO6_NEW_COMB.seq:*

3: /cgn2_6/ptodata/2/pna/USO8_NEW_COMB.seq:*

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5: /cgn2_6/ptodata/2/pna/USO9_NEW_COMB.seq:*

6: /cgn2_6/ptodata/2/pna/USO9_NEW_COMB.seq:*

7: /cgn2_6/ptodata/2/pna/USO9_NEW_COMB.seq:*

8: /cgn2_6/ptodata/2/pna/USO9_NEW_COMB.seq2:*

8: /cgn2_6/ptodata/2/pna/USO0_NEW_COMB.seq2:*
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         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-60-252-833-32245
US-60-278-561-657
US-09-516-667-73
US-09-516-667-73
US-09-516-667-74
US-09-516-667-74
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US-09-518-90
US-09-574-376B-124
US-09-574-376B-124
US-09-574-376B-124
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US-09-747-391-16
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Maximum Match 100%
Listing first 45 summaries
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Match Length
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Length 36; Indels

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Futreal, P. Andrew
TITLE OF INVENTION: 179-Linked Breast and Ovarian Cancer
Susceptibility Gene
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 02-May-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg, Ernst & Manbeck, P.C.
STREET: 555 Thirteenth Street, N.W., Suite 701-E
CITY: Washington
STATE: DC
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Indels
                                      Sequence 32225...
Sequence 3225...
GENERAL INFORMATION:
APPLICANT: Glenn, Matthew
APPLICANT: Glenn, Mutray R
TITLE OF INVENTION: Compositions isolated from bovine
TITLE OF INVENTION: tissues and methods for their use.
FILE REFERENCE: 1052P2
CURRENT APPLICATION NUMBER: US/60/252,833
CURRENT FILING DATE: 2000-11-21
NUMBER OF SEQ ID NOS: 43335
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 32245
                                                                                                                                                                                                                                                                                                                                                                                                                     Score 13.6; DB 8;
Pred. No. 2.8e+03;
); Mismatches 4;
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FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/409,305
FILING DATE: 24-MAR-1995
APPLICATION NUMBER: US 08/348,824
FILING DATE: 29-NOV-1994
APPLICATION NUMBER: US 08/308,104
FILING DATE: 16-SEP-1994
APPLICATION NUMBER: US 08/300,266
FILING DATE: 02-SEP-1994
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Shattuck-Eidens, Donna M.
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US-08-850-062A-75
Sequence 75, Application US/08850062A
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Skolnick, Mark H. Goldgar, David E. Miki, Yoshio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Swenson, Jeff
Kamb, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                     68.0%;
80.0%;
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Best Local Similarity 80.0
Matches 16; Conservative
                         JS-60-252-833-32245/c
                                                                                                                                                                                                                                                                                                                                   ORGANISM: Bovine US-60-252-833-32245
                                                                                                                                                                                                                                                                                                                    TYPE: DNA
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Sequence 83, Application US/09900590
GENERAL INFORMATION:
APPLICANT: Huse, William D.
Glaser, Scott M.
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
Anti-bodies, Nucleic Acids Encoding Same and Methods of Use
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                                                                                                                                             69.0%; Score 13.8; DB 6; Length 21; 88.2%; Pred. No. 2.1e+03; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/09/900,590
FILING DATE: 06-Jul-2001
CLASSIFICATION: CUNKNOWN>
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                                                                                                                                                                                        2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 13.8; DB 6;
Pred. No. 2.2e+03;
0; Mismatches 2;
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REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 2965
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-8949
INFORMATION FOR SEQ ID NO: 83:
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APPLICATION NUMBER: 09/016,061
FILING DATE: <Unknown>
                                                              ; OTHER INFORMATION: antisense oligomer US-09-726-774-70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: California
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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Matches 15; Conservative
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Best Local Similarity 88.2
Matches 15; Conservative
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GENERAL INFORMATION:
APPLICANT: Incuye, Masayori
APPLICANT: Vananaka, Kunitoshi
TITLE OF INVENTION: COLD-SHOCK REGULATORY ELEMENTS, CONSTRUCTS THEREOF, AND
TITLE OF INVENTION: METHODS OF USE
FILE REFERENCE: 1053-00
CURRENT APPLICANCE: 2001-08-01
CURRENT FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 87
SEQ ID NO 35
                                                            TITLE OF INVENTION: COLD-SHOCK REGULATORY ELEMENTS, CONSTRUCTS THEREOF, AND TITLE OF INVENTION: METHODS OF USE FILE REFERENCE: 1053-00 CURRENT APPLICATION NUMBER: US/09/516,667 CURRENT FILING DATE: 2001-08-01 NUMBER OF SEQ ID NOS: 87 SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 36, Application US/09516667
GENERAL INFORMATION:
APPLICANT: Inouye, Masayori
APPLICANT: Wang, Nan
APPLICANT: Yamanaka, Kunitoshi
TITLE OF INVENTION: METHODS OF USE
TITLE OF INVENTION: METHODS OF USE
FILE REFERENCE: 1053-00
CURRENT APPLICATION NUMBER: US/09/516,667
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Pred. No. 1.3e+04;
0; Mismatches 3; Indels
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82.4%; Pred. No. 1.3e+04;
.ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: Oligonucleotide US-09-516-667-35
                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence:
COTHER INFORMATION: Oligonucleotide
US-09-516-667-73
                         APPLICANT: Wang, Nan
APPLICANT: Yamanaka, Kunitoshi
                                                                                                                                                                                                                                                                           TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 82.4%;
Matches 14; Conservative
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Matches 14; Conservative
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LENGTH: 47
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Sequence 657, Application US/60278561
Sequence Databases, and Single Nucleotide Sequence Databases, and Single Nucleotide TITLE OF INVENTION: Polyuncleotide Sequence Databases, and Single Nucleotide TITLE OF INVENTION: Polyuncleotide Sequence Databases, and Single Nucleotide STILE REFERENCE: GX-0012-1 P
CURRENT APPLICATION NUMBER: US/60/278,561
CURRENT FILING DATE: 2001-03-23
NUMBER OF SEQ ID NOS: 15598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63.0%; Score 12.6; DB 4; 78.9%; Pred. No. 8.1e+03; Live 0; Mismatches 4;
                                                     ATLORARIA CABLAI ALL CARRALLOS.

REGISTRATION NUMBER: 28,957

REFERENCE/DOCKET NUMBER: 2318-137

TELECOMMUTICATION INFORMATION:

TELEPHONE: 202-783-6031

INFORMATION FOR SEQ ID NO: 75:

SEQUENCE CHARACTERISTICS:

LENGTH: 30 base pairs

TYPE: nucleic acid

STYPE: nucleic acid

STYPE: nucleic acid

STYPE: nucleic acid
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OTHER INFORMATION: Incyte ID No: SNP00057293
APPLICATION NUMBER: US 08/289,221
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 75:
US-08-850-062A-75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: 017559.1, 21, G->A US-60-278-561-657
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                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
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Best Local Similarity 78.9
Matches 15; Conservative
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Best Local Similarity 78.9
Matches 15; Conservative
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LOCATION: 21
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FEATURE:
Description of Artificial Sequence:
OTHER INFORMATION: Oligonucleotide
US-09-516-667-75
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86.7%;
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82.4%;
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Best Local Similarity 75.0
Matches 15; Conservative
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Best Local Similarity 82.4
Matches 14; Conservative
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Matches 13; Conservative
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US-60-253-652-14008
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US-09-516-667-74/C
Sequence 74, Application US/09516667
Sequence 74, Application US/09516667
GENERAL INFORMATION:
APPLICANT: Inouye, Masayori
APPLICANT: Wang, Nan
TITLE OF INVENTION: COLD-SHOCK REGULATORY ELEMENTS, CONSTRUCTS THEREOF, AND
TITLE OF INVENTION: METHODS OF USE
FILE REFERENCE: 1053-00
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GENERAL INFORMATION:
APPLICANT: Inouye, Masayori
APPLICANT: Wang, Nan
APPLICANT: Wang, Nan
APPLICANT: Yamanaka, Kunitoshi
TITLE OF INVENTION: COLD-SHOCK REGULATORY ELEMENTS, CONSTRUCTS THEREOF, AND
TITLE OF INVENTION: METHODS OF USE
FILE REFERENCE: 1053-00
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Pred. No. 1.3e+04;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                    3; Indels
                                                                                                                                    FEATURE:

CTHER INFORMATION: Description of Artificial Sequence:

CTHER INFORMATION: Oligonucleotide

US-09-516-667-36
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Pred. No. 1.3e+04;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/516,667
CURRENT FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 74
LENGTH: 48
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CURRENT FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 75
LENGTH: 48
NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 36
LENGTH: 48
                                                                                                                       ORGANISM: Artificial Sequence
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Best Local Similarity 82.4%;
Matches 14; Conservative (
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Best Local Similarity 82.4%;
Matches 14; Conservative
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24 ttcccctttcattatt 40
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                                                                                                        TYPE: DNA
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Pred. No. 1.9e+04;
0; Mismatches 2; Indels
     Length 48;
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                                                                                                                                                                                                                                                             Sequence 98.24, Application US/60252833
GENERAL INFORMATION:
APPLICANT: Glenn, Matthew
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions isolated from bovine
TITLE OF INVENTION: tissues and methods for their use.
FILE REFERENCE: 105.2P2
CURRENT APPLICATION NUMBER: US/60/252,833
CURRENT FILING DATE: 2000-11-21
NUMBER OF SEQ ID NOS: 43535
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 14008, Application US/60253652
GENERAL INFORMATION:
APPLICANT: Glen, Matthew
APPLICANT: Grigor, Murray R
TITLE OF INVENTION: Compositions isolated from bovine
TITLE OF INVENTION: Lissues and methods for their use.
FILE REFERENCE: 105592
Score 12.2; DB 6;
Pred. No. 1.3e+04;
0; Mismatches 3;
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CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 29954
SOFTWARE: PASTSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                    Score 11.6; DB 8; Length 29;
Pred. No. 2.4e+04;
0; Mismatches 4; Indels
US-60-253-456-15489
Sequence 15489, Application US/60253456
GENERAL INFORMATION:
TOTALE OF INVENTION: Polynucleotides, isolated from
TITLE OF INVENTION: Plants, and methods for their use.
FILE REFERENCE: 1054P1
CURRENT PELING DATE: 2000-11-27
NUMBER OF SEQ ID NOS: 37096
SEQ ID NO 15489
LENGTH: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
US-09-574-376B-90/C
; Sequence 90, Application US/09574376B
; GENERAL INFORMATION:
; APPLICANT: Warrington, Janet
; APPLICANT: Gingeras, Thomas Raymond
; APPLICANT: Gingeras, Thomas Raymond
APPLICANT: Affymetrix, Inc.
; TILLE OF INVENTION: Human Lymphoblast Polymorphisms
; FILE REFERENCE: 3229.2
; CURRENT APPLICATION NUMBER: US/09/574,376B
; CURRENT FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 1330
; SEQ ID NO 90
; SEQ ID NO 90
; LENGTH: 31
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                                                                                                                                                                                                                                                                                                                                                                                  Query Match 58.0%;
Best Local Similarity 77.8%;
Matches 14; Conservative
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Best Local Similarity 70.09
Matches 14; Conservative
                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Pinus radiata
US-60-253-456-15489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
CRGANISM: Homo sapiens
PUBLICATION INFORMATION:
US-09-574-376B-90
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Search completed: October 2, 2001, 16:55:00 Job time: 17663 sec

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(without alignments)
16.701 Million cell updates/sec
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/cgn2_6/ptodata/1/pna/US06_COMB.seq:*
/cgn2_6/ptodata/1/pna/US08_COMB.seq:*
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                     14155048 seqs, 7388405095 residues
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                                                                                                                                                  October 2, 2001, 21:50:08
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                                                                                                  OM nucleic - nucleic search, using sw model
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Perfect score:
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/cgn2_6/ptodata/1/pna/US6028_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Description | Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 247462, | Sequence 26, Sequence 26, Sequence 26, Sequence 26, Sequence 169 | Sequence 2372, Sequence 7628, Sequence 7568 Sequence 35341 Sequence 35341 Sequence 1603, Sequence 1603, | | Sequence 14, Sequence 14, Sequence 14, Sequence 14, Sequence 11, Sequence 15, Sequence 12, Sequence 12, Sequence 12, Sequence 12, Sequence 25, Seque | 2777 |
|---------------------|---|--|---|--|--|---|
| MARIES | -US00-18999-6 -09-377-310-6 -09-757-100B- | PCT-US00-18999-26 US-09-377-310-26 US-09-757-1008-26 US-60-233-166-169359 US-60-233-166-169359 | -09-660-220 -09-660-220 -60-233-166- -60-233-166- -60-233-166- -00-310-298- | US-60-233-166-250484 US-60-233-166-250515 US-60-233-620-33139 US-60-233-620-33145 US-60-233-620-33146 US-60-234-017-31881 US-60-234-017-31891 US-60-234-049-10183 | US-60-233-166-142291 US-60-233-166-341643 US-60-233-166-36183 US-60-234-017-150021 US-60-234-017-427143 US-60-234-017-427143 US-60-234-017-427143 US-60-234-017-427143 US-60-164-320-12274 US-60-164-320-12274 US-60-164-320-12274 US-60-183-18-15 US-90-201-2284-4597 US-60-233-166-75953 US-60-233-166-75953 US-60-233-166-75953 US-60-233-166-75953 US-60-233-166-75953 US-60-233-166-75953 | T-US96-13455-12 S-09-116-115-12 S-09-541-762-12 |
| Length DB | 7000 7000 7000 7000 | 44986 | 9 H 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 | | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 7 7 7 |
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| Score | 20 20 20 15.2 | ппппп | ਂਚਰਚਰਚਰਰ | | | 13.4 13.4 13.4 |
| Result No. | | | 0 0 0 0 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 | C 18 C 19 20 21 22 23 24 25 | 0 0 0 000000 0 0 0 0 0 0 0 0 0 0 0 0 0 | C 44 C 45 |

GENERAL INFORMATION:

APPLICANT: Monia, Brett P. APPLICANT: Gaarde, William A. APPLICANT: Gaarde, William A. APPLICANT: Nero, Pamela S. TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase; TITLE OF INVENTION: Expression FILE REFRENCE: ISPH-0533 CURRENT APPLICATION NUMBER: US/09/757,100B CURRENT FILING DATE: 2001-03-15 PRIOR FILING DATE: 2001-03-15 PRIOR FILING DATE: 2000-07-13 NUMBER OF SEQ ID NOS: 44 SOFTWARE: PATHUR PATHUR DATE: 2000-07-13 NUMBER OF SEQ ID NOS: 44 SOFTWARE: PATHUR DATE: 2000-07-13 ö Gaps APPLICANT: Monid, Brett P. APPLICANT: Gaarde, William A. APPLICANT: Garde, William A. APPLICANT: Nero, Pamela S. TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase APPLICANT: Monia, Brett P. APPLICANT: Monia, Brett P. APPLICANT: Gaarde, William A. ATITLE OF INVENTION: Antibense Modulation of Focal Adhesion Kinase TITLE OF INVENTION: Expression FILE REFERENCE: ISPH-0389 CURRENT PELLIG DATE: 1999-08-19 NUMBER OF SEQ ID NOS: 43 SEQ ID NO 6 LENGTH: 20 DB 17; Length 20; 13; Score 20; DB 1; Pred. No. 13; Mismatches ALIGNMENTS FILE REFERENCE: ISPH-0476 CURRENT APPLICATION NUMBER: PCT/USOO/18999 CURRENT FILING DATE: 2000-07-13 PRIOR APPLICATION NUMBER: 09/377,310 PRIOR FILING DATE: 1999-08-19 SOFTWARE: PATENTIN VOC: 2.0 100.0%; Score 20; 100.0%; Pred. No. Isis Pharmaceuticals, Inc. ; OTHER INFORMATION: antisense sequence PCT-US00-18999-6 ; OTHER INFORMATION: antisense sequence US-09-377-310-6 Sequence 6, Application PC/TUS0018999 GENERAL INFORMATION: Sequence 6, Application US/09377310A GENERAL INFORMATION: 100.0%; Sc 100.0%; Pr tive 0; 1 gaaactgcagaaggcactga 20 ORGANISM: Artificial Sequence 1 gaaactgcagaaggcactga 20 TYPE: DNA ORGANISM: Artificial Sequence Query Match Best Local Similarity 100. Matches 20; Conservative Query Match 100. Best Local Similarity 100. Matches 20; Conservative RESULT 1 PCT-US00-18999-6 RESULT 2 US-09-377-310-6 SOFTWARE: Pa SEQ ID NO 6 LENGTH: 20 APPLICANT: APPLICANT: ò ద

ORGANISM: Artificial Sequence

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APPLICANT: Monia, Brett P.
APPLICANT: Gaarde, William A.
APPLICANT: Nero, Pamela S.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
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                                                                                                                                                                                                                                                                        Sequence 247462, Application US/60233166
GENERAL INFORMATION:
APPLICANT: Mittmann
APPLICANT: Mittmann
TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
TITLE OF INVENTION: Genome
FILE REFERENCE: 3112
CURRENT APPLICATION NUMBER: US/60/233,166
CURRENT APPLICATION NUMBER: US/60/233,166
CURRENT FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 420907
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 247462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 25;
                                                                     Length 20;
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Pred. No. 3.1e+03;
0; Mismatches 3;
                                                                     DB 29;
                                                                                                          Mismatches
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; DATABASE ACCESSION NUMBER: GenBank AI043982
US-60-233-166-247462
                                                                     Score 20;
Pred. No.
; OTHER INFORMATION: antisense sequence US-09-757-1008-6
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100.0%;
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85.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best_Local Similarity 85.0
Matches 17; Conservative
                                                                                                          20; Conservative
                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                           RESULT 4
US-60-233-166-247462/c
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PCT-US00-18999-26
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Gaps

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Mismatches

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RESULT 3 US-09-757-100B-6

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NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver.
SEQ ID NO 26
LENGTH: 15
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US-60-233-166-169359/c
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GENERAL INFORMATION:
APPLICANT: Monia, Brett P.
APPLICANT: Gaarde, William A.
APPLICANT: Moro, Pamela S.
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0533
CURRENT APPLICATION NUMBER: US/09/757,100B
CURRENT FILING DATE: 2001-03-15
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 2000-07-13
PRIOR FILING DATE: 2000-07-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Monital Brett P.
APPLICANT: Gaarde, William A.
TILLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TILLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0389
CURRENT APPLICATION NUMBER: US/09/377,310A
CURRENT APPLICATION NUMBER: 43
SOFTWARE: Patentin Ver. 2.0
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3.5e+03;
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. 3.5e+03;
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100.0%; Pred. No. ...
0; Mismatches
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                FILE REFERENCE: ISPH-0476
CURRENT APPLICATION NUMBER: PCT/USOO/18999
CURRENT FILING DATE: 2000-07-13
PRIOR APPLICATION NUMBER: 09/377,310
PRIOR FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                    ; OTHER INFORMATION: antisense sequence PCT-USO0-18999-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.09-377-310-26
Sequence 26, Application US/09377310A
GENERAL INFORMATION:
 TITLE OF INVENTION: Expression
                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                              Query Match 75.0
Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
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APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
TITLE OF INVENTION: Genome
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; Sequence 169364, Application US/60233166
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; TITLE OF INVENTION: Genome
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100.0%; Pred. No. 3.9e+03;
Live 0; Mismatches 0;
                                                                                                                                                      Score 15; DB 29; Pred. No. 3.5e+03;
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100.0%; Pred. No. ...
0; Mismatches
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PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank AA955408
US-60-233-166-169359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 312
CURRENT APPLICATION NUMBER: US/60/233,166
CURRENT FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 420907
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 169359
LENGTH: 25
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CURRENT APPLICATION NUMBER: US/60/233,166
CURRENT FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 420907
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 169364
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 169359, Application US/60233166; GENERAL INFORMATION:
                                           FEATURE:
COTHER INFORMATION: antisense sequence
US-09-757-100B-26
TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                      Query Match 75.0
Best Local Similarity 100.
Matches 15; Conservative
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Matches 15; Conserv
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Query Match
Best Local Similarity
                                  US-60-233-166-75968/c
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LENGTH: 25
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GENERAL INFORMATION:
APPLICANT: Mittmann et al.
TITLE OF INVENTION: Methods of Genetic Analysis of Human FILE REFERENCE: 3102.1
CURRENT APPLICATION WUMBER: US/09/660,220
CURRENT FILING DATE: 2000-09-12
PRIOR APPLICATION WUMBER: 06.0164,973
PRIOR FILING DATE: 1999-11-11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7628
LENGTH: 25
   Length 25;
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TITLE OF INVENTION: Methods of Genetic Analysis of Rat
TITLE OF INVENTION: Toxicology
FILE REFRENCE: 3109.1
CURRENT APPLICATION NUMBER: US/09/660,080
CURRENT FILING DATE: 2000-09-12
PRIOR PELLING DATE: 1999-10.28
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Pred. No. 4.9e+03;
0; Mismatches 2;
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Pred. No. 4.9e+03;
0; Mismatches 2;
75.0%; Score 15; DB 55; I
100.0%; Pred. No. 3.9e+03;
iive 0; Mismatches 0;
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; DATABASE ACCESSION NUMBER: GenBank AA819500
US-09-660-080-2372
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2372
LENGTH: 25
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; Sequence 2372, Application US/09660080
; GENERAL INFORMATION:
; APPLICANT: Mittmann et al.
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Best Local Similarity 88.9
Matches 16; Conservative
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Best Local Similarity 88.9
Matches 16; Conservative
                  Best_Local Similarity 100.
Matches 15; Conservative
                                                                       1 gaaactgcagaaggc 15
                                                                                           21 GAAACTGCAGAAGGC 7
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   Query Match
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                                      APPLICANT: Mittenin
APPLICANT: Mittenin
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
TITLE OF INVENTION: Gene
FILE REFRENCE: 3112
CURRENT APPLICATION WIMBER: US/60/233,166
CURRENT FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 420907
SOFTWARE: FastsEQ for Windows Version 4.0
LENGTH: 25
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Sequence 247458, Application US/60233166
Sequence 247458, Application US/60233166
Sequence 247458, Application US/60233166
SEQUENCE INFORMATION:
TITLE OF INVERTION: Methods of Genetic Analysis of the Rat TITLE OF INVERTION: Genome
FILE REFERENCE: 3112
CURRENT APPLICATION NUMBER: US/60/233,166
CURRENT APPLICATION NOSE: 2000-10-24
NUMBER OF SEQ IN NOS: 420907
SOFTWARE: FastSEQ for Windows Version 4.0
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Sequence 353412, Application US/60233166
Sequence 353412, Application US/60233166
GENERAL INFORMATION:
APPLICANT: Mittmann
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
TITLE OF INVENTION: Genome
FILE REFERENCE: 3112
CURRENT APPLICATION NUMBER: US/60/233,166
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Pred. No. 7.7e+03;
); Mismatches 1;
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Pred. No. 4.9e+03;
0; Mismatches 2;
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; DATABASE ACCESSION NUMBER: GenBank AA819500
US-60-233-166-75968
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; DATABASE ACCESSION NUMBER: GenBank AI043982
US-60-233-166-247458
; Sequence 75968, Application US/60233166; GENERAL INFORMATION:
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93.8%;
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Best Local Similarity 93.8
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7140, Application US/6023357
GENERAL INFORMATION:
APPLICANT: Mittmann:
TITLE OF INVENTION: Methods of Genetic Analysis of Rat:
TITLE OF INVENTION: Neurobiology
FILE REFERENCE: 3114
CURRENT APPLICANTON WUMBER: US/60/233,357
CURRENT PILLING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 21305
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 25
CURRENT FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 420907
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 25
                                                                                         TYPE: DNA
ORGANISM: Rattus norvegicus
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: GenBank U59126
US-60-233-166-353412
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ORGANISM: Rattus norregicus
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: GenBank D49836
US-60-233-357-7140
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Best Local Similarity 84.29
Matches 16; Conservative
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223, App 3, Appli 2, Appli

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2027, Ap 6556, Ap 4964, Ap 45, Appl

Sequence 2 Sequence 4 Sequence 7 Sequence 3 Sequence 2 Sequence 2 Sequence 2 Sequence 4 Sequence 4 Sequence 3 Sequence 3

370, App 370, App

18382, A 2, Appli

Run on:

Title:

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TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE THE REFERENCE: AEDMICA-7 CURRENT APPLICATION NUMBER: US/09/866,108 CURRENT FILING DATE: 2001-05-25
              US-09-866-108-4949
US-09-928-614-2
US-09-928-614-2
US-09-928-614-2
US-09-806-769-33
US-09-801-274-223
US-09-86-172-2
US-09-866-108-4964-3
US-09-866-108-4964-3
US-09-866-108-4964-3
US-09-893-23-496-3
US-09-91-274-1777
US-09-724-55-11980
US-09-724-55-11980
US-09-724-55-11880
US-09-724-55-18382
US-09-708-690-14557
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PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR APPLICATION NUMBER: GB 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PELLING DATE: 2000-10-30
PRIOR PELLING DATE: 2001-01-30
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APPLICANT: JI, YONGGANG
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, MAIK
US-09-866-108-2022/c
                                                                                                                                     SEQ ID NO 2022
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19.290 Million cell updates/sec
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Sequence 4953,
Sequence 4954,
Sequence 4955,
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Sequence 4957,
Sequence 4959,
Sequence 4969,
Sequence 1595,
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1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*

2: /cgn2_6/ptodata/2/pna/USO6_NEW_COMB.seq:*

3: /cgn2_6/ptodata/2/pna/USO8_NEW_COMB.seq:*

4: /cgn2_6/ptodata/2/pna/USO8_NEW_COMB.seq:*

5: /cgn2_6/ptodata/2/pna/USO9_NEW_COMB.seq:*

6: /cgn2_6/ptodata/2/pna/USO9_NEW_COMB.seq:*

7: /cgn2_6/ptodata/2/pna/USO9_NEW_COMB.seq:*

8: /cgn2_6/ptodata/2/pna/USO9_NEW_COMB.seq2:*
                 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-866-108-4951

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US-09-866-108-4960

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US-09-866-108-4961

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US-09-724-648-6
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US-09-919-478-15
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                                                                                                                                                         October 2, 2001, 16:54:59
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Maximum Match 100%
Listing first 45 summaries
                                                                                                               - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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APPLICANT: RANK, David R.

APPLICANT: HANKEL, David R.

APPLICANT: SHANKON, MARK

TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

CURRENT APPLICANTON NUMBER: US/09/866,108

PRIOR APPLICANTION NUMBER: 08 24263.6

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-10-30

PRIOR FILING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR APPLICANTON NUMBER: PCT/US01/00669

PRIOR PLING DATE: 2001-01-30

PRIOR PLING PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

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PRIOR PLING DATE: 2001-01-30
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Pred. No. 1.1e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Acomica Sequence Listing Engine
                                                                                                                                                  RESULT 3
US-09-866-108-4951/c
; Sequence 4951, Application US/09866108
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4952, Application US/09866108; GENERAL INFORMATION:
APPLICANT: GU, Yizhong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72.0%;
93.8%;
                                                                                                                                                                                                                                                                           APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 93.8
Matches 15; Conservative
5 ctgcagaaggcactga 20
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                                   16 CTGCAGAAGGCACCGA 1
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US-09-866-108-4952/c
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US-09-866-108-4951
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APPLICANT: 01, Yalahong
APPLICANT: 01, Yalahong
APPLICANT: 01, Yalahong
APPLICANT: 01, Yonggang
APPLICANT: David K.
APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, MAIK
TITLE OF INVENTION WIMBER: US/09/866,108
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2000-05-25
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-06-26
PRIOR PLING DATE: 2000-06-26
PRIOR PLING DATE: 2000-06-26
PRIOR PLING DATE: 2001-01-30
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                                                                                                                                                                                  Length 17;
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Pred. No. 1e+03;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                              Indels
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Pred. No. 1e+03;
0; Mismatches 1;
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SOFTWARE: Acomica Sequence Listing Engine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2023, Application US/09866108 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72.0%;
93.8%;
                                                                                                                                                                               72.0%;
93.8%;
                                                                                                                                                                  Query Match 12.0
Best Local Similarity 93.8
Matches 15; Conservative
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Best Local Similarity 93.8
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-2022
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; ORGANISM: Homo sapiens
US-09-866-108-2023
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LENGTH: 17
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APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
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Pred. No. 1.1e+03;
0; Mismatches 1;
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OR APPLICATION NUMBER: US 60/236,359
OR FILING DATE: 2000-09-27
OR PILING DATE: 2001-01-30
OR FILING DATE: 2001-01-30
OR PRICATION NUMBER: PCT/US01/00667
OR PRILING DATE: 2001-01-30
                      PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-09-27
PRIOR PLILING DATE: 2000-09-27
PRIOR PLILING DATE: 2000-09-27
PRIOR PLILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR PELLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR PILING DATE: 2001-01-30
PRIOR PELLING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PELLING DATE: 2000-09-21
PRIOR PELLING DATE: 2000-09-21
PRIOR PELLING DATE: 2000-09-20
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CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO 4953
LENGTH: 25
                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/USO1/00664
FILING DATE: 2001-01.30
APPLICATION NUMBER: PCT/USO1/00669
FILING DATE: 2001-01.30
APPLICATION NUMBER: PCT/USO1/00669
APPLICATION NUMBER: PCT/USO1/00665
                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
                                                                                                                 FILING DATE: 2000-09-27
PPILING DATE: 2000-09-27
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00670
FILING DATE: 2001-01-30
FILING DATE: 2000-05-26
APPLICATION NUMBER: GB 24263.6
FILING DATE: 2000-10-04
APPLICATION NUMBER: US 60/236,359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4954, Application US/09866108 GENERAL INFORMATION:
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APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, Dayld K.
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US-09-866-108-4953
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Best Local Similarity
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TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
TITLE REFERENCE: ABOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
                                                                                                    APPLICANT: SHANNON, MATCHER GENE EXPRESSED IN HUMAN HEART AND MUSCLE FILE REFERENCE: AEOMICA-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Pred. No. 1.1e+03; 
0; Mismatches 1; Indels
                                                                                                                                                                                            CURRENT FELING DATE: 105/09/866,108

CURRENT FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: US/09/866,108

CURRENT FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-06-26

PRIOR FILING DATE: 2000-10-04

PRIOR FILING DATE: 2000-10-04

PRIOR FILING DATE: 2000-10-04

PRIOR PILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/0066

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR PILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR PILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR APPLICATION NUMBER: PCT/US01/00670

PRIOR APPLICATION NUMBER: PCT/US01/00670

PRIOR PLING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00670

PRIOR PLING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00670

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00670
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SEQ ID NO 4952
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR FALING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
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93.8%;
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APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 72.0
Best Local Similarity 93.8
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-4952
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Gaps

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APPLICANT: GU, Yizhong
APPLICANT: GI, Yizhong
APPLICANT: JI, Yongquag
APPLICANT: David K.
APPLICANT: RANZEL, David K.
APPLICANT: RANZEL, David R.
APPLICANT: RANZEL, David R.
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
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Pred. No. 1.1e+03;
); Mismatches 1;
               PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PAPLICATION NUMBER: PCT/USO1/00661
PRIOR PAPLICATION NUMBER: PCT/USO1/00670
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Acomica Sequence Listing Engine
SEQ ID NO 4955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-06-36

PRIOR PILING DATE: 2000-09-37

PRIOR PILING DATE: 2000-09-27

PRIOR PILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30
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R APPLICATION NUMBER: PCT/US01/00669

R FILING DATE: 2001-01-30

R APPLICATION NUMBER: PCT/US01/00665

R PILING DATE: 2001-01-30

R APPLICATION NUMBER: PCT/US01/00668

R APPLICATION NUMBER: PCT/US01/00668

PR APPLICATION NUMBER: PCT/US01/00668
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APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00661
FILING DATE: 2001-01-30
PCT/US01/00662
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APPLICATION NUMBER: US 60/234,687
FILING DATE: 2000-09-21
APPLICATION NUMBER: US 60/266,860
FILING DATE: 2001-02-05
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93.8%;
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Best Local Similarity 93.8
Matches 15; Conservative
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US-09-866-108-4955
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APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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         PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 1575-2
SOFTWARE: ABOMICA SEQUENCE LISTING ENGINE
SENGTHARE: 350
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CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-04
PRIOR PELICATION NUMBER: US 60/236,359
PRIOR PELICATION NUMBER: US 60/236,359
PRIOR PELICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR PELICATION NUMBER: PCT/US01/00667
PRIOR PELICATION NUMBER: PCT/US01/00667
PRIOR PELICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR PELICATION NUMBER: PCT/US01/00669
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FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
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93.8%;
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APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
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Best Local Similarity 93.8
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-4954
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Gaps

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Indels

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APPLICANT: CHEN, WENSINGON
APPLICANT: CHEN, WENSINGON
TITLE OF INVERTION: WOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REPEBRACE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,666
PRIOR PILING DATE: 2000-10-0-4
PRIOR PILING DATE: 2000-10-0-3
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DA
       Pred. No. 1.1e+03;
0; Mismatches 1;
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Pred. No. 1.1e+03;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                  Sequence 4958, Application US/09866108
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
   93.88;
       Best Local Similarity 93.8
Matches 15; Conservative
                                                                                                         Query Match 72.0
Best Local Similarity 93.8
Matches 15; Conservative
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; ORGANISM: Homo sapiens
US-09-866-108-4958
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US-09-866-108-4958/c
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US-09-866-108-4959/c
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APPLICANT: 01, YIZADON
APPLICANT: 01, YIZADON
APPLICANT: 01, YIZADON
APPLICANT: PENN, Sharron G.
APPLICANT: PENN, Sharron G.
APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, MAIX
TITLE OF INVENTION WOMER: US/09/866,108
CURRENT APPLICATION WOMER: US/09/866,108
CURRENT FILING DATE: 2000-05-25
FRIOR FLING DATE: 2000-05-26
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/0663
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PRING DATE: 2001-01-30
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Pred. No. 1.1e+03;
0; Mismatches 1;
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Acomica Sequence Listing Engine
SEQ ID NO 4956
LENGTH: 25
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LENGTH: 25
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93.8%;
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US-09-866-108-4956
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Best Local Similarity
Matches 15; Conserv
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US-09-866-108-4957/c
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DB 6; Length 25;

72.0%; Score 14.4;

Query Match

Length 25;

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                                                        APPLICANT: GU, Yizhong
APPLICANT: JI, Yongang
APPLICANT: PENN, Sharron G.
APPLICANT: RANK, David R.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, MAIK
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
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Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                        FILE KEFEKENCE: ALOMICA-/
CURRENT APPLICATION NUMBER: US/99/866,108
CURRENT PILING DATE: 2001-05-25
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-06-26
PRIOR FILING DATE: 2000-06-26
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-07
PRIOR FILING DATE: 2001-01-30
PRIOR PRILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : Aeomica Sequence Listing Engine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
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GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: PENN, Sharron G.
APPLICANT: PENN, Sharron G.
APPLICANT: RANK, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2000-09-21
PRIOR PAPLICATION NUMBER: US 60/266,860
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Acomica Sequence Listing Engised In Nos 1959
LENGTH: 25
Sequence 4959, Application US/09866108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72.0%;
93.8%;
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Matches 15; Conservative
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US-09-866-108-4959
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US-09-866-108-4960/c
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Gaps
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cargill, Michele
APPLICANT: Ireland, James S.
APPLICANT: Lander, Elic S.
TITLE OF INVEWION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
FILE REFERENCE: 2825,2009-001
CURRENT APPLICATION NUMBER: US/09/801,274
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 60/187,510
PRIOR FILING DATE: 2000-03-07
PRIOR FILING DATE: 2000-03-07
PRIOR FILING DATE: 2000-03-07
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Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
PRINKE TITLING DATE: 2010-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PELICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-09-27
PRIOR PELICATION NUMBER: PCT/USO1/00665
PRIOR FILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1595
LENGTH: 31
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Matches 15; Conservative
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US-09-801-274-1595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: HOMO US-09-866-108-4960
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US-09-801-274-1595
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Application US/09866108
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93.3%;
                                                                                        T: GU, Yizhong
T: JI, Yonggang
T: PENN, Sharron G.
T: HANZEL, David K.
T: RANK, David R.
T: CHEN, Wensheng
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Best Local Similarity 93.3
Matches 14; Conservative
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US-09-866-108-2024
                            Sequence 2024, Applica
GENERAL INFORMATION:
APPLICANT: GU, YIZHON
SAPPLICANT: JI, YONGG;
APPLICANT: JI, YONGG;
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APPLICANT:
APPLICANT:
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APPLICANT: TJ, YONGGANG
APPLICANT: TJ, YONGGANG
APPLICANT: TJ, YONGGANG
APPLICANT: TRANK, SHALTON G
APPLICANT: HANZEL, David R.
APPLICANT: RANK, David R.
APPLICANT: CHEM, WENDERCE: LOS 106-108
CURRENT: SHANNOM, MAIN
TITLE REPRENEUE: ADDOLLCA-7
CURRENT: FILING DATE: 2001-05-25
PRIOR FLILING DATE: 2000-05-36
PRIOR FLILING DATE: 2000-06-36
PRIOR FLILING DATE: 2000-09-37
PRIOR FLILING DATE: 2000-09-37
PRIOR FLILING DATE: 2000-09-37
PRIOR FLILING DATE: 2001-01-30
PRIOR PRILCATION NUMBER: PCT/US01/00665
PRIOR FLILING DATE: 2001-01-30
PRIOR PRIOR
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Query Match 69.0%; Score 13.8; DB 6; Length 31; Best Local Similarity 78.9%; Pred. No. 2.3e+03; Matches 15; Conservative 1; Mismatches 3; Indels
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LENGTH: 17
                                                                                                                                                                                                                                                                                                                              Sequence 2021, Application US/09866108 GENERAL INFORMATION:
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                                                                                                                       1 gaaactgcagaaggcactg 19
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; ORGANISM: Homo sapiens
US-09-866-108-2021
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Best Local Similaritÿ
Matches 14; Conserv
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TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE TELE REFERENCE: AEOMICA-7 CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
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Pred. No. 3.2e+03;
0; Mismatches 1;
                                                                                                           CURRENT FILING DATE: 2010-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR PLILOR DATE: 2000-10-04
PRIOR PLILOR DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR PLILOR DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR PLILOR DATE: 2001-01-30
PRIOR PPLICATION NUMBER: PCT/US01/00661
PRIOR PLILOR DATE: 2001-01-30
PRIOR PPLICATION NUMBER: PCT/US01/00670
PRIOR PPLICATION NUMBER: PCT/US01/00670
PRIOR PPLICATION NUMBER: PCT/US01/00670
PRIOR PPLICATION NUMBER: PCT/US01/00670
PRIOR PLILOR DATE: 2001-01-30
PRIOR PPLILOR DATE: 2001-01-30
PRIOR PPLILOR DATE: 2001-01-30
PRIOR PPLILOR DATE: 2001-01-30
PRIOR PPLICATION NUMBER: PCT/US01/00670
PRIOR PPLICATION NUMBER: PCT/US01/00670
PRIOR PPLICATION NUMBER: PCT/US01/00670
PRIOR PLILOR DATE: 2001-01-30
PRIOR PLILOR DATE: 2001-01-30
PRIOR PPLICATION NUMBER: PCT/US01/00670
PRIOR PPLICATION NUMBER: PCT/US01/00670
PRIOR PPLICATION NUMBER: US 60/256,860
PRIOR PRIOR POLICATION NUMBER: US 60/256,860
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3865, Ap 6, Appli 12058, A 14335, A 23884, A 81, Appl 10, Appl 19893, A

355, App 1025, App 33, Appl 1280, Ap 3050, Ap 3277, Ap 180, App

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Searched:

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Result No.

Sequence:

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APPLICANT: Garner, Harold R.
APPLICANT: Wreb. Johathan D.
APPLICANT: Minna, John D.
TITLE OF INVENTION: Polymorphic Repeats in Human Genes
FILE REFERENCE: UTSD0667
CURRENT FILING DATE: 1999-12-31
NUMBER OF SEQ ID NOS: 346
SEQ ID NO 204
LENGTH: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Grigor, Murray R
TITLE OF INVENTION: Compositions isolated from bovine
TITLE OF INVENTION: Compositions isolated from bovine
TITLE OF INVENTION: tissues and methods for their use.
FILE REPERENCE: 1052P2
CURRENT APPLICATION NUMBER: US/60/252,833
CURRENT FILING DATE: 2000-11-21
NUMBER OF SEQ ID NOS: 43535
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26301
                    Score 12.2; DB 8;
Pred. No. 9.1e+03;
0; Mismatches 3;
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1 ggcgccgtgcaccgagg 17
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  ; ORGANISM: Bovine
US-60-252-833-26301
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CRGANISM: human
US-09-475-947A-204
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US-09-475-947A-204
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Best Local Simi
Matches 14;
  TYPE: DNA
QQ
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1, Appli
1, Appli
23, Appl
6500, Ap
185, App
10876, A
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22, Appl
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Sequence 6
Sequence 2
Sequence 1
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1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*

2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*

3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*

4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*

5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*

6: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*

7: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq1:*

8: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq1:*
                       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-447-9478-204
US-09-441-949-1086
US-09-817-879-1279
US-09-817-879-1504
US-09-817-879-1505
US-09-817-879-3551
US-09-574-3768-157
US-09-574-3768-157
US-09-910-402-26
US-09-910-402-26
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US-09-910-629-185
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US-09-800-6294-185
US-09-800-6294-185
US-09-800-6294-185
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US-00-23-378-63-10876
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US-09-817-879-6300
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                                                                                                                     - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Perfect score:
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Best Local Similarity 75.0
Matches 15; Conservative
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Best Local Similarity 86.7
Matches 13; Conservative
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ORGANISM: Homo sapiens
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US-09-817-879-1279/c
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US-09-817-879-1504/c
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TITLE OF INVENTION: Nucleic Acids Containing Single Nucleotide
TITLE OF INVENTION: Polymorphisms and Methods of Use Thereof
FILE REFERENCE: 15966-534C
CURRENT APPLICATION NUMBER: US/09/442,849B
CURRENT FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: 60/109,024
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: 09/443,199
PRIOR APPLICATION NUMBER: 09/442, 129
PRIOR APPLICATION NUMBER: 09/412, 129
SPRIOR APPLICATION NUMBER: 09/412, 129
SPRIOR APPLICATION NUMBER: 09/412, 129
PRIOR APPLICATION NUMBER: 09/412, 129
PRIOR APPLICATION NUMBER: 09/412, 129
PRIOR OF SEQ ID NOS: 1592
SOFTWARE: Curaden Patent Formatter Version 0.9
SEQ ID NO 1086
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GENERAL INFORMATION:
APPLICANT: Shimkets, Richard A.
APPLICANT: Shimkets, Richard A.
TILLE OF INVENTION: Nucleic Acids Containing Single Nucleotide
TITLE OF INVENTION: Polymorphisms and Methods of Use Thereof
TITLE OF INVENTION: Polymorphisms and Methods of Use Thereof
FILE REFERENCE: 15966-334A
CURRENT PELLING DATE: 1999-11-16
PRIOR FILING DATE: 1999-11-17
NUMBER OF SEQ ID NOS: 1272
SOFTWARE: Curaden Patent Formatter Version 0.9
SEQ ID NO 1086
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LOCATION: (26)...(0)
OTHER INFORMATION: 2 of 2 allelic variants (1085 is other entry)
NAME/KEY: misc_feature
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OTHER INFORMATION: nucleotide deleted between bases 25 and 26
LOCATION: (0)...(0)
                     Length 35;
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                                                                      5; Indels
                  Score 12; DB 7; 1
Pred. No. 1.1e+04;
0; Mismatches 5;
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P. OTHER INFORMATION: Accession number cg44923068
US-09-442-849B-1086
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                  Query Match 60.0%; Scr
Best Local Similarity 75.0%; Pro
Matches 15; Conservative 0;
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Best Local Similarity 75.0
Matches 15; Conservative
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Sequence 1279, Application US/09817879
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals Inc.
APPLICANT: Ribozyme Pharmaceuticals Inc.
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Rel
TITLE OF INVENTION: Hepatitis C Virus Infection
FILE REFERENCE: MBHB00-801-F
CURRENT APPLICATION NUMBER: US/09/817,879
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9703
SOFTWARE: PatentIn version 3.0
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; Sequence 1504, Application US/09817879
; GENERAL INFORMATION:
    APPLICANT: Ribozyme Pharmaceuticals Inc.
    TITLE OF INVENTION: Bizymatic Nucleic Acid Treatment of Diseases or Conditions Rel
    TITLE OF INVENTION: Hepatitis C Virus Infection
    FILE REPERENCE: MRH800-801-F
    CURRENT APPLICATION NUMBER: US/09/817,879
    CURRENT FILING DATE: 2001-03-26
    NUMBER OF SEQ ID NOS: 9703
    SEQ ID NO 1504
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LOCATION: (26)...(0)
OTHER INFORMATION: 2 of 2 allelic variants (1085 is other entry)
NAME/KEY: misc_feature
LOCATION: (25)...(25)
OTHER INFORMATION: nucleotide deleted between bases 25 and 26
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Pred. No. 1.4e+04;
0; Mismatches 2;
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COTHER INFORMATION: Accession number cg44923068
US-09-443-199C-1086
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ORGANISM: artificial sequence
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ORGANISM: artificial sequence
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APPLICANT: Ribozyme Pharmaceuticals Inc.
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Rel
TITLE OF INVENTION: Hepatitis C Virus Infection
FILE REPERENCE: MBHB00-801-F
CURRENT APPLICATION NUMBER: US/09/817,879
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9703
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3276
LENGTH: 17
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APPLICANT: Shah, Nila
APPLICANT: Shah, Nila
APPLICANT: Gingeras, Thomas Raymond
APPLICANT: Affgmeras, Thomas Raymond
APPLICANT: Affgmerix, Inc.
TITLE OF INVENTION: Human Lymphoblast Polymorphisms
FILE REPERENCE: 3229.2
CURRENT APPLICATION NUMBER: US/09/574,376B
CURRENT FILLNG DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 1330
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 157
LENGTH: 31
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Pred. No. 1.4e+04;
1; Mismatches 2;
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Pred. No. 1.4e+04;
0; Mismatches 2;
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; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-3276
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; GENERAL INFORMATION:
; APPLICANT: Watson, James D
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86.7%;
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Best Local Similarity 80.0
Matches 12; Conservative
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; PUBLICATION INFORMATION:
US-09-574-376B-157
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Best Local Similarity
Matches 13; Conserv
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US-09-724-671-4282/c
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US-09-817-879-3276
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US-09-574-376B-157
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TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
TITLE OF INVENTION: Hepatitis C Virus Infection
FILE REFERENCE: MBHB00-801-F
CURRENT APPLICATION NUMBER: US/09/817,879
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEC ID NOS: 9703
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                               Sequence 1505, Application US/09817879
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT RIDOZYME Pharmaccuticals Inc.
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
TITLE OF INVENTION: Hepatitis C Virus Infection
FILE REFERENCE: MBHB00-801-F
CURRENT APPLICATION NUMBER: US/09/817,879
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9703
SOFTWARE: PATENTIN VERSION 3.0
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                                                                                             Score 11.8; DB 6;
Pred. No. 1.4e+04;
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86.7%; Pred. No. 1.4e+04;
tive 0; Mismatches 2;
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Pred. No. 1.4e+04;
0; Mismatches 2;
    ; LOCATION:
; JOTHER INFORMATION: oligonucleotide substrate
US-09-817-879-1504
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                                                                                             Query Match 59.0%;
Best Local Similarity 86.7%;
Matches 13; Conservative
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ilarity 86.7%;
Conservative
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Best Local Similarity 86.7
Matches 13; Conservative
                                                                                                                                                                              5 ccgtgaagcgaaggc 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 gcgccgtgaagcgaa 16
                                                                                                                                                                                                 17 CCGCGAAGCGAACGC 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                            US-09-817-879-1505/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 1505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 3051
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: RNA
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: RNA
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TTILE OF INVENTION: Transfection, Storage and Transfer of
TTILE OF INVENTION: Transfection, Storage and Transfer of
TTILE OF INVENTION: Transfection, Storage and Transgenic Stem
TTILE OF INVENTION: Cells
TTILE OF INVENTION: Cells
TTILE OF INVENTION: Cells
FILE REPERENCE: 18810-81602
CURRENT APPLICATION NUMBER: US/09/919,042
CURRENT FILING DATE: 2001-7-30
PRIOR FILING DATE: 1999-04-15
PRIOR FILING DATE: 1999-04-15
PRIOR FILING DATE: 1998-11-13
PRIOR FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: US 60/065,825
PRIOR APPLICATION NUMBER: PCT/US98/24238
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF IMMUNE
TITLE OF INVENTION: CAPACID DISEASES
FILE REFERENCE: P2833R1C1
CURRENT APPLICATION NUMBER: US/09/929,404
CURRENT PILING DATE: 2001-08-13
NUMBER OF SEQ ID NOS: 310
SEQ ID NO 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Single-stranded oligonucleotide US-09-919-042-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 11.6; DB 7;
Pred. No. 1.7e+04;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : Sequence 282, Application US/09929404
; GENERAL INFORMATION:
        Koeffler, H. Phillip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58.0%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stewart, Timothy A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumas, Daniel
Watanabe, Colin K.
Wood, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Henzel, William
Kabokoff, Rhona C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ggcgccgtgaagcgaagg 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gurney, Austin L.
Hebert, Caroline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 58.0
Best Local Similarity 77.8
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Smith, Victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pennica, Diane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lu,Yanmei
Pan,James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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APPLICANT: Murison, James G
TITLE OF INVENTION: Polynucleotides, polypeptides expressed
TITLE OF INVENTION: Polynucleotides and methods for their use.
TITLE REPERENCE: 105002
CURRENT APPLICATION NUMBER: US/09/724,671
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US. No. 60/171,678
PRIOR FILING DATE: 1999-12-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 26, Application US/09918889
GENERAL INFORMATION:
APPLICANT: Readhead, Carol W.
APPLICANT: Winston, Robert
APPLICANT: Winston, Robert
APPLICANT: Winston, Robert
APPLICANT: Winston, Robert
APPLICANT: Willer, Carsten
TITLE OF INVENTION: WCLEIC ACID CONSTRUCTS CONTAINING A
TITLE OF INVENTION: CYCLIN A1 PROMOTER, AND KIT
FILE REFERENCE: 18810-81603
CURRENT APPLICATION NUMBER: US/09/918,889
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US 09/292,723
PRIOR APPLICATION NUMBER: US 09/191,920
PRIOR FILING DATE: 1999-04-15
PRIOR FILING DATE: 1999-11-13
PRIOR FILING DATE: 1999-11-14
PRIOR FILING DATE: 1999-11-13
PRIOR FILING DATE: 1999-11-13
SUSPEMBER OF SEQ ID NOS: 32
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FESTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 11.8; DB 7; Length 3 Pred. No. 1.4e+04; Dred. Mismatches 2; Indels
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                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 21907
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4282
LENGTH: 31
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GENERAL INFORMATION:
APPLICANT: Readhead, Carol W.
APPLICANT: Winston, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
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86.7%;
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Best Local Similarity 86.7
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Mouse
US-09-724-671-4282
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US-09-919-042-26/c
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GENERAL INFORMATION:
APPLICANT: Setera Sciences, Inc.
TILE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING
TITLE OF INVENTION: TELOMERASE REVERSE TRANSCRIPTASE (TERT) EXPRESSION
FILE REFERENCE: SIER 00500
CURRENT APPLICATION NUMBER: PC/TUS01/25861
CURRENT PILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 60/237,865
PRIOR PILING DATE: 2000-08-24
PRIOR FILING DATE: 2000-09-01
PRIOR PILING DATE: 2000-09-01
PRIOR PILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 25
NUMBER OF SEQ ID NOS: 25
TYPE: DNA
TYPE: DNA
CRGANISM: human
PCT-US01-25861-1
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                       Gaps
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                       0;
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Pred. No. 1.8e+04;
0; Mismatches 4; Indels
Best Local Similarity 77.8%; Pred. No. 1.8e+04; Matches 14; Conservative 0; Mismatches 4; Indels
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| | | | | | | | | | | | | | | |
6 gtcgctgtgaagccaacg 23
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Best Local Similarity 77.87
Matches 14; Conservative
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PCT-US01-25861-1/c
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Search completed: October 2, 2001, 16:54:59 Job time: 17662 sec

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(without alignments)
16.701 Million cell updates/sec
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| Cgn2_6/ptodata/1/pna/USO6_COMB.seq:*
| Cgn2_6/ptodata/1/pna/USO6_COMB.seq:*
| Cgn2_6/ptodata/1/pna/USO8_COMB.seq:*
| Cgn2_6/ptodata/1/pna/USO8_CO
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//cgn2_6/ptodata/1/pna/US6009_COMB.seq:
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/cgn2_6/ptodata/1/pna/US6011_COMB.seq:
                      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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/ptodata/1/pna/US6016_COMB.seq:
/cgn2_6/ptodata/1/pna/US6012_COMB.seq
/cgn2_6/ptodata/1/pna/US6013_COMB.seq
/cgn2_6/ptodata/1/pna/US6014_COMB.seq
/cgn2_6/ptodata/1/pna/US6015_COMB.seq
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| Description | 4 | ₹. | Sequence 4, | Sequence 24, Appl | 24 | 13 | 14, | e 949 | e 3520 | 11, App | 40172, | 4. | 45792 | П, | 10497 | e 10498 | edneuce 10201 | 5687 | 56872 | 56873 | 2687 | 19599, | 12063 | 2002 | c | 2588, A | 2593, A | e 78332, | e 83352, | 4741, | 4 | 4/44, | 4746, | 4754, | 4788, | 4789, | 4790, | 4791, | 4792, | 4793, | 479 | 5481, | 29410, | Sequence 73099, A |
|------------------------|--------------|--------------|--------------|---------------------------------------|-------------|---------------|----------------|-----------|----------------|-----------------|-------------------|----------------|--------------------|--------------|--------------|--------------|---------------|----------|-------------|------------|-------------|------------------|-------------------|-------------------|-----------------|-----------------|------------------|-----------------|----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------|------------------|-----------------|-----------------|-------------------|-----------------|-------------------|
| ΩI | -0800-18999- | -09-377-310- | -09-757-100B | FCT-USUU-18999-24 HS-09-377-310-24 | 9-757-100B- | 08-448-223-13 | -08-448-223-14 | -234-017- | S-60-234-017-3 | S-09-812-913-11 | S-09-404-520-4017 | S-09-404-520-4 | S-60-232-638-45792 | S-60-233-166 | S-60-233-Tec | S-60-233-166 | -00-233-100 | -234-017 | -60-234-017 | -60-234-01 | -60-234-017 | -09-660-080-1959 | -09-660-220-12063 | S-60-233-166-2005 | -60-233-166-309 | -60-233-620-258 | -60-233-620-2593 | -60-233-620-783 | 0-233-620-8335 | -60-234-049-474 | -60-234-049-474 | -60-234-049-4/4 | -60-234-049-474 | -60-234-049-475 | -60-234-049-478 | -60-234-049-478 | -60-234-049-479 | 4-049-479 | S-60-234-049-479 | -60-234-049-479 | S-60-234-049-47 | 5-60-234-049-5481 | -60-234-049-294 | |
| Length DB | 20 1 | 0 | ا د | 15 1 | | . 60 | 2 | 5 | 5 | 9 | 7 | | ر د | in i | ות | ເບເ | U. | ហ | 5 | 25 55 | 5 | 5 | 5 | 5 | 5 | 5 | r L | 5 | S I | ر. د د | ກ | ດ : | 2 . | 5 | 5 | 5 | 5 | 5 | 5 5 | 5 | S. | in i | 5 | 5 |
| % Query Match Le | 0.0 | \circ | 100.0 | 75.0 | | 4 | 4 | ä | ъ. | دی | ω, | σοι | ٠ | ۰۰ | ٠, | 66.0 | ٠. | 65.0 | Š. | 65.0 | ς. | 4 | 4 | ₹. | 4 | 4 | 4 | 4 | 64.0 | 4. | • | Ţ. | - | ₹. | 64.0 | ▼ | 64.0 | 64.0 | ₹. | ₹. | • | 4 | 64.0 | 64.0 |
| Score | 20 | 20 | 20 | 15 | 15 | 4. | 4 | 4 | <u>ښ</u> | ω. | m | ش ر | | | ή, | | ή. | 13 | | 13 | ٦, | 7 | ~. ~! | α. | ς. (3 | | ~ | ς. | ٠. | | • | | • | | ~ | ~ | ~ | ~ | ς. | ~ | ~ | ~. N | 12.8 | 12.8 |
| Result No. | - | CV (| v) = | 4 K | o vo | 7 | 80 | | c 10 | - | 12 | 13 | 14 | c 15 | ٦, | Η, | ٦. | 19 | 20 | 21 | 22 | 23 | ~ | ~ | c 26 | 7 | ~ | 29 | 30 0 | (| יו ריי | ν, (| י ניי | m | 36 | 37 | 38 | 39 | 40 | 41 | 42 | | 44 | c 45 |

GENERAL INFORMATION: δλ Dβ ŏ ρp .; 0 ö SUBLICAL INFORMATION: APPLICANT: Monia, Brett P. APPLICANT: Monia, Brett P. APPLICANT: Monia, Brett P. APPLICANT: Garade, William A. APPLICANT: Garade, William A. APPLICANT: OBERCH. APPLICANT: OBERCH. APPLICANT: Nero, Panela S. TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase; TITLE OF INVENTION: Expression FILE REFERENCE: ISPH-0476 CURRENT APPLICATION NUMBER: PCT/US00/18999 CURRENT APPLICATION NUMBER: PCT/US00/18999 PRIOR FILING DATE: 1999-08-19 NUMBER OF SEQ ID NOS: 43 SOFWWARE: PatentIn Ver. 2.0 SEQ ID NO 4 LENGTH: 20 Gaps Gaps APPLICANT: Monia, Brett P. APPLICANT: Gaarde, William A. TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase TITLE OF INVENTION: Expression FILE REFERENCE: ISPH-0389 CURRENT APPLICATION NUMBER: US/09/377,310A CURRENT FILING DATE: 1999-08-19 NUMBER OF SEQ ID NOS: 43 SOFTWARE: Patentin Ver. 2.0 SED ID NO 4 LENGTH: 20 ; 0 ò Query Match 100.0%; Score 20; DB 17; Length 20; Best Local Similarity 100.0%; Pred. No. 14; Matches 20; Conservative 0; Mismatches 0; Indels Length 20; Indels .; 0); DB 1;). 14; Mismatches ALIGNMENTS 100.0%; Score 20; 100.0%; Pred. No. CT-US00-18999-4 ; OTHER INFORMATION: antisense sequence US-09-377-310-4 Sequence 4, Application PC/TUS0018999 GENERAL INFORMATION: Sequence 4, Application US/09377310A GENERAL INFORMATION: Sequence 4, Application US/09757100B ö 1 ggcgccgtgaagcgaaggca 20 1 ggcgccgtgaagcgaaggca 20 1 ggcgccgtgaagcgaaggca 20 TYPE: DNA ORGANISM: Artificial Sequence 1 ggcgccgtgaagcgaaggca 20 TYPE: DNA ORGANISM: Artificial Sequence Query Match 100. Best Local Similarity 100. Matches 20; Conservative RESULT 3 US-09-757-100B-4 RESULT 2 US-09-377-310-4 ò 셤 ô g

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APPLICANT: Monia, Brett P.
APPLICANT: Gaarde, William A.
APPLICANT: Garde, William A.
APPLICANT: Nero, Pamela S.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
FILE REFREENCE: ISPH-0533
CURRENT APPLICATION NUMBER: US/09/757,100B
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: 09/377,310
PRIOR APPLICATION NUMBER: PCT/US00/18999
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 2000-07-13
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 4
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Monia, Brett P.
APPLICANT: Gaarde, William A.
APPLICANT: Garde, William A.
APPLICANT: Nero, Pamela S.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase TITLE OF INVENTION: Expression
FILLE REFERENCE: ISPH-0476
CURRENT APPLICATION NUMBER: PCT/USO0/18999
CURRENT FILLING DATE: 2000-07-13
PRIOR PPPLICATION NUMBER: 09/377,310
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Pred. No. 3.8e+03;
0; Mismatches .0;
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Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                           ; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-757-100B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isis Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: antisense sequence PCT-USO0-18999-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 24, Application PC/TUS0018999
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 24, Application US/09377310A; GENERAL INFORMATION:
APPLICANT: Monia, Brett P.
                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Scu-
100.0%; Pre
0;
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100.0%;
                                                                                                                                                                                                                                                                                                 LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ggcgccgtgaagcgaaggca 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 20; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
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PCT-US00-18999-24
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US-09-377-310-24
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SEQ ID NO 24
LENGTH: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Abramson, Richard D.
APPLICANT: Gelfand, David H.
APPLICANT: Kalman, Lisa V.
APPLICANT: Reichert, Fred L.
TITLE OF INVENTION: Thermostable DNA Polymerases With
TITLE OF INVENTION: Altered Discrimination Properties
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,223
                                                                                                                                                                            E: Floppy disk
IBM PC compatible
SYSTEM: PC DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 14.8; DB 8;
Pred. No. 4.9e+03;
0; Mismatches 2;
                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448, 223
                                 Hoffmann-La Roche Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Hoffmann-La Roche Inc. 340 Kingsland Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 14, Application US/08448223
GENERAL INFORMATION:
APPLICANT: Abramson, Richard D.
                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: 518s, Stacey R.
REGISTRATION NUMBER: 32,630
REFERENCE/POCKET NUMBER: 9134
TELEPHONE: (510) 814-2863
TELEPHONE: (510) 814-2977
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 9134
                      ATTORNEY/AGENT INFORMATION:
NAME: Sias, Stacey R.
REGISTRATION NUMBER: 32,630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74.0%;
88.9%;
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Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 45 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
           CORRESPONDENCE ADDRESS:
                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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STATE: New Jersey
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                                                                  Nutley: New Jersey
RY: U.S.A.
                                                                                                                                                                                                  COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
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COUNTRY: U.E.
07110
                                                                                                            COUNTRY: U.
                                                                                                                                                                                                                                                                                                            FILING DATE:
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US-08-448-223-14
                                                                                          STATE:
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Gaarde, William A.

APPLICANT: Garde, William A.

APPLICANT: Nero, Pamela S.

TITLE OF INVENTION: Expression

FILE REFERENCE: ESPH-0533

CURRENT APPLICATION NUMBER: US/09/757,100B

CURRENT FILING DATE: 12001-03-15

PRIOR APPLICATION NUMBER: PCT/USO0/18999

PRIOR FILING DATE: 1999-08-19

PRIOR FILING DATE: 1999-08-19

PRIOR FILING DATE: 2000-07-13

NUMBER OF SEQ ID NOS: 44

SOFTWARE: PatentIn Ver. 2.0
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
FITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0389
CURRENT APPLICATION NUMBER: US/09/377,310A
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 24
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APPLICANT: Gelfand, David H.
APPLICANT: Kelman, Lisa V.
APPLICANT: Reichert, Fred L.
TITLE OF INVENTION: Thermostable DNA POlymerases With
TITLE OF INVENTION: Altered Discrimination Properties
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 75.0%; Score 15; DB 29; I Best Local Similarity 100.0%; Pred. No. 3.8e+03; Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                 Query Match 75.0%; Score 15; DB Best Local Similarity 100.0%; Pred. No. 3.6 Matches 15; Conservative 0; Mismatches
                                                                                                                                                                                                                                                               ; OTHER INFORMATION: antisense sequence US-09-377-310-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) OTHER INFORMATION: antisense sequence US-09-757-100B-24
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GENERAL INFORMATION:
APPLICANT: Abramson, Richard D.
                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 cgccgtgaagcgaag 17
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LENGTH: 15
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                                                                                                                                                                                                                                                            Length 45;
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US-60-234-017-94926/c
; Sequence 94926, Application US/60234017
; GENERAL INFORMATION:
   APPLICANT: Mittmann, M
   APPLICANT: Mittmann, M
   TITLE OF INVENTION: Methods of Genetic Analysis of Mus
   TITLE OF INVENTION: Musculus
   FILE REFERENCE: 3115
   CURRENT FILING DATE: 2000-09-20
   NUMBER OF SEQ ID NOS: 605887
   SOFTWARE: FastSEQ for Windows Version 4.0
   SEQ ID NO 94926
   LENGTH: 25
   TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 352075, Application US/60234017

Sequence 352075, Application US/60234017

Septicant: Mittmann, M

APPLICANT: Mittmann, M

APPLICANT: Affymetrix, Inc.

TITLE OF INVENTION: Methods of Genetic Analysis of Mus

FILE REFERENCE: 3115

CURRENT APPLICATION NUMBER: US/60/234,017

CURRENT FILING DATE: 2000-09-20

NUMBER OF SEQ ID NOS: 605887

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 352075

LENGTH: 25
                                                                                                                                                                                                                                                                                                 2; Indels
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                                                                                                                                                                                                                                                        Score 14.8; DB 8;
Pred. No. 4.9e+03;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank AJ243852
US-60-234-017-94926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank AI506367
US-60-234-017-352075
                TELEPHONE: (510) 814-2863
TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TELECOMMUNICATION INFORMATION:
                                                                                                                                                       ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-448-223-14
                                                                                                                                                                                                                                                          74.0%;
88.9%;
                                                                                                                                                                                                                                                                                                                                 Query Match 74.0
Best Local Similarity 88.9
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Mus musculus
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US-60-234-017-352075/c
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Sequence 11, Application US/09812913
Sequence 11, Application US/09812913
GENERAL INFORMATION:
APPLICAMT: Weeks, Donald
APPLICAMT: Cerutii, Heriberto
TITLE OF INVENTION: Accetolactate synthase gene and construct for the transformatio
TITLE OF INVENTION: Accetolactate synthase gene and construct for the transformatio
TITLE OF INVENTION: Accetolactate synthase gene and construct for the transformatio
TITLE OF INVENTION: Accetolactate synthase gene and construct for the transformatio
TITLE OF INVENTION: Accetolactate synthase gene and construct for the transformatio
CURRENT APPLICATION WUMBER: US/09/812,913
CURRENT APPLICATION WUMBER: 60/190,668
PRIOR APPLICATION WUMBER: 60/190,668
PRIOR APPLICATION WUMBER: 60/190,668
PRIOR APPLICATION UNDER: 2000-03-20
NUMBER OF SEQ ID NOS: 26
SSOFTWARE: PatentIn Version 3.0
SEG ID NO 11
LENGTH: APPLICATION WINDER: APPLICA
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APPLICANT: Ghodssi, Azita
APPLICANT: Ghodssi, Azita
APPLICANT: Hinke, Gregory J.
APPLICANT: Hinke, Gregory J.
APPLICANT: Timberlake, William E.
APPLICANT: Timberlake, William E.
APPLICANT: Yu. Jaehyuk
TITLE OF INVENTION: Emericella nidulans Genome Sequence and Uses Thereof
FILE REFERENCE: 38-10(15498)A
CURRENT APPLICATION NUMBER: US/09/404,520
CURRENT FILING DATE: 1999-09-23
NUMBER OF SEQ ID NOS: 44345
SEQ ID NO 40172
LENGTH: 41
                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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           Length 25;
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Pred. No. 1.9e+04;
0; Mismatches 4;
       Score 13.6; DB 55;
Pred. No. 1.9e+04;
); Mismatches 4;
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Pred. No. 1.9e+04;
0; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Chlamydomonas reinhardtil
US-09-812-913-11
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CRGANISM: Aspergillus nidulans
US-09-404-520-40172
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80.0%;
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80.0%;
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Query Match
Best Local Similarity 80.0
Matches 16; Conservative
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Best Local Similarity 80.0
Matches 16; Conservative
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Best Local Similarity
Matches 16; Conserv
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                                                                            APPLICANT: Gao, Yongwei
APPLICANT: Ghodssi, Azita
APPLICANT: Ghodssi, Azita
APPLICANT: Hinler, Gregory J.
APPLICANT: Hinler, Gregory J.
APPLICANT: Timberlake, William E.
APPLICANT: Tu, James
APPLICANT: Tu, James
APPLICANT: Tu, Jaehyuk
TITLE OF INVENTION: Emericella nidulans Genome Sequence and Uses Thereof
FILE REFERENCE: 38-10(15498)A
FILE REFERENCE: 1999-09-23
NUMBER OF SEQ ID NOS: 44345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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US-60-232-638 45792
US-60-232-638 45792
Sequence 45792, Application US/60232638
SEMERAL INFORMATION:
APPLICANT: Mittmann
APPLICANT: Mittmann
APPLICANT: Mittmann
TITLE OF INVENTION: Methods of Genetic Analysis of Yeast
FILE REFERENCE: 3110
CURRENT APPLICATION NUMBER: US/60/232,638
CURRENT FILING DATE: 2000-09-14
NUMBER OF SEQ ID NOS: 138410
SEQ ID NO 45792
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Mittmann
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
FITLE OF INVENTION: Genome
FILE REFERENCE: 3112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 68.0%; Score 13.6; DB 18; Best Local Similarity 80.0%; Pred. No. 1.9e+04; Matches 16; Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 13.2; DB 55;
Pred. No. 2.9e+04;
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CURRENT APPLICATION NUMBER: US/60/233,166
CURRENT FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 420907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: SGD YDL200C
US-60-232-638-45792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
US-60-233-166-104969/c
; Sequence 104969, Application US/60233166
; GENERAL INPORMATION:
                                        Sequence 40466, Application US/09404520 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Saccaromyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Aspergillus nidulans US-09-404-520-40466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ggcgccgtgaagcgaaggca 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 66.0%;
Best Local Similarity 83.3%;
Matches 15; Conservative
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RESULT 13
US-09-404-520-40466
                                                                                                                                                                                                                                                                                                                          SEQ ID NO 40466
LENGTH: 41
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Run on:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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7 US-09-377-310-3

9 US-09-377-310-3

PCT-US00-18999-3

7 US-09-377-310-23

9 US-09-560-220-37376

9 US-09-660-220-37376

10 US-09-660-220-37376

10 US-00-33-166-18790

10 US-00-233-166-18790

10 US-00-233-166-18790

10 US-00-233-166-279728

10 US-00-233-166-279728

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10 US-00-233-160-239-186-279728

10 US-00-233-017-28844
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US-09-724-866-18952
US-09-724-866-18962
US-09-321-94A-6
US-09-326-203A-31
US-60-232-638-136549
US-60-232-638-136549
US-60-234-017-217855
US-60-234-166-410983
US-60-234-17-242830
US-09-006-298-11
US-09-006-298-11
US-09-606-298-173
US-09-549-848B-57
US-09-549-848B-57
US-09-549-848B-57
US-09-60-233-166-30520
US-60-233-166-30520
US-60-233-166-30520
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US-60-234-017-480869
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                                                                      (without alignments)
16.701 Million cell updates/sec
                                                              Search time 17695.9 Seconds
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/cgn2_6/ptodata/1/pna/US6006_COMB.seq
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/cgn2_6/ptodata/1/pna/US6010_COWB.seq
/cgn2_6/ptodata/1/pna/US6010_COWB.seq
           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                             14155048 segs, 7388405095 residues
                                                                                                                                                                              of hits satisfying chosen parameters:
                                                              October 2, 2001, 15:01:27;
                                                                                                                                                                                                                                    Maximum Match 100%
Listing first 45 summaries

    nucleic search, using sw model

                                                                                                                   ccgcgggctcacagtggtcg 20
                                                                                                                                    IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                US-09-757-100B-3
20
                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
                                                                                                                                                                                                Minimum DB seq length: 0 Maximum DB seq length: 50
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                                                                                                                                    Scoring table:
                                                                                                                                                                                rotal number
                                             OM nucleic
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                                                                                                                    Sequence:
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Sequence 3, Appli Sequence 3, Appli

Sequence 23, Appl Sequence 23, Appl Sequence 23, Appl

Sequence 3, Appli Sequence 3, Appli

Description

Sequence 37376, A Sequence 18579, A Sequence 18577, A Sequence 27527, A Sequence 279728, Sequence 278728, Sequence 248844, Sequence 2, 48911, Sequence 2, 48911,

6, Appli 31, Apr

Sequence 18962, A Sequence 18962, A Sequence 18962, A Sequence 18062, A Sequence 13649, Sequence 217856, Sequence 410893, Sequence 41518, Sequence 125344, Sequence 228330, Sequence 228330,

546, App

Sequence 54 Sequence 11

Sequence Sequence

Sequence

Sequence 37375, A Sequence 30520, A Sequence 40877, A Sequence 185404, Sequence 235736, Sequence 272127,

Sequence Seguence Sequence Sequence

Sequence 480869

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APPLICANT:
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                                                                                                                                                APPLICANT: Monia, Brett P.
APPLICANT: Monia, Brett P.
APPLICANT: Gaarde, William A.
APPLICANT: Garde, William A.
APPLICANT: Moro, Pamela S.
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0476
CURRENT APPLICATION NUMBER: PCT/US00/18999
CURRENT APPLICATION NUMBER: 09/377,310
PRIOR APPLICATION NUMBER: 09/377,310
PRIOR SPLICE DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 20
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APPLICANT: Gaarde, William A.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0389
CURRENT APPLICATION NUMBER: US/09/377,310A
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
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100.0%; Pred. No. 15;
tive 0; Mismatches 0
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ALIGNMENTS
                                                                                                                                    Isis Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: antisense sequence PCT-US00-18999-3
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                                                                                             Sequence 3, Application PC/TUS0018999 GENERAL INFORMATION:
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US-09-757-100B-3
; Sequence 3, Application US/09757100B
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 20; Conservative
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PCT-US00-18999-3
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US-09-377-310-3
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LENGTH: 20
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APPLICANT: Gaarde, William A.
APPLICANT: Gaarde, William A.
APPLICANT: Gaarde, William A.
TAPLICANT: Nero, Pamela S.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0476
CURRENT APPLICATION NUMBER: 2000-07-13
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-08-19
SPRIOR FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 23
APPLICANT: Gaarde, william A.
APPLICANT: Gaarde, william A.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase;
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0533
CURRENT APPLICATION NUMBER: US/09/757,100B
CURRENT FILING DATE: 2001-03-15
PRIOR PRIJNG DATE: 1999-08-19
PRIOR APPLICATION NUMBER: 09/377,310
PRIOR FILING DATE: 2000-07-13
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
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Pred. No. 15;
; Mismatches 0;
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Pred. No. 4.1e+0.0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: antisense sequence PCT-US00-18999-23
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; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 20; Conservative
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GENERAL INFORMATION:
APPLICANT: Mittmann et al.
APPLICANT: Mittmann et al.
TITLE OF INVENTION: Methods of Genetic Analysis of Human TITLE OF INVENTION: Methods of Genetic Analysis of Human FILE OF INVENTION: Methods of Genetic Analysis of Human CURRENT APPLICATION NUMBER: US/09/660,220
CURRENT FILING DATE: 2000-09-12
PRIOR PELICATION NUMBER: 60/164,973
PRIOR FILING DATE: 1999-11-11
NUMBER OF SEQ ID NOS: 140981
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 25
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APPLICANT: Affymetrix, Inc.
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
FILE REFERENCE: 3112
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Pred. No. 5.1e+03;
0; Mismatches 2;
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Pred. No. 5.1e+03;
0; Mismatches 2;
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US-60-233-166-185790
               SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 37376
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                                                                                                                                                    ; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank L11931
US-09-660-220-37376
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; DATABASE ACCESSION NUMBER: GenBank L11931
US-09-660-220-37377
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CURRENT FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 420907
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88.9%;
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ilarity 88.9%;
Conservative
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Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                              TYPE: DNA
ORGANISM: Homo Sapiens
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Best Local Similarity
Matches 16; Conserv
        PRIOR FILING DATE:
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APPLICANT: Monia, Brett P.
APPLICANT: Monia, Pamela S.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
FILE REFERENCE: 1SPH-0533
CURRENT FILING DATE: 1999-08-15
PRIOR APPLICATION NUMBER: 09/377,310
PRIOR APPLICATION NUMBER: 09/377,310
PRIOR APPLICATION NUMBER: 09/377,310
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 2000-07-13
PRIOR FILING DATE: 2000-07-13
SOFTWARE: PATENTING DATE: 2000-07-13
SOFTWARE: PATENTING DATE: 1950-08-19
SEQ ID NO 23
LENGTH: 15
APPLICANT: Gaarde, William A.

TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0389
CURRENT APPLICATION NUMBER: US/09/377,310A
CURRENT APPLICATION NUMBER: US/09/377,310A
SUFTWAREN FILING DATE: 1999-08-19
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 23
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APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis of Human FILE REFERENCE: 3102.1
CURRENT APPLICATION NUMBER: US/09/660,220
CURRENT FILING DATE: 2000-09-12
PRIOR APPLICATION NUMBER: 60/164,973
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Sequence 37376, Application US/09660220
SEMEAL INFORMATION:
APPLICANT: Mitmann et al.
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Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
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69.0%;
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2 cggactcacagtgatcg 18
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Best Local Similarity 100.
Matches 14; Conservative
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US-60-233-166-319513
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   Length 25;
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GENERAL INFORMATION:
APPLICANT: Mittmann, M
TITLE OF INVENTION: Methods of Genetic Analysis of Mus
TITLE OF INVENTION: Methods of Genetic Analysis of Mus
TITLE OF INVENTION: Methods of Genetic Analysis of Mus
FILE REFERENCE: 3115
CURRENT APPLICATION NUMBER: US/60/234,017
CURRENT FILING DATE: 2000-09-20
NUMBER OF SEQ ID NOS: 605887
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 75527
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APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis of Mus
TITLE OF INVENTION: Methods of Genetic Analysis of Mus
TITLE OF INVENTION: musculus
FILE REFERENCE: 3115
CURRENT APPLICATION NUMBER: US/60/234,017
CURRENT FILIGE DATE: 2000-09-20
NUMBER OF SEQ ID NOS: 605887
SEQ ID NO 55657
LENGTH: 25
Score 14.8; DB 55;
Pred. No. 5.1e+03;
0; Mismatches 2;
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Pred. No. 1e+04;
0; Mismatches 3;
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Pred. No. 1e+04;
0; Mismatches 3;
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; DATABASE ACCESSION NUMBER: GenBank AF048838
US-60-234-017-75527
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; DATABASE ACCESSION NUMBER: GenBank U76759
US-60-234-017-55657
                                                                                                                                                                                                 ; Sequence 55657, Application US/60234017; GENERAL INFORMATION:
74.0%;
88.9%;
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Best Local Similarity 84.2%;
Matches 16; Conservative
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84.2%;
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Matches 16; Conserva
                   Best Local Similarity
Matches 16; Conserv
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Query Match
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US-60-233-166-279728/c

Sequence 279728, Application US/60233166

Sequence 279728, Application US/60233166

Separate Mitthman

APPLICANT: Affymetrix, Inc.

TITLE OF INVENTION: Methods of Genetic Analysis of the Rat

TITLE OF INVENTION: Genome

FILE REFERENCE: 3112

CURRENT APPLICATION NUMBER: US/60/233,166

CURRENT FILIG DATE: 2000-10-24

NUMBER OF SEQ ID NOS: 420907

SOFTWARE: FastSEQ for Windows Version 4.0

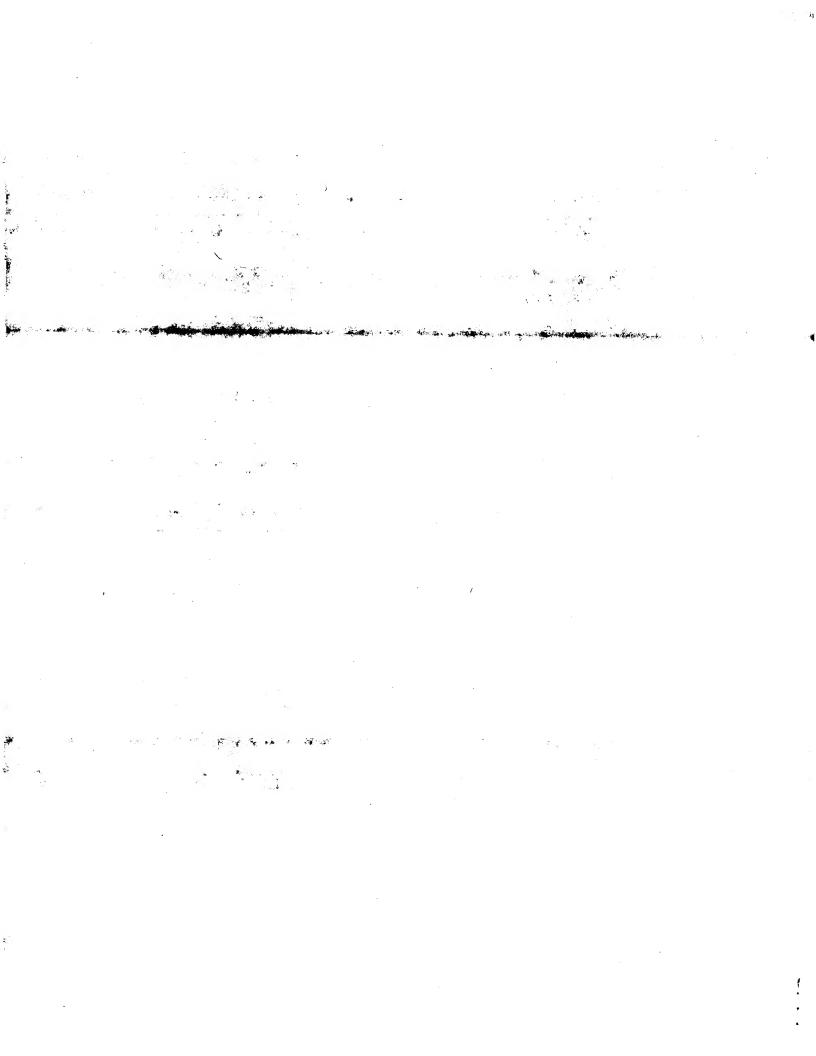
SEQ ID NO 279728

LENGTH: 25
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GENERAL INFORMATION:
APPLICANT: Mittmann:
APPLICANT: Mittmann:
APPLICANT: Mittmann:
APPLICANT: Mittmann:
TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
TITLE OF INVENTION: Genome
FILE REPRENCE: 311.
CURRENT PILION NUMBER: US/60/233,166
CURRENT PILION DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 420907
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 319513
LENGTH: 25
TYPE: DNA
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GENERAL INFORMATION:
APPLICANT: MitLmann, M
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis of Mus
TITLE OF INVENTION: musculus
FILE REFERENCE: 3115
CURRENT APPLICATION UNBER: US/60/234,017
CURRENT FILING DATE: 2000-09-20
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Pred. No. 1.6e+04;
0; Mismatches 2;
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DATABASE ACCESSION NUMBER: GenBank A1639107
US-60-233-166-279728
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US-60-233-166-319513
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US-60-234-017-248844
; Sequence 248844, Application US/60234017
; GENERAL INFORMATION:
   APPLICANT: Mittmann, M
   APPLICANT: Affymetrix, Inc.
   TITLE OF INVENTION: musculus
   FILE REFERENCE: 3115
CURRENT APPLICANTON: Methods of Genetic Analysis of Mus
   FILE REFERENCE: 3115
CURRENT PFLLING DATE: 2000-09-20
NUMBER OF SEQ ID NOS: 605887
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 248844
CURGHH: 25
LENGTH: 25
LENGTH: 25
LYPE: DATE ACCESSION NUMBER: GenBank AW049900
US-60-234-017-248844
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Pred. No. 1.6e+04;
0; Mismatches 2;
                                                                 TYPE: DNA
ORGANISM: Mus musculus
POBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank AF055638
US-60-234-017-10846
NUMBER OF SEQ ID NOS: 605887
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10846
LENGTH: 25
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Best Local Similarity 88.2%;
Matches 15; Conservative
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Best Local Similarity 88.2
Matches 15; Conservative
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Search completed: October 2, 2001, 21:50:08 Job time: 24521 sec

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ORGANISM: Artificial Sequence
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US-09-688-071-57
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                                Compugen Ltd.
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US-09-688-071-57
US-09-688-071-51
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US-09-735-271-2037
US-09-735-271-2037
US-09-735-271-10
US-09-915-060-9
US-09-915-060-43
US-09-915-060-43
US-09-915-271-1558
US-09-787-252-17
US-09-88-17728-4196
US-09-787-25-17
US-09-78-5-55
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            GenCore version 4.5
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ALIGNMENTS

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105-09-688-069-57

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APPLICANT: Lassner, M.; Post-Beittenmiller, M.; Savidge, B.; Weiss, J.; Mitsky, T. APPLICANT: Lassner, M.; Post-Beittenmiller, M.; Savidge, B.; Weiss, J.; Mitsky, T. APPLICANT: Valentin, H.
TITLE OF INVENTION: Nucleic Acid Sequences to Proteins Involved in Tocopherol Synt FILE REPERENCE: 16515.055
CURRENT PAPLICATION NUMBER: US/09/688,071
CURRENT FILING DATE: 1099-04-15
PRIOR APPLICATION NUMBER: US 60/129,899
PRIOR FILING DATE: 1999-04-15
PRIOR FILING DATE: 1999-04-14
PRIOR FILING DATE: 1999-04-14
PRIOR FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-09-14
PRIOR FILING DATE: 2000-09-14
PRIOR FILING DATE: 2000-09-14
PRIOR FILING DATE: 2000-09-14
                                                                                                                                                                                                                           Sequence 53, Application US/0968069
GENERAL INFORMATION:
APPLICANT: Subramaniam, S.; Slater, S.; Karberg, K.; Chen, R.; Valentin, H.; Wong, TILLE OF INVENTION: Nucleic Acid Sequences to Proteins Involved in Tocopherol Synt FILE REFERENCE: 16515.054
CURRENT APPLICATION NUMBER: US/09/688,069
CURRENT FILING DATE: 2000-10-14
NUMBER OF SEQ ID NOS: 114
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                                            Gaps
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    Length 41;
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Score 12.2; DB 7;
Pred. No. 9.4e+03;
0; Mismatches 3;
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Pred. No. 9.4e+03;
0; Mismatches 3;
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Pred. No. 9.4e+03;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Synthetic Oligonucleotides US-09-688-069-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Synthetic Oligonucleotides US-09-688-071-53
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0
    61.0%;
82.4%;
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82.4%;
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82.4%;
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                                                                                   1 ccgcgggctcacagtgg 17
                                                                                                                 5 ccgcggccgcacatgg 21
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Best Local Similarity 82.4
Matches 14; Conservative
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                                            14; Conservative
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                 Best Local Similarity
Matches 14; Conserv
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Best Local Similarity
Matches 14; Conserv
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US-09-688-069-53
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US-09-688-071-53
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    Query Match
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TITLE OF INVENTION: Nucleic Acid Sequences to Proteins Involved in Tocopherol Synthes FILE REFERENCE: 16515.055
CURRENT PAPLICATION NUMBER: US/09/688,071
CURRENT FILING DATE: 2000-10-14
PRIOR APPLICATION NUMBER: US 60/129,899
PRIOR APPLICATION NUMBER: US 60/146,461
PRIOR PILING DATE: 1999-04-15
PRIOR FILING DATE: 1999-07-30
PRIOR FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-04-14
SEQ ID NOS: 114
SEQ ID NO 51
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 51, Application US/09688069

GENERAL INFORMATION:
APPLICANT: Subramaniam, S.; Slater, S.; Karberg, K.; Chen, R.; Valentin, H.; Wong, Y.
TITLE OF INVENTION: Nucleic Acid Sequences to Proteins Involved in Tocopherol Synthes
FILE REFERENCE: 16515.054
CURRENT APPLICATION NUMBER: US/09/688,069
CURRENT FILING DATE: 2000-10-14
SEQ ID NOS: 114
SEQ ID NOS: 114
SEQ ID NOS: 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lassner, M.; Post-Beittenmiller, M.; Savidge, B.; Weiss, J.; Mitsky, T.;
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                                                                                                                                                                    Length 50;
                                                                                                                                                                                                          Indels
                                                                                                                                                                Score 13.2; DB 7;
Pred. No. 2.9e+03;
0; Mismatches 3;
                                                                                 ; OTHER INFORMATION: Synthetic Oligonucleotides US-09-688-071-57
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                     TYPE: DNA ORGANISM: Artificial Sequence
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82.4%;
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ilarity 83.3%;
Conservative
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Best Local Similarity
Matches 15; Conserva
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Best Local Similarity
Matches 14; Conserv
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  LENGTH: 50
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                                                             FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Kster, Hubert
TITLE OF INVENTION: DNA Diagnostics Based on Mass Spectrometry
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Pred. No. 1.8e+04;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Heller Ehrman White & McAuliffe LLP
STREET: 4350 La Jolla Village Drive
CITY: San Diego
                                                                                                                                                                                                                                                  Score 11.6; DB 6;
Pred. No. 1.8e+04;
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NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24736-2002M
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                       ed. No. 1.86
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/879,341 FILING DATE: 11-Jun-2001 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 09/786,416
FILING DATE: 28 FEB-2001
APPLICATION NUMBER: 09/287,679
FILING DATE: 06-APR-1999
APPLICATION NUMBER: 08/617,256
FILING DATE: 18-MAR-1996
APPLICATION NUMBER: 08/406,199
FILING DATE: 03-MAR-1995
                                                                                                            TOPOLOGY: linear MOLECULE TYPE: cDNA SEQUENCE DESCRIPTION: SEQ ID NO: 12: US-09-879-341-12
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SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-879-341-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10, Application US/09879341 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Diskette
                                            LENGTH: 25 base pairs
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                                                                 TYPE: nucleic acid
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                 6 GCGGCCAACCAGTCGTTG 23
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Best Local Similarity 77.8
Matches 14; Conservative
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ZIP: 92122-1246
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Best Local Similarity
Matches 14; Conserv
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TITLE OF INVENTION: DNA Diagnostics Based on Mass Spectrometry
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Haller Ehrman White & McAuliffe LLP
STREET: 4350 La Jolla Village Drive
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COMPUTER: IBM COmpatible
COMPUTER: IBM Compatible
COMPUTER: IBM COmpatible
COMPUTER: Datentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,341
FILING DATE: 10-10n -2001
APPLICATION NUMBER: 09/786,416
FILING DATE: 28-FEB-2001
APPLICATION NUMBER: 09/287,679
FILING DATE: 06-APR-1999
APPLICATION NUMBER: 08/406,199
FILING DATE: 01-MAR-1996
APPLICATION NUMBER: 08/406,199
FILING DATE: 01-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 25;
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REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24736-2002M
                                                                                                                                                  APPLICANT: Rioux, John APPLICANT: Siminovitch, Kathy TITLE OF INVENTION: IBD-RELATED POLYMORPHISMS FILE REFERENCE: 2825.1025-002 CURRENT APPLICATION NUMBER: US/09/735,271 CURRENT FILING DATE: 2000-12-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 1.5e; Mismatches
                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 2058
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/170,257
PRIOR FILING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: US 60/196,046
PRIOR FILING DATE: 2000-04-10
                                        Sequence 2037, Application US/09735271
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TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 12, Application US/09879341 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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86.7%;
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Best Local Similarity 86.7
Matches 13; Conservative
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ZIP: 92122-1246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 cgcgggctcacagtg 16
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; ORGANISM: Homo sapiens
US-09-735-271-2037
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US-09-879-341-12
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LENGTH: 25
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APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN GROWTH FACTOR WITH HOMOL
TITLE OF INVENTION: EPIDERMAL GROWTH FACTOR, BGS-8, EXPRESSED HIGHLY IN IMMUNE TI
FILE REFERENCE: D0166 PSP
CURRENT APPLICATION NUMBER: US/60/298,340
CURRENT FILING DATE: 2001-06-14
NUMBER OF SEQ ID NOS: 26
SOFWARE: Patentin version 3.0
SEQ ID NO 21
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Sequence 17, Application US/09787252

Sequence 17, Application US/09787252

SERREAL INFORMATION:
APPLICANT: Lex M. COWSETt

TITLE OF INVENTION: ANTISENSE MODULATION OF RhOG EXPRESSION
FILE REFERENCE: RTSP-0106

CURRENT APPLICATION NUMBER: US/09/787,252

CURRENT FILING DATE: 2001-03-15

PRIOR APPLICATION NUMBER: 09/161,015

PRIOR FILING DATE: 1998-09-25

NUMBER OF SEQ ID NOS: 47

SEQ ID NO 17

LENGTH: 18
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GENERAL INFORMATION:
APPLICANT: Cargill, Michele
APPLICANT: Ireland, James S.
APPLICANT: Lander, Eric S.
TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
FILE REFERENCE: 2825.2009-001
CURRENT APPLICATION NUMBER: US/09/801,274
CURRENT FILING DATE: 2001-03-07
PRIOR FILING DATE: 2000-03-07
PRIOR FILING DATE: 2000-03-07
PRIOR FILING DATE: 2000-05-05
NUMBER OF SQL ID NOS: 1802
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 629
                                                                                                                                                                                                                                                                                                                                           Length 39;
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Pred. No. 1.9e+04;
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Pred. No. 2.3e+04;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Antisense Oligonucleotide US-09-787-252-17
                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57.0%;
92.3%;
                                                                                                                                                                                                                                                                                                                                         58.0%;
77.8%;
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Best Local Similarity 92.3
Matches 12; Conservative
                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-298-340-21
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                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 14; Conserv
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GENERAL INFORMATION:
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                                                                                                                                                                                                               LENGTH: 39
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TITLE OF INVENTION: Novel internal ribosome entry site, vector containing same and th
TITLE OF INVENTION: LAFACOF
TITLE OF INVENTION: LAFACOF
TITLE REPRENCE: 2676-4976US
CURRENT APPLICATION NUMBER: 09/09/915,060
CURRENT FILING DATE: 2001-07-25
PRIOR FILING DATE: 1999-01-26
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin version 3.1
SEQ ID NO 43
LENGTH: 30
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                                                                                                                                                     Sequence 9. Application US/09915060
GENERAL INFORMATION:
APPLICAMY: Valams Internulversitair Instituut voor Biotechnol
TITLE OF INVENTION: thereof
CURRENT APPLICATION NUMBER: 08/09/915,060
CURRENT FILING DATE: 2001-07-25
PRIOR FILING DATE: 1999-01-26
NUMBER OF SEQ ID NOS: 51
SOCTHARRE: PATENTIN VERSION 3.1
SEQ ID NO 9
LENGTH: 30
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Pred. No. 1.9e+04;
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US-09-915-060-43
; Sequence 43, Application US/09915060
; GENERAL INFORMATION:
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US-60-298-340-21/c
; Sequence 21, Application US/60298340
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 77.8%;
Matches 14; Conservative
                 3 gegggeteacagtggteg 20
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                                              20 GCGGCAAACAGTCGTTG 3
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Matches 14; Conservative
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Pred. No. 2.4e+04;
0; Mismatches 1; Indels
                                                                                                                                                                   Score 11.4; DB 6; Length 31;
Pred. No. 2.3e+04;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
US-09-735-271-1558/C

Sequence 1558, Application US/09735271

SEGUENCE INFORMATION:
APPLICANT: Hudson, Thomas J.
APPLICANT: Lander, Eric S.
APPLICANT: Rioux, John
TITLE OF INVENTION: BOHIOVICH, Kathy
TITLE OF INVENTION: IBD-RELATED POLYMORPHISMS
FILE REFERENCE: 2825.1025-002
CURRENT FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: US/09/735,271
PRIOR PRILING DATE: 1999-12-10
PRIOR FILING DATE: 1999-12-10
PRIOR FILING DATE: 2000-12-11
PRIOR FILING DATE: 2000-12-11
PRIOR FILING DATE: 2000-12-10
PRIOR FILING DATE: 2000-12-10
SPRIOR FILING DATE: 2000-04-10
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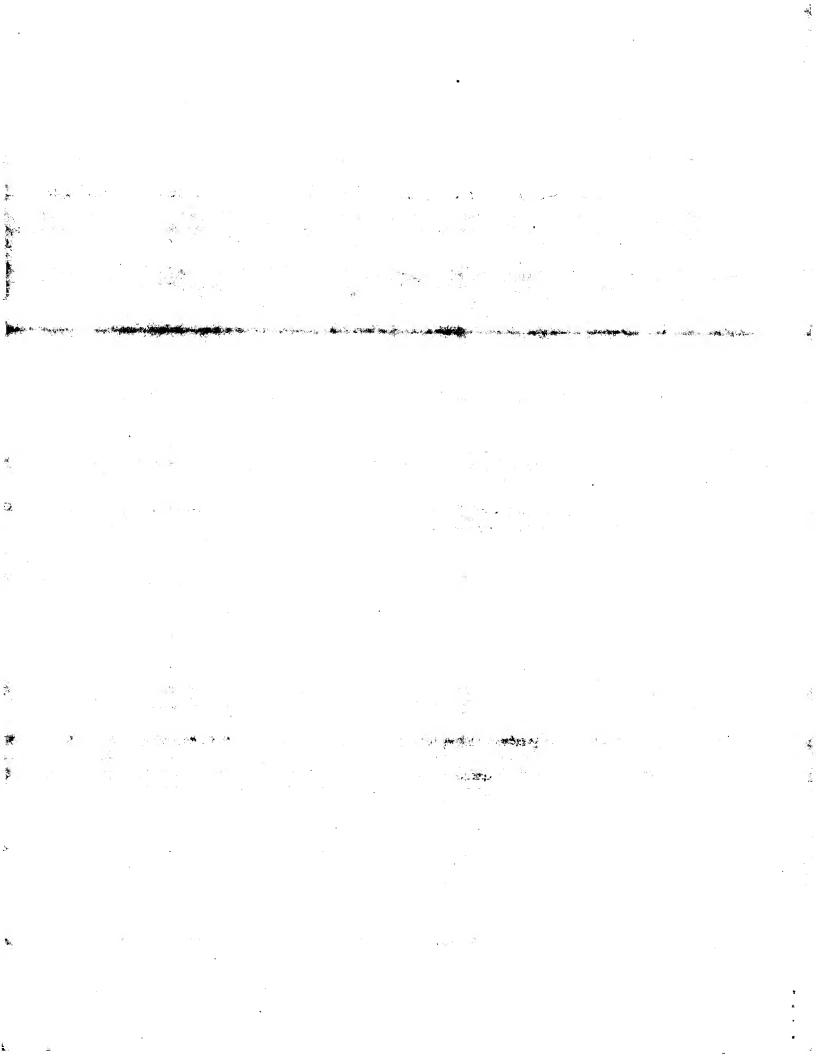
NAME/KEY: misc_feature

LOCATION: (1)...(40)

OTHER INFORMATION: n = A,T,C or G
US-09-735-271-1558
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Best Local Similarity 80.0%;
Matches 12; Conservative
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Best Local Similarity 92.3%;
Matches 12; Conservative
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3 gggtcacagtggcsg 17
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-801-274-629
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35 GCGGGTCACAGT 23
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ORGANISM: Homo sapiens
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Search completed: October 2, 2001, 16:54:58 Job time: 17661 sec

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Sequence:

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Sequence 9, Application US/09377310B
Fatent No. 6133031
GENERAL INFORMATION:
APPLICANT: Monia, Brett P.
APPLICANT: Monia, Brett P.
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0389
CURRENT APPLICATION NUMBER: US/09/377,310B
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
LENGTH: 20
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APPLICANT: Monia, Brett P.
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0389
CURRENT APPLICATION NUMBER: US/09/377,310B
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 29
LENGTH: 15
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100.0%; Pred. No. 0.041;
iive 0; Mismatches 0;
             US-08-471-791-39
PCT-US91-01746-39
PCT-US91-01750-10
US-08-781-891.0
US-08-445-4638-63
US-08-445-4638-63
US-08-445-4638-63
US-08-445-4638-62
US-08-790-963-2
US-08-790-963-2
US-08-790-774-2
US-08-790-774-2
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US-08-790-774-2
US-08-790-774-2
US-08-790-774-2
US-08-790-774-2
US-08-790-774-2
US-08-790-774-04
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; OTHER INFORMATION: antisense sequence
US-09-377-310-9
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; Patent No. 6133031
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 20; Conservative
 GENERAL INFORMATION:
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US-09-377-310-29
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US-09-377-310-9
TYPE: DNA
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                                                                                                                               (without alignments)
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                                                                                                                 Search time 417.38 Seconds
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Sequence 39,
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
            version 4.5
- 2000 Compugen Ltd.
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US-09-377-310-8
US-08-219-012-39
US-08-219-012-39
US-08-687-421-22
US-09-377-310-28
US-09-377-310-28
US-08-686-968C-28
US-08-686-968C-32
US-08-686-968C-32
US-08-686-968C-32
US-08-686-968C-32
US-08-388-653-8
US-08-388-653-8
US-08-388-653-8
US-08-087-716-8
US-09-157-753-8
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length: 50
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APPLICANT: Gold, Larry
APPLICANT: Gold, Larry
APPLICANT: Tasie, Nebojsa
APPLICANT: Tasset, Diane
TITLE OF INVENTION: HIGH-AFFINITY LIGANDS OF BASIC
TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR AND
TITLE OF INVENTION: THROMBIN
NUMBER OF SEQUENCES: 445
CORRESPONDENCE ADDRESS:
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8400 E. Prentice Avenue, Suite 200
                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                           Score 13.6; |
Pred. No. 98;
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SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,421
FILING DATE: 08-MAY-1996
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: 08/195,005
BITTING CAM
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PRIOR APPLICATION DATA:
PAPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 227, Application US/08687421 Patent No. 6177557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,333
FILING DATE: 11.NOVEMBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/219,012
FILING DATE: 28-MARCH-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07/536,428
                                                      REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 850-9900
TELEFAX: (303) 850-9401
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                           68.0%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 11-JUNE-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       2 TTTTGGTATAGGCTAGGTGT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-JUNE-1991
     ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                     1 ttttgctagatgctaggtat
                           Swanson
                                                                                                                                                                                                                                                                                                                                                  Conservative
                                 REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA: APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80111
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                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
US-08-687-421-227
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                                                                                                                                                                                                                                                    US-08-219-012-39
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APPLICANT: Montal, Brett P.
APPLICANT: Montal, Brett P.
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0389
CURRENT APPLICATION NUMBER: US/09/377,310B
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 20
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                                                                                               DB 3; Length 15;
17;
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17;
                                                                                                                                    0; Indels
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STREET: 4582 South Ulster Street Parkway, Suite #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY.
ZIP: 80237
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
- COMPUTER: IBM COMPATIBLE
- COMPUTER: IBM COMPATIBLE
                                                                                  75.0%; Scor.
100.0%; Pred. No. 10.
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Larry Gold
APPLICANT: Diane Tasset
TITLE OF INVENTION: Ligands of Thrombin
NUMBER OF SEQUENCES: 92
CORRESPONDENCE ADDRESS:
ADDRESSEE: Beaton & Swanson, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: antisense sequence
US-09-377-310-8
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-377-310-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/219,012
                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/09377310B Patent No. 6133031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 39, Application US/08219012 Patent No. 5543293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Printive 0;
                                                                                               Query Match 75.C
Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
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PRIOR APPLICATION DATA:
                                                                                                                                                                        6 ctagatgctaggtat 20
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STATE: Colorado
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-219-012-39
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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MEDIUM TYPE: Floppy Disk
COMPUTER: IBM compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: OHKAWA, HIDEO
APPLICANT: IMAISHL, HIROMASA
TITLE OF INVENTION: NOVEL CYTOCHROME P450 GENE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: PILLSBURY, MADISON & SUTRO
STREET: 1100 NEW YORK AVENUE, N.W.
                                                                                                SUFINARE: PARTENTIA RELEASE #1.0, Vers CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/792,832A FILING DATE: 30-JAN-1997 CLASSIFICATION: 435 PRIOR APPLICATION DATA: 435 APPLICATION NUMBER: US 60/000,955 FILING DATE: 07-JUL-1995 APPLICATION NUMBER: US 08/678,435 FILING DATE: 03-JUL-1996 ATTORNEY/AGENT INNORMATION: NAME: Hibler, David W. REGISTRATION NUMBER: 41,071 REFERENCE/DOCKET NUMBER: TAMK:190 TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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US-09-033-055A-10
Sequence 10, Application US/09033055A;
Patent No. 6069241;
GENERAL INFORMATION:
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NAME: PAGU. E. WHITE, JR.
REGISTRATION NUMBER: 32,011
REFERENCE/DOCKET NUMBER: 9437
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 861-3651
TELEFAX: 6714627 GUSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.0%;
82.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 ttgctagatgctaggta 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 14; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1100 NEW CITY: WASHINGTON STATE: D.C.
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APPLICANT: Monia, Brett P.
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: Expression
FILE OF INVENTION: Expression
FILE REPERENCE: ISPH-0389
CURRENT APPLICATION NUMBER: US/09/377,310B
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SSCTWARE: Patentin Ver. 2.0
SEQ ID NO 28
LENGTH: 15
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Patent No. 6017734
GENERAL INFORMATION:
APPLICANT: Summers Dr., Max D.
APPLICANT: Braunagel Dr., Sharon C.
APPLICANT: Hong Dr., Tao
TITLE OF INVENTION: UNIQUE NUCLEOTIDE AND AMINO ACID
TITLE OF INVENTION: SEQUENCE AND USES THEREOF
NUMBER OF SEQUENCES:
ADDRESSEE: Annold, White & Durkee
                                                                                                                                                                                                                                                                                                                     Pred. No. 98;
; Mismatches
                                                                                                                                                                                                                                                                                               68.0%; Score 13.6;
80.0%; Pred. No. 98
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                 REFERENCE/DOCKET NUMBER: NEX07/PCT TELECOMMUNICATION INFORMATION: TELEPHONE: (303) 793-3333
TELEPAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 227: SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: antisense sequence US-09-377-310-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
US-00-377-310-28
Sequence 28, Application US/09377310B
Patent No. 6133031
  REGISTRATION NUMBER: 33,215
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                                                                                                                                                                                                                                                                                                                   Best Local Similarity 80.03
Matches 16; Conservative
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Best Local Similarity 100.
                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
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77210
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US-08-687-421-227
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; OTHER INFORMATION: Description of Artificial Sequence: primer US-08-686-9686-32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 35;
   Indels
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Pred. No. 5.4e+02;
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Pred. No. 5.4e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 34, Application US/08686968C

Patent No. 6221361

GENERAL INFORMATION:
APPLICANT: Occhran, Mark D.
TITLE OF INVENTION: Recombinant Swinepox Virus
FITE REFERENCE: 39119+4/0.
CURRENT APPLICATION NUMBER: US/08/686,968C
CURRENT FILING DATE: 1996-07-25
NUMBER OF SEQ ID NOS: 231
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 34
LENGTH: 35
                                                                                                                                                                                                                 APPLICANT: Cochian, Mark D.
APPLICANT: Cochian, Mark D.
TITLE OF INVENTION: Recombinant Swinepox Virus
FILE REFERENCE: 39119-H/JML
CURRENT APPLICATION NUMBER: US/08/686,968C
CURRENT FILING DATE: 1996-07-25
NUMBER OF SEQ ID NOS: 231
SEQ ID NO 32
LENGTH: 35
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                 ; Sequence 32, Application US/08686968C
; Patent No. 6221361
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82.4%;
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82.4%;
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                                        2 tttgctagatgctaggt 18
                                                         2 tttgctagatgctaggt 18
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 Matches 14; Conservative
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Best Local Similarity 82.4
Matches 14; Conservative
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Best Local Similarity 82.4
Matches 14; Conservative
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                                                                                                                               RESULT 11
US-08-686-968C-32
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US-08-686-968C-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
US-08-478-386A-8
                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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                                                                                                                                                                Length 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 12.2; DB 4; Length 35;
Pred. No. 5.4e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 35;
                                                                                                                                                                                                      3; Indels
                                                                                                                                                              Score 12.2; DB 3;
Pred. No. 5.3e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Cochran, Mark D.
TITLE OF INVENTION: Recombinant Swinepox Virus
FILE REFERENCE: 39119-H/JML
CURRENT APPLICATION NUMBER: US/08/686,968C
NUMBER OF SEQ ID NOS: 231
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 28
LENGTH: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 12.2; DB 4;
Pred. No. 5.4e+02;
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APPLICANT: Cochean, Mark D.
TILE APPLICANTION: Recombinant Swinepox Virus
FILE REFERENCE: 39119-H/JML
CURRENT APPLICATION NUMBER: US/08/686,968C
NUMBER OF SEQ ID NOS: 231
SOFTWARE: PALENT VET. 2.1
SEQ ID NO 30
LENGTH: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
US-08-686-968C-30
; Sequence 30, Application US/08686968C
; Patent No. 6221361
                                                                                                                                                                                                                                                                                                                                                                Sequence 28, Application US/08686968C Patent No. 6221361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                              Query Match 61.0%;
Best Local Similarity 82.4%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 61.0%;
Best Local Similarity 82.4%;
Matches 14; Conservative
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82.4%;
                                                                                                                                                                                                                                                           2 TTGCTTATTGCTAGGTA 18
                                                                                                                                                                                                                                      3 ttgctagatgctaggta 19
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                   ; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-09-033-055A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                 US-08-686-968C-28
                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
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Pred. No. 5.5e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: 6..11
OTHER INFORMATION: /note= "Xho I restriction site."
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MEDIUM TYPE: Floppy disk
COMPUTER: Elbopy disk
COMPUTER: Elbopy disk
COMPUTER: Elb PC COMPATIBLE
OPERATING SYSTEM: PC/DOS/MS/DOS
SOFTWARE: PATENTIN BATA:
APPLICATION NUMBER: US/08/292,597
FILING DATE: 18/AUG/1994
CLASSIFICATION 135
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                          APPLICANT: Spencer, David M.
APPLICANT: Wandless, Thomas J.
APPLICANT: Wandless, Thomas J.
APPLICANT: Belshaw, Peter
TITLE OF INVENTION: Regulated Apoptosis
NUMBER OF SEQUENCES: 81
ANDRESSEE: ARRAD Pharmaceuticals, Inc.
                                                                                                                                                                                          E: ARIAD Pharmaceuticals, Inc. 26 Landsdowne Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Figg, E. Anthony
REGISTRATION UNBER: 27,195
REFERENCE/DOCKET NUMBER: 2054-108A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 783-6040
TELEPHONE: (202) 783-6040
TELEPHONE: (202) 783-6031
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
LENGTH: 41 base pairs
LENGTH: 41 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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CHER INFORMATION: /note= "A to G."
US-08-292-597-8
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; Sequence 8, Application US/08388653
; Patent No. 5869337
; GENERAL INFORMATION:
APPLICANT: Crabtree, Gerald R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61.0%;
ilarity 82.4%;
Conservative
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OTHER INFORMATION:
OTHER INFORMATION:
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CITY: Cambridge
STATE: Massachuse
COUNTRY: USA
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Best Local Similarity
Matches 14; Conserv
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        APPLICANT: Crabtree, Gerald R.
APPLICANT: Schreiber, Stuart L.
APPLICANT: Spencer, David M.
APPLICANT: Spencer, David M.
APPLICANT: Wandless, Thomas J.
APPLICANT: Wandless, Thomas J.
APPLICANT: Belshaw, Peter
TITLE OF INVENTION: REGULATED TRANSCRIPTION OF TARGETED
TITLE OF INVENTION: GENES AND OTHER BIOLOGICAL EVENTS
INVERS OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSES: ALIAD Pharmaceuticals, Inc.
STRREET: 26 Landsdowne Street
CITY: Cambridge
STRYE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 61.0%; Score 12.2; DB 2; Length 41; Best Local Similarity 82.4%; Pred. No. 5.5e+02; Matches 14; Conservative 0; Mismatches 3; Indels
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OTHER INFORMATION: /note= "Region of homology with OTHER INFORMATION: target sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: 6.11
OTHER INFORMATION: /note= "Xho I restriction site.
                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER LOSA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

SOFTWARE: PatentIn Release #1.0, Version #1.25

SOFTWARE: PALICATION DATA:

APPLICATION NUMBER: US/08/478,386A

FILING DATE: 07/JUN/195

CLASSIFICATION: 514

ATTORNEY_AGENT INFORMATION:

NAME: Figg, E. Anthony

REGISTRATION NUMBER: 2054-114A

TELEPHONE: (202) 783-6040

TELEPHONE: (202) 783-6040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 28
CHER INFORMATION: /note= "A to G."
US-08-478-386A-8
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Sequence 8, Application US/08292597

Patent No. 5834266

GENERAL INFORMATION:

APPLICANT: GERBIA Crabtree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: 12..41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: cDNA
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GENERAL INFORMATION:
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APPLICANT: Schreiber, Stuart L.
APPLICANT: Schreiber, Stuart L.
APPLICANT: Spencer, David M.
APPLICANT: Cambridge Control of Street Control
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Db 13 TCTGCTAGCTAGGT 29

Search completed: October 2, 2001, 16:03:48

Job time: 14592 sec

Nucleotide sequenc Maize rpob gene pr Mutagenic PCR prim Reverse primer amp Petunia flower bud CPV VP2 gene PCR CPV VP2 gene PCR CPV VP1/2 gene PCR CPV VP1/2 gene PCR CPV VP1/2 gene PCR CPV VP1/2 gene PCR CD3 transmembrane Murine signalling Murine signalling Murine signalling Murine signalling Murine signalling Murine signalling PCB Primer #3. Uniden PCR primer #3. Uniden PCR primer for amp HPV16 E6-coding re 3/ junction sequen Nucleotide fragmen PCR primer for amp HPV16 E6-coding re 3/ junction sequen Nucleotide fragmen PCR primer for amp HUM IIIB gp160 PCR HIV IIIB gp160 gene amp PKPINV expression

| 12.6 63.0 37 20 12.4 62.0 27 20 12.2 61.0 29 18 12.2 61.0 29 19 12.2 61.0 35 19 12.2 61.0 35 19 12.2 61.0 35 19 12.2 61.0 35 19 12.2 61.0 41 17 12.2 61.0 41 17 12.2 61.0 41 12 12.2 61.0 41 12 | 2.2 61.0 41 22 AACF7538 2.2 61.0 24 122 AACB3458 12 60.0 26 12 AAX55038 12 60.0 27 20 AAX5503 12 60.0 33 19 AAX0554 12 60.0 33 20 AAX8959 12 60.0 39 16 AAV3442 12 60.0 42 16 AAV3442 12 60.0 42 16 AAT01098 12 60.0 43 18 AAT0135 12 60.0 43 18 AAT0151 12 60.0 43 18 AAT0151 12 60.0 43 18 AAT0151 12 60.0 20 143 18 AAV31551 12 85.0 20 14 AAV3151 1.8 59.0 22 18 AAX83010 | RESULT 1 AAC65541 ID AAC65541 ID AAC65541 XX AC AAC65541; XX AC AAC65541; XX AC AAC65541; XX DF 12-FBB-2001 (first entry) XX DE Human focal adhesion kinase antisense sequence #7. XX KW Human; focal adhesion kinase; FAK; signal transduction; cancer; KW EMBYONIC development disorder; anglogenic disorder; wound healing; XX | AX | ISIS-) ISIS PH onia BP, Gaar PI; 2001-00614 ew antisense c |
|--|--|---|---|--|
| Gencore (c) 1993 , using sv , 2001, 16 | Gapop 10.0 , Gapext 1.0 730101 seqs, 313950809 res its satisfying chosen para ngth: 0 Minimum Match 0% Maximum Match 100% Listing first 45 summaries N_Geneseq_0601: /SIDSB/gcgdata/geneseq,:/SIDSB/gcgdata/geneseq,:/SIDSB/gcgdata/geneseq,:/SIDSB/gcgdata/geneseq,:/SIDSB/gcgdata/geneseq,:/SIDSB/gcgdata/geneseq,:/SIDSB/gcgdata/geneseq,:/SIDSB/gcgdata/geneseq,:/SIDSB/gcgdata/geneseq,:/SIDSB/gcgdata/geneseq,:/SIDSB/gcgdata/geneseq,:/SIDSB/gcgdata/geneseq,:/SIDSB/gcgdata/geneseq,:/SIDSB/gcgdata/geneseq,:/SIDSB/gcgdata/geneseq,:/SIDSB/gcgdata/geneseq,:/SIDSB/gcgdata/geneseq, | 6: /SIDSB/gcgdata/geneseq/geneseqn/NA1985.DAT:* 7: /SIDSB/gcgdata/geneseq/geneseqn/NA1986.DAT:* 8: /SIDSB/gcgdata/geneseq/geneseqn/NA1986.DAT:* 9: /SIDSB/gcgdata/geneseqf/geneseqn/NA1980.DAT:* 10: /SIDSB/gcgdata/geneseqn/NA1980.DAT:* 11: /SIDSB/gcgdata/geneseqn/NA1990.DAT:* 12: /SIDSB/gcgdata/geneseqn/NA1991.DAT:* 13: /SIDSB/gcgdata/geneseqn/NA1991.DAT:* 14: /SIDSB/gcgdata/geneseqn/NA1991.DAT:* 15: /SIDSB/gcgdata/geneseqn/NA1992.DAT:* 16: /SIDSB/gcgdata/geneseqn/NA1995.DAT:* 16: /SIDSB/gcgdata/geneseqn/NA1995.DAT:* 17: /SIDSB/gcgdata/geneseqn/NA1996.DAT:* 18: /SIDSB/gcgdata/geneseqn/NA1999.DAT:* 19: /SIDSB/gcgdata/geneseqn/NA1999.DAT:* 11: /SIDSB/gcgdata/geneseqn/NA1999.DAT:* 12: /SIDSB/gcgdata/geneseqn/NA1999.DAT:* 13: /SIDSB/gcgdata/geneseqn/NA1999.DAT:* 14: /SIDSB/gcgdata/geneseqn/NA1999.DAT:* 15: /SIDSB/gcgdata/geneseqn/NA1999.DAT:* 16: /SIDSB/gcgdata/geneseqn/NA1999.DAT:* 17: /SIDSB/gcgdata/geneseqn/NA1999.DAT:* 18: /SIDSB/gcgdata/geneseqn/NA1999.DAT:* | Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SUMMARIES \$ Score Match Length DB ID Description | 20 100.0 20 22 AAC65541 Human focal adhesi 15 75.0 15 22 AAC65561 Human focal adhesi 15 70 20 22 AAC65540 Human focal adhesi 3.8 69.0 20 AAX33269 PEBP2 alpha A gene 3.6 68.0 31 AAA48327 PEBP2 alpha A gene 3.6 68.0 31 AAX700213 Thrombin DNA ligan 3.1 68.0 31 22 AAX293950 CaMY Calibrator pr 3.2 66.0 27 21 AAA293950 Human genomic DNA 3.2 66.0 31 23 AAA79014 Human genomic DNA |

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The present invention describes a number of phosphorothioate antisense sequences to the human focal adhesion kinase (FAK) protein. This protein is involved in integrin-mediated signal transduction, and is implicated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEBP2 alpha A gene expression regulating DNA PCR primer SEQ ID NO:26.
                                                                                                                                                                                                                                                                                              Human; focal adhesion kinase; FAK; signal transduction; cancer;
embryonic development disorder; anglogenic disorder; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in cancer, particularly colon, breast and oral tumours, embryonic development disorders, angiogenic disorders and wound healing. The antisense sequences, including the one shown here, can be used in treatment of all of these.
                                                                                                                                                                                                                                                        Human focal adhesion kinase antisense sequence #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20 BP; 4 A; 4 C; 5 G; 7 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 15;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Column 23; 30pp; English.
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100.0%; Fig.
                                                                                                                                                                                                                                                                                                                                       antisense; phosphorothioate; ss.
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Matches 15; Conservative
                      AAC65540 standard; DNA;
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                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-AUG-1999;
                                                                                                                                                                                                                   12-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                               US6133031-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Monia BP,
                                                                                                                                                                               AAC65540;
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ID AAX3
XX
AC AAX3
XX
DT 30-JI
XX
XX
DE PEBP:
XX
XW
KW
PEBP:
KW OStee
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                                    The present invention describes a number of phosphorothioate antisense sequences to the human focal adhesion kinase (FAK) protein. This protein is involved in integrin-mediated signal transduction, and is implicated in cancer, particularly colon, breast and oral tumours, embryonic development disorders, anglogenic disorders and wound healing. The antisense sequences, including the one shown here, can be used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a number of phosphorothioate antisense sequences to the human focal adhesion kinase (FAK) protein. This protein is involved in integrin-mediated signal transduction, and is implicated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in cancer, particularly colon, breast and oral tumours, embryonic development disorders, angiogenic disorders and wound healing. The antisense sequences, including the one shown here, can be used in the treatment of all of these.
                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; focal adhesion kinase; FAK; signal transduction; cancer; embryonic development disorder; angiogenic disorder; wound healing; antisense; phosphorothloate; ss.
                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                        Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 15;
                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human focal adhesion kinase antisense sequence #27.
                                                                                                                                                                                                                                                                                            .;
0
                                                                                                                                                                                                                                                      DB 22;
0.16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22;
                                                                                                                                                                                             Sequence 20 BP; 4 A; 2 C; 5 G; 9 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15 BP; 3 A; 2 C; 5 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1
                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75.0%; Score 15; DB 100.0%; Pred. No. 61;
                                                                                                                                                                                                                                                      Score 20;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Column 25; 30pp; English
Claim 3; Column 23; 30pp; English
                                                                                                                                                                                                                                                    Query Match 100.0%; S
Best Local Similarity 100.0%; P
Matches 20; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP.
                                                                                                                                                                                                                                                                                                                                                   1 ttttgctagatgctaggtat 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99us-0377310.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC65561 standard; DNA; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                       antisense sequences, inclutreatment of all of these.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaarde WA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-006141/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-AUG-1999;
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Gaps

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Indels

.; 0

PEBP2 alpha A gene; expression; regulation; bone disease; osteoporosis; PCR primer; ss.

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Gaps

; 0

Conservative

Query Match

22; Length 20;

DB 63;

Monia BP,

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A new method for developing vaccines has been identified, in which a non-naturally occurring molecular scaffold, having a core particle and a covalently attached organiser, is attached to an antigen or antigenic determinant. The scaffold and antigen or antigenic determinant interact to form an ordered and repetitive antigen array. The composition is useful as a vacche against infectious diseases, to induce immune responses in farm animals and also in the treatment of cancer and allergies. The present sequence is the PCR primer, gpl40CysEcoRI. This primer was used to amplify the coding sequence for the gpl40 gene of human immunodeficiency virus (HVV). The PCR product was then used as an antigen in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                     Composition for use as vaccine against infectious diseases and in treatment of cancer and allergies comprises non-naturally occurring molecular scaffold and antigen or antigenic determinant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Family 1; family 2; ligand; thrombin; systematic evolution of ligands by exponential enrichment; SELEX; heparin; selection; region of homology; inhibitor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identification of ligands to basic fibroblast growth factor and thrombin - which can be modified for increased in vivo stability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                69.0%; Score 13.8; DB 21;
88.2%; Pred. No. 2.8e+02;
1ve 0; Mismatches 2;
 Ξ
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 36 BP; 11 A; 10 C; 6 G; 9 T; 0 other;
 Bachmann
                                                                                                                                                 Example 26; Page 77; 102pp; English.
Nieba L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 39; Page 95; 236pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thrombin DNA ligand, clone #17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94US-019012.
94US-0195005.
90US-0536428.
91US-0714131.
93US-0061691.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gold L, Janjic N, Tasset
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (NEXS-) NEXSTAR PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 tgctagatgctaggtat 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 TGCTAGCTGCTAGGAAT 6
 Hennecke F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1995-293073/38.
                                    WPI; 2000-412159/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-FEB-1994;
11-JUN-1990;
10-JUN-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-AUG-1995.
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Renner WA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT00213;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes DNA which participates in the regulation of expression of PEBP2 alpha A gene. The DNA produces a regulator protein with the activity of promoting bone formation and can serve as a promoter for prevention and treatment of bone diseases including osteoporosis. The present sequence represents a PCR primer used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                      DNA regulating expression of PEBP2 alphaA gene to produce regulator protein, useful as promoter for prevention or/and treatment of bone diseases e.g. osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69.0%; Score 13.8; DB 20; Length 20; 88.2%; Pred. No. 2.6e+02; ive 0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                               Katsumata T, Nakatsuka M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20 BP; 6 A; 1 C; 6 G; 7 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HIV gp140 gene PCR primer, gp140CysEcoRI.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 6; Page 39; 118pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CYTO-) CYTOS BIOTECHNOLOGY AG.
                                                                                                                                                                                                                                          (SUMU ) SUMITOMO PHARM CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immunodeficiency virus.
                                                                                                                                                               98JP-0114135.
97JP-0254250.
97JP-0299407.
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                                                                                                                            98WO-JP03920
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 tttgctagatgctaggt 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 tttgataaatgctaggt 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 88.2
Matches 15; Conservative
                                                                                                                                                                                                                                                                             M, Harada H,
Tagashira S;
                                                                                                                                                                                                                                                                                                                                   WPI; 1999-243621/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HIV; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200032227-A2
                                                    WO9911787-A1
                                                                                                                            02-SEP-1998;
                                                                                                                                                                 08-APR-1998;
02-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-NOV-1999;
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                                                                                                                                                                                                     15-0CT-1997;
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                                                                                         11-MAR-1999
                                                                                                                                                                                                                                                                               Fujiwara M,
                 Synthetic.
                                                                                                                                                                                                                                                                                                  Ogawa S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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ð g Sequence 31 BP; 5 A; 3 C; 11 G; 12 T; 0 other;

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of ligands to thrombin. These sequences were isolated using the single stranded DNA molecules given in AATO0201 and AAT00226 which comprise a 30N and a 60N variable region, respectively. These ligands were isolated using systematic evolution of ligands by exponential enrichment (SELEX). The selection was conducted in a buffer solution at 37 deg. C. After 12 rounds of selection, no additional improvement in binding was seen. By studying regions of homology between the isolated ligands, a retains high affinity binding and inhibits clotting. These ligands are inhibitors of thrombin and are therefore useful in treating thrombin mediated conditions and in studying the structure and binding of
                                                                                                                                                                                                                                                                                                                                ;
0
sequences given in AAT00202-25 and AAT00227-57 represent two groups
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to a purified and isolated non-naturally occurring DNA ligands to basic flibroblast growth factor (bFGF). The ligands are useful as part of gene therapy treatments and for diagnosing pathogenesis of vascular diseases including intitation and progression of atherosclerosis, acute coronary syndromes, vein graft disease and restrenosis following coronary angloplasty. The ligands have improved stability in vivo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acid ligands to basic fibroblast growth factor that are useful as inhibitors of basic fibroblast growth factors and 2'-amino modified RNA ligands, exhibit increased in vivo stability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ligand; basic fibroblast growth factor; bFGF; gene therapy; vascular; atherosclerosis; angloplasty; stability; ss.
                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                            68.0%; Score 13.6; DB 16; Length 31; 80.0%; Pred. No. 3.5e+02;
                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                          Sequence 31 BP; 5 A; 3 C; 11 G; 12 T; 0 other;
                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 19; Column 57-58; 153pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thrombin high affinity ligand #12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAF70765 standard; DNA; 31 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gold L, Tasset D;
                                                                                                                                                                                                                                                                                                                                                                 1 ttttgctagatgctaggtat 20
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91US-0714131.
92US-0973333.
94US-0195005.
                                                                                                                                                                                                                                                                                                                                                                                   2 ttttggtataggctaggtgt 21
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                                                                                                                                                                                                                                                                                                                              16; Conservative
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                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US6177557-B1
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                                                                                                                                                                                                         thrombin.
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                                                                                                                                                                                                                                                                                            Query Match
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AAF70765
3399999999999888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quantitative detection of nucleic acids, based on the use of a calibrator, suitable primers and probes, and a nucleic acid polymerase with 5' \cdot 3' nuclease activity
                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                    Detection; identification; PCR; polymerase chain reaction; probe; primer; calibrator; diagnosts; pathogen; virus; bacteria; HHV-6; HHV-7; HHV-8; human herpes virus; human immunodeficiency virus; HIV; AIDS; acquired immune deficiency syndrome;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ပ်
Length 31;
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                                          Indels
                                                                                                                                                                                                                                                                                                                                            CaMV Calibrator probe sequence used in detection method
  DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Locatelli G, Lusso P, Malnati M, Salvatori F,
Score 13.6; DB 22
Pred. No. 3.5e+02;
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                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 13; 39pp; English.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis; ss
                                                                                                                                                                                                                          BP
68.0%;
80.0%;
                                                                               1 ttttgctagatgctaggtat 20
                                                                                                                   21
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                                                                                                                                                                                                                        AAZ93950 standard; DNA; 27
                                                                                                                                                                                                                                                                                                      29-AUG-2000 (first entry)
                                                                                                    |||||| || || ||||||| || ttttggtataggctaggtgt
                                       16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-387819/33.
  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200029613-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                              AAZ93950;
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                                          Matches
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Sequence 31 BP; 9 A; 8 C; 8 G; 5 T; 1 other;
                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                          12-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US6133031-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-0CT-2000.
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                                                                                                                                                                                                                                                                     10
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                                                                                                                         Matches
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ID AAZ9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a nucleic acid segment of 10-100 contiguous bases chosen from one of 632 fragments (AAA78631 to AAA79651, where the segment comprises a polymorphic site or an immediately adjacent base, or the complement of the segment. Also described are: (1) an allele-specific oligonucleotide that hybridises to a segment of the novelty; (2) an isolated nucleic acid comprising a sequence of the novelty where the polymorphic site within the sequence is cecupied by a base other than the reference base indicated in the specification; and (3) analysing a nucleic acid, comprising obtaining a nucleic acid from an individual, and determining a base occupying any one of the polymorphic sites of the novelty. The nucleic acid sequences for the presence of polymorphisms. The method can also be used to test for a disease phenotype and correlate the presence of the phenotype with a new or the presence of the phenotype with a new or many or the presence of the phenotype with a new or many or the nucleic acid sequences for the prasming and or new or the nucleic acid sequences for the presence of polymorphisms. The method can also be used to test for a disease phenotype and correlate the presence of the phenotype with a new or new or the presence of the phenotype with a new or new or the nucleic acid sequences for new or new or new or the nucleic acid sequences for the presence of polymorphisms. The method can also be used to test for a new or new 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human genomic polymorphic nucleic acid segments, allele specific primers and probes, and methods of analysis, useful for e.g. forensics, paternity testing, genetic mapping,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               particular polymorphism. The presence of polymorphic sites are useful
                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for, e.g. forensics, paternity testing, correlation of polymorphisms with phenotypic traits and for genetic mapping of phenotypic traits.

AAA78631 to AAA79262 represent sequence tags of human genomic DNA fragments containing polymorphic sites. The base occupying the polymorphic site is indicated using IUPAC-IUB nomenclature.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; genomic DNA; polymorphism; genome; allele-specific; primer;
probe; hybridisation; polymorphic site; forensic; paternity testing;
medicine; phenotypic trait; genetic analysis; genetic mapping; ds.
virus (HIV). The method provides an enhanced sensitivity, accuracy, and precision and a reduced measure viability. For specific probe, primer and calibrator sequences used in the method, see GENESEQ records AA293935-293965.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human genomic DNA polymorphic site sequence tag SEQ ID NO:384.
                                                                                                                                                             Score 13.2; DB 21; Length 27;
Pred. No. 5.6e+02;
0; Mismatches 3; Indels (
                                                                                                 Sequence 27 BP; 5 A; 7 C; 7 G; 8 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 15; 141pp; English.
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                                                                                                                                                                                                                                                                                                                                                                  AAA79014/c
ID AAA79014 standard; DNA; 31 BP.
                                                                                                                                                             66.0%;
ilarity 83.3%;
Conservative
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                                                                                                                                                                                                                                             3 ttgctagatgctaggtat 20
                                                                                                                                                                                                                                                                     2 tcgctacatgctaggcat 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AFFY-) AFFYMETRIX INC.
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                                                                                                                                                               Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shah N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EP1024200-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                              AAA79014;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a number of phosphorothicate antisense sequences to the human focal adhesion kinase (FAK) protein. This protein is involved in integrin-mediated signal transduction, and is implicated in cancer, particularly colon, breast and oral tumours, embryonic development disorders, angiogenic disorders and wound healing. The antisense sequences, including the one shown here, can be used in the
                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antisense compounds for inhibiting focal adhesion kinase expression, especially useful for inhibiting retinal neovascularization, or for diagnosing and treating e.g. colon cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; focal adhesion kinase; FAK; signal transduction; cancer; embryonic development disorder; angiogenic disorder; wound healing; antisense; phosphorothioate; ss.
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  Length 31;
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                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human focal adhesion kinase antisense sequence #26.
66.0%; Score 13.2; DB 21;
75.0%; Pred. No. 5.7e+02;
ive 1; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65.0%; Score 13; DB 22; L 100.0%; Pred. No. 6.7e+02; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15 BP; 4 A; 2 C; 4 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Column 25; 30pp; English.
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                                                                                                                                                                                                                                                                                                 AAC65560 standard; DNA; 15 BP
                                                                                                          1 ttttgctagatgctaggtat 20
                                                                                                                                         24 TTCTGCTCRATGCTAGAGAT 5
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                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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Best Local Similarity 100.
Matches 13; Conservative
                                                        15; Conservative
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AAZ99288;

Synthetic.

Key

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The present sequence represents a fragment from a clone of a method for including the 3'-untranslated region of a DNA molecule comprising KIAAO111. specification describes a method for removing the 3'-untranslated region of a DNA molecule comprises providing an open reading frame (ORF). The method comprises providing a DNA molecule having an ORF and a 3'-untranslated region, the DNA having a 5' overhang and a blunt end at the 3' end, and treating the DNA molecule with a 3'-5' exonuclease followed by a single-stranded used to produce RNA-protein fusion libraries. The fusion libraries can be used for the identification of protein-protein interactions, identification of drug targets, and hybridisation to solid supports to erreate protein chips (or beads). The RNA-protein molecules may be arranged in spatially defined arrays on the protein chips to carry out large scale screening for protein or compound identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Producing nucleic acids lacking 3'-untranslated regions to optimise production of fusion proteins, used to produce fusion libraries for identification of protein:protein interactions and drug targets for the production of protein chip:
                                                                                                                                                                                                            a
"an unspecified number of bases are present
between these nucleotides"
Nucleotide sequence of a clone from a RNA-protein fusion library.
                                             RNA-protein fusion; protein-protein interaction; drug target;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Promoter; nuclear encoded plastid RNA polymerase; NEP; rpoB; chloroplast; transgenic plant; maize; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 12.6; DB 21;
Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 36 BP; 6 A; 9 C; 10 G; 11 T; 0 other;
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                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Fig 14; 52pp; English.
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AAV99615/c
XX
AC AAV99615;
XX
AC AAV99615;
XX
DT 29-MAR-1999 (first entry)
XX
DE Maize rpoB gene primer rpoB#3.
XX
XX
XX
W Promoter; nuclear encoded plasti
XW Promoter; nuclear encoded plasti
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78.9%;
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Best Local Similarity 78.9
Matches 15; Conservative
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| ttttggatgaagctaggta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PHYL-) PHYLOS INC.
                                                                   protein chip; ss.
                                                                                                                                                                                                                                                                                                     WO200009737-A1
                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                 16-AUG-1999;
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                                                                                                                 Synthetic.
g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a fragment from a clone of a mak-protein fusion library comprising KIAA0111. specification describes a method for removing the 3'-untranslated region of a DNA molecule comprising an open reading frame (ORF). The method comprises providing a DNA molecule having an ORF and a 3'-untranslated region, the DNA having a 5' overhang and a blunt end at the 3' end, and treating the DNA molecule with a 3'-5' exonuclease followed by a single-stranded nuclease to remove the 3'-untranslated region. The products can be used for the identification of protein-protein interactions, identification of drug targets, and hybridisation to solid supports to create protein chips (or beads). The RNA-protein molecules may be arranged in spatially defined arrays on the protein chips to carry out
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Producing nucleic acids lacking 3'-untranslated regions to optimise production of fusion proteins, used to produce fusion libraries for identification of protein:protein interactions and drug targets for the production of protein chips.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                     a "an unspecified number of bases are present between these nucleotides"
                                                                                         Nucleotide sequence of a clone from a RNA-protein fusion library
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                                                                                                                                    fusion; protein-protein interaction; drug target;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       large scale screening for protein or compound identification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 36 BP; 6 A; 9 C; 10 G; 11 T; 0 other;
                                                                                                                                                                                                                                                   Location/Qualifiers
18..19
/*tag= a
/note= "an unspecifie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Fig 14; 52pp; English.
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                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-224362/19.
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                                                                                                                                      RNA-protein fusio
protein chip; ss.
                                                                                                                                                                                                                                                                                                                                                                                                 WO200009737-A1.
                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-AUG-1998;
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                                           03-JUL-2000
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Gaps

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Indels

AAZ99289;

AAZ99289 ID AAZ9: XX AC AAZ9: XX DT 03-JI

Query Match

Best Loc Matches

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Length 36;

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The present invention relates to the use of apoptotic genes in the the production of transgenic plants with improved resistance characteristics. The present sequence is the mutagenic PCR primer Bcl2-3. This primer was used with primer Bcl2-5 (AAA48984) to introduce a 5' Nco1 site and a 3' Xbar site in the human apoptotic gene bcl-2. Specifically the primer introduced an Ala residue between the Met (position 1) and His (position 2) residues of the native protein. The altered bcl-2 sequence was used in the creation of the final vector used to transform plants. The improved resistance characteristics of the plants helps protect against bacterial, viral and other pathogens. Resistance to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-terminal transport polypeptide; insect pest control; cell cycle; Autographa californica multinucleocapsid nuclear polyhedrosis virus; AcMNPV; occlusion derived virus; ODV; 66 kD envelope protein; ODV-866; membrane protein; intranuclear viral-induced microvesicle; GFP; URF-13; beta-galactosidase; b-gal; green fluorescent protein; marker; primer; polymerase chain reaction; PCR; amplify; ss.
                                                                                                   Transgenic plants with improved resistance characteristics comprising nucleic acids encoding apoptotic proteins \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reverse primer amplifies fragment encoding ODV-E66 residues 1-23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62.0%; Score 12.4; DB 21; Length 27; 92.9%; Pred. No. 1.5e+03; ive 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated transport polypeptide from AcMNPV - can direct localisation of desired proteins to occlusion derived virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 27 BP; 2 A; 5 C; 8 G; 12 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                 abiotic challenges may also be conferred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Summers MD
                                                                                                                                                               Example 3; Page 58; 109pp; English.
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95US-0000955
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 tttttctagatgct 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ttttgctagatgct 14
                                                          WPI; 2000-365634/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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                   Dickman MB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The 5' nucleotide of the primer corresponds to nucleotide 21394 of the complementary strand of the maize plastid genome sequence. The primer was designed to add a Xhol restriction site downstream of an amplified rpoB fragment following PCR amplification. The PCR product was cloned into vector pBSKS+ and used to generate protecting RNA for use in in vitro capping experiments. The invention provides isolated rpoB, atpB, clpP and 16S rDNA NEP and PEP promoter elements (see AAV99569-99) useful for producing exogenous proteins of interest in plant plastids.
                                                                                                                                                                                                                                                                                                                                                                                       Isolated nuclear-encoded plastid RNA polymerase promoter sequences useful for expressing exogenous protein in plant plastids such as chloroplasts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mutagenic PCR primer Bcl2-3 targeted to anti-apoptotic gene bcl-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This is the nucleotide sequence of maize rpoB gene primer rpoB#3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62.0%; Score 12.4; DB 20; 92.9%; Pred. No. 1.5e+03; ive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 27 BP; 9 A; 5 C; 6 G; 7 T; 0 other;
                                                                                                                                                                                                                                                                (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 17; 79pp; English.
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99US-0138303.
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Best Local Similarity 92.9
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                         Maliga P, Silhavy D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCR primer; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 TIGCTAGATTCTAG
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                                                                           W09855595-A1
                                                                                                                                                           03-JUN-1998;
                                                                                                                                                                                                    12-SEP-1997;
03-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-OCT-1999;
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09-JUN-1999;
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                 Synthetic.
                                        Zea mays.
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RESULT 14 AAA48985

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Gaps

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The sequences given in AAT59548-49 are primers which were used to amplify the sequence encoding residues 1-23 of Autographa californica multi- nucleacopsia nuclear polyhedrosls virus (ACMNPV) occlusion derived virus (ODV) 66 kD envelope protein (ODV-E66). ODV-E66 is an integral membrane protein of the ODV envelope. In an infected cell nuclear, ODV-E66 is present in the intranuclear viral-induced microvesicles and ODV envelope, providing evidence that the microvesicles microvesicles in mimediate precursor in the assembly of the ODV envelope. In infected cells, ODV-E66 localises to the ODV envelope. The ambranes of the nuclear envelope and cytoplasmic membranes in close juxtaposition to the nuclear envelope. The amplified sequence encodes the N-terminal, target sequence domain of ODV-E66. The target sequence may be used to target beta galactosiaase (b-gal), green cluorescent protein (GFP) and URF-13 to the membranes of the nuclear envelope which are further transported into the intranuclear correction envelope. The target protein for one of proteins to the ODV envelope and intranuclear microvesicles. It can be used for insect pest control, for therapeutic applications, e.g. correction proteins to the ODV envelope and intranuclear microvesicles. Correction proteins to the ODV envelope and intranuclear microvesicles. Correction proteins to the ODV envelope and intranuclear microvesicles. The correction proteins to the oDV envelope and intranuclear microvesicles. Correction proteins to the oDV envelope and intranuclear microvesicles. Correction proteins to the oDV envelope and intranuclear microvesicles. The membrane which will alter the cell cycle and for diagnostics, e.g. to insert a marker specific for a disease or abnormality into a cell tissue correction manifesting such abnormalities.
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Sequence 29 BP; 5 A; 3 C; 6 G; 15 T; 0 other;

ö Gaps ó Ouery Match 61.0%; Score 12.2; DB 18; Length 29; Best Local Similarity 82.4%; Pred. No. 1.9e+03; Matches 14; Conservative 0; Mismatches 3; Indels (

3 ttgctagatgctaggta 19 ö g

Search completed: October 2, 2001, 16:18:38 Job time: 15482 sec

Reverse PCR primer Human MTS1Elbeta g

Human multiple tum Human MTS1E1-beta

PCR primer for PCR primer for

Nucleotide sequenc Human MTS1El-beta

Reverse primer #1. Human catenin-bind

Reverse primer use

Human catenin-bind

HIV packaging cons pHP-1d1.28 WT nucl

Human KDR primer

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Post-processing:

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score:

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plasmid pBS-HĪV ol HIV anti-viral oli Human focal adhesi

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DGH gene 3' antise
MHC class I allele
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MHC CW3 cDNA forwa
Probe EF-4 for HIV
Probe EF-7 for HIV
HIV-1 proviral DNA
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Hammerhead ribozym
Primer for HIV RNA
PCR primer used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antisense compounds for inhibiting focal adhesion kinase expression, especially useful for inhibiting retinal neovascularization, or for diagnosing and treating e.g. colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; focal adhesion kinase; FAK; signal transduction; cancer; embryonic development disorder; angiogenic disorder; wound healing; antisense; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                           Human focal adhesion kinase antisense sequence #6.
                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                 AAQ49810
AAQ85851
AAQ85781
AAQ85745
                                                                                                                                                  AAZ31530
AAZ11016
         AAV53849
AAV11268
AAV70613
AAA95647
AAA11178
AAA39383
AAA48786
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AAC88772
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AAC88771
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AAV34760
AAQ34171
AAZ48824
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AAV64682
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 99US-0377310.
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                                                                                                                                                                                                                                                                                                                                                                       AAC65540 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
 (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaarde WA;
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19-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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Monta BP,
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RESULT
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CaMV Calibrator pr
Human focal adhesi
c-fos position 339
PCR primer 2 for a
Human Fas signal s
PCR primer for 1-2
Human tumour suppr
Multiple tumour su
Human MTSIE1-beta
                                                          Search time 876.95 Seconds (without alignments)
14.320 Million cell updates/sec
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                                                                                                                                                                                                                                                                                   (SIDSB/)qqdata/qeneseq/,qeneseqn/NA1982.DAT:*
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        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                            Potal number of hits satisfying chosen parameters:
                                                                                                                                                            730101 segs, 313950809 residues
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                                                           2, 2001, 16:18:37
                                                                                                                                                                                                                       Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                           - nucleic search, using sw model
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AAC93950
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AAT87799
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                                                                                                                                 IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Match Length
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227
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12.8 12.8 12.8 12.6 12.6

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Score

Result š presence of

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of the extracted target nucleic acid. The reaction in the presence of the calibrator nucleotide permits quantitation of the calibrator columber. The reaction in the presence of both permits calculation of the total number of target templates and calibrator, allowing
                                                                                                                                                                                                                                                                                                                                                                                                     AAC65560
                                                                                                                                                                                                                                                                                                                                                                                        RESULT
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                          The present invention describes a number of phosphorothioate antisense sequences to the human focal adhesion kinase (FAK) protein. This protein is involved in integrin-mediated signal transduction, and is implicated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quantitative detection of nucleic acids, based on the use of a calibrator, suitable primers and probes, and a nucleic acid polymerase with 5'-3' nuclease activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sample which uses a calibrator, suitable primers and probes, and a nucleic acid polymerase with 5-3' nuclease activity is described. The method comprises adding a calibrator nucleotide to the sample, the calibrator nucleotide having the same sequence as the target with the calibrator nucleotide having the same sequence as the target with a probe labeled with a reporter and quencher, or which hybridize with a probe and with 2 or more primers. These regions have a different, randomized nucleotide sequence and a similar Tm. Then extracting the calibrator and target nucleotides from the sample. Probes and primers are then added to the extracted sample/calibrator
                                                                     in cancer, particularly colon, breast and oral tumours, embryonic development disorders, anglogenic disorders and wound healing. The antisense sequences, including the one shown here, can be used in the treatment of all of these.
                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detection; identification; PCR; polymerase chain reaction; probe; primer; callbrator; diagnosis; pathogen; virus; bacteria; HHV-6; HHW-7; HHV-8; human herpes virus; human immunodeficiency virus; HIV; AIDS; acquired immune deficiency syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mixture and PCR is performed. Reaction in the presence of the target nucleic acid specific probe permits quantitation of the copy number
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                                                                                                                                                                                    DB 22; Length 20; 0.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SANR-) FOND CENT SAN RAFFAELE DEL MONTE TABOR.
                                                                                                                                           Sequence 20 BP; 4 A; 4 C; 5 G; 7 T; 0 other;
                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                      100.0%; Score 20; 100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 13; 39pp; English.
Claim 3; Column 23; 30pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium tuberculosis; ss.
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Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
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calculation of the percentage of calibrator recovery. The method may be used for the diagnosis of viral and any other pathogenic agents in body fluids, and to monitor safety and/or genetic composition of waters, foods, and plant species used in the alimentary field. The method is used to quantitatively detect the genomic nucleic acid of human herpes virus (HHV)-6, HHV-7, HHV-8 and human immunodeficiency virus (HIV). The method provides an enhanced sensitivity, accuracy, and precision and a reduced measure viability. For specific probe, primer and calibrator sequences used in the method, see GENESEQ records AA23935-293965.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antisense compounds for inhibiting focal adhesion kinase expression, especially useful for inhibiting retinal neovascularization, or for diagnosing and treating e.g. colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; focal adhesion kinase; FAK; signal transduction; cancer; embryonic development disorder; angiogenic disorder; wound healing; antisense; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human focal adhesion kinase antisense sequence #26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 15.8; DB
Pred. No. 28;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 27 BP; 5 A; 7 C; 7 G; 8 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 15 BP; 4 A; 2 C; 4 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Column 25; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79.0%;
89.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0377310.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0377310.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ctagatgctaggtatctgt 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 ctacatgctaggcatctgt 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAC65560 standard; DNA; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 79.0
Best Local Similarity 89.5
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Monia BP, Gaarde WA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-006141/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US6133031-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-0CT-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAC65560;
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AND PERSONS

AAC65541;

AAC65541

RESULT

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The sequences given in AAQ50202-70 are oligonucleotides which were used to illustrate the method of the invention for the mutagenesis of inhibitory/instability signals (INS). Mutation in an INS produced using oligonucelotides such as these, increases the stability and/or utilisation of mRNA without changing its protech coding capacity, or if the sequence is changed, its function is maintained. Other genes encoding such mRNA molecules include growth factor, interferon,
                                                                           HIV-1; p17gag; inhibition; gag; M1; M2; M3; M4; silent mutation; mRNA vector; p17; point mutation; p17M1234; HLtat cells; gene replacement; inhibitory/instability signal; INS; stability; utilisation; vaccine; interferon; interleukin; fos proto-oncogene protein; growth factor; env; attenuated; AIDS-related disease; latent infection; gene therapy; Human immunodeficiency virus type 1; p24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diseases by preventing HIV from establishing a latent infection, as is possible using the INS, and thus escaping immune system surveillance. The constructs may also be according to the constructs and the constructs are become as a construct to the constructs and the constructs are become as a construct to the constructs and the constructs are become as a construct to the constructs and the constructs are become as a construct to the constructs are also become as a construct to the constructs are also become as a construct to the construct to th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Receptor tyrosine kinase; vascular endothelial cell growth factors;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The constructs may also be used in gene therapy for
nt by homologous recombination with a target gene in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  encoding such mRNA molecules include growth factor, interferon, interleukin, fos proto-oncogene protein and HIV env and gag gene proteins. Nucleic acid constructs in which INS function has been
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eliminating inhibitory-instability regions in mRNA to improve stability and expression - by making multiple point mutations within A-T rich regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCR primer 2 for a novel type III RTK gene - the KDR gene
                        c-fos position 3392-3434 INS mutagenic oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 13.4; DB 14.
Pred. No. 5.1e+02;
0; Mismatches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 43 BP; 9 A; 11 C; 5 G; 18 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer; tumour; diagnosing; monitoring; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3; Page 69; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                             long terminal repeat; LTR; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.0%;
93.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92US-0858747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       See also AAQ50200-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (USSH ) US SEC DEPT HEALTH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pavlakis GN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 gatgctaggtatctg 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19 GAAGCTAGGTATCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1993-336919/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene replacement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                            WO9320212-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                     14-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Felber BK,
                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ28274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ28274
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequences to the human focal adhesion kinase (FAK) protein. This protein is involved in integrin-mediated signal transduction, and is implicated in cancer, particularly colon, breast and oral tumours, embryonic development disorders, angiogenic disorders and wound healing. The antisense sequences, including the one shown here, can be used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a number of phosphorothioate antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antisense compounds for inhibiting focal adhesion kinase expression, especially useful for inhibiting retinal neovascularization, or for diagnosing and treating e.g. colon cancer
                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; focal adhesion kinase; FAK; signal transduction; cancer; embryonic development disorder; angiogenic disorder; wound healing; antisense; phosphorothioate; ss.
                                                                              ó
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0
            DB 22; Length 15;
69;
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                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human focal adhesion kinase antisense sequence #7
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75.0%; Scor.
100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 75.0%; Score 15; Local Similarity 100.0%; Pred. No. les 15; Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Column 23; 30pp; English
                                                                                                                                                                                                                                                                                                                                              BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВР.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0377310.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0377310.
                                                                                                                                                                                                                                                                                                                                           AAC65541 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ50213 standard; DNA; 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antisense sequences, inclu
treatment of all of these.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-MAY-1994 (first entry)
                                                                              Conservative
                                                                                                                                    3 agatgctaggtatct 17
                                                                                                                                                                                       1 agatgctaggtatct 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ctagatgctaggtat 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaarde WA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-006141/01.
                  Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US6133031-A.
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Monia BP,

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Indels

AAQ50213;

Z X X E

AAQ50213/c

RESULT

Query Match

Best Loca Matches

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Length 43;

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This oligonucleotide Fas1 is used for the generation of a Fas signal sequence for post translational modification of a novel human Fas ligand (hFasL) fusion protein. This novel protein comprises of hFasL or a truncated or functionally equivalent variant that retains the Fas truncated to Incorporate inducing properties of hFasL. This is liked to Glycosyl-Phosphatidyl inositol (GFI) at its C-terminus. DNA encoding hFasL amino acids, a linker sequence and a human Fas signal sequence derived from human CDIG. The fusion protein can be produced by culturing COS cells transformed by the expression vector product. This novel fusion protein can incorporate its lipid tail can be produced. This novel fusion protein can incorporate its lipid tail can be protein on the cell surface. This can bind to Fas receptor present on other cells, particularly T lymphocytes, and thereby induce their apoptosis. This is useful for preventing or treating tissue or organ allograft or xenograft rejection. This provides a specific treatment for activated T lymphocytes, i.e. only for T lymphocytes that expresses the Fas antigen, which attack the transplanted tissue or organ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1-2-rhamnosyl-transferase; hesperidin conversion; orange peel; NHDC; flavone-7-0-glucosidase-2"-0-rhamnosyl-transferase; flavanoid glycoside; sweetener; neohesperidin dihydrochalcone; grapefruit; pomelo;
                                                                                                       Human Fas Ligand fused to carboxy-terminal glycophospholipid - useful for preventing or treating tissue or organ allograft or xenograft rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCR primer for 1-2-rhamnosyl-transferase cDNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 12.8; DB 18
Pred. No. 9.9e+02;
); Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 24 BP; 3 A; 5 C; 9 G; 7 T; 0 other;
                                                                                                                                                                                          Example 1; Page 11; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (YEDA ) YEDA RES & DEV CO LTD. (ISRA ) ISRAEL MIN AGRIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gressel J, Eyal Y, Fluhr R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64.0%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                citrus fruit; PCR primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-JAN-2000; 2000WO-IL00038.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
AAA37664/c
ID AAA37684 standard; DNA; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 64.0
Best Local Similarity 87.5
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 agatgctggggatctg 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-289283/26
(SANO ) SANDOZ-ERF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200043490-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-JUL-2000
                                      Buehler T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Citrus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA37684;
g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This PCR primer is designed from a region of the kinase domain 5' to the kinase insert domain of a consensus sequence of known type III str gene catalytic domains. It is used with AAQ28273 to amplify human endothelial cDNA producting 251 and 420 bp products. Sequencing of the 251bp product revealed a novel sequence containing both primers but with little homology to known tyrosine kinases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human Fas ligand; hFasL; fusion protein; truncated; T lymphocyte;
glycosyl-phosphatidylinositol; GPI; treatment; allograft; xenograft;
Fas signal sequence; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding type III receptor tyrosine kinase - useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human Fas signal sequence generating oligonucleotide Fasl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65.0%; Score 13; DB 13; Length 38
68.4%; Pred. No. 8.1e+02;
ive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 38 BP; 5 A; 10 C; 8 G; 10 T; 5 other;
                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 16; Fig 2; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnosing the onset of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAT97310 standard; DNA; 24 BP
                                                                                                                                                                                                                                                                                                          (AMCY ) AMERICAN CYANAMID CO.
                                                                                             /*tag= a
/mod_base= I
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                                                                                                                                                                                                                                                                      91US-0657236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                   Terman BI;
                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1992-316117/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
nes 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SANO ) SANDOZ
(SANO ) SANDOZ
                                                                       modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                  Homo sapiens
                                                                                                                                                                                                                               20-FEB-1992;
                                                                                                                                                                                                                                                                      22-FEB-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-NOV-1996;
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                                                                                                                                                                                                                                                                                                                                                   Carrion ME,
                                                                                                                                                    W09214748-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT97310;
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Best Loc Matches

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Sequences AAZ87797-812
                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detecting polymorphism associated with cancer pre:disposition - also DNA, vectors and host cells e.g. for gene or protein replacement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         An individual can be diagnosed as having a predisposition to cancer by detecting an alteration in the wild type multiple tumour suppressor (MTS) gene, using gene probes which hybridise to the MTSIElbeta gene OFF (amplified using the PCR primers AAT00719-21). The above assay can also be used in the diagnosis and prognosis of melanoma, lymphoma, leukaemia and pancreas, breast and thyroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Multiple tumour suppressor; MTS1Elbeta; cancer; diagnosis; assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Multiple tumour suppressor 1 exon 1 beta gene PCR reverse primer.
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                                                                                                                      Length 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         predisposition; melanoma; leukaemia; lymphoma; prognosis; pancreas; breast; thyroid; PCR reverse primer; exon 1; ss
                                                                                                                                                              Indels
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may be used for gene therapy and protein therapy. Seq
represent PCR primers for sequencing the TMPRSS2 CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63.0%; Score 12.6; DB 16; 78.9%; Pred. No. 1.2e+03; tive 0; Mismatches 4;
                                                                                                                    Score 12.8; DB 21;
Pred. No. 1e+03;
0; Mismatches 2;
                                                          Sequence 39 BP; 9 A; 11 C; 7 G; 12 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 21 BP; 5 A; 3 C; 7 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Skolnick MH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 10; Page 64; 148pp; English.
                                                                                                                                                                                                                                                                                                                                            BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kamb A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94US-0251938.
94US-0214582.
94US-0215086.
94US-0215087.
                                                                                                                    64.0%;
87.5%;
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                                                                                                                                                                                                                                                                                                                                          AAT00720 standard; cDNA; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94US-0227369
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                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                  Query Match 64.0 Best Local Similarity 87.5 Matches 14; Conservative
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                                                                                                                                                                                                   20
                                                                                                                                                                                                                                         30 ATGATAGGTATCCGTC 15
                                                                                                                                                                                                   5 atgctaggtatctgtc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1995-344626/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches .15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-MAR-1994;
18-MAR-1994;
18-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancers, etc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
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                                                                                                                                                                                                             to a polynucleotide encoding a polypeptide with flavone-7-0-glucosidase-2"-0-rhamnosyl-transferase catalytic activity (such as 1-2-rhamnosyl-transferase). The enzyme is useful for converting hesperidin from orange peels to the sweetener neohesperidin dihydrochalcone (NHDC), and to provide genetically modified plants of the citrus genus including an antisense or sense (for co-suppression) construct, or knockout integrated construct, to provide less bitter grapefruits, pomelos and other citrus fruits containing flavanoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The TWPRSS2 polynucleotides and polypeptides can be used in methods for diagnosing and prognosing predisposition to cancer in humans. The polypeptides may also be used in assays to screen for compounds with anti-cancer or therapeutic properties. The polypeptides are also useful for rational drug design. The TWPRSS2 polynucleotides and polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention provides a new tumour suppressor gene, designated TMPRSS2
                                     Polynucleotide encoding a flavone-7-0-glucosidase-2"-0-rhamnosyl-transferase, useful for converting hesperidin from orange peels to the sweetener neohesperidin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tumor suppressor TMPRSS2 used for the diagnosis and prognosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumour suppressor gene; TMPRSS2; cancer; human; drug design;
gene therapy; protein therapy; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human tumour suppressor TMPRSS2 cDNA sequencing primer 1B.
                                                                                                                                                                              This sequence represents a PCR primer for DNA encoding a 1-2-rhamnosyl-transferase. The invention relates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 12.8; DB 21;
Pred. No. 1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 27 BP; 11 A; 6 C; 5 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tavtigian SV, Teng DHF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; Page 53; 89pp; English.
                                                                                                                                       Example; Page 24; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAZ87799 standard; DNA; 39 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ctagatgctaggtate 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27 CTTGATGCTTGGTATC 12
                                                                                                 dihydrochalcone (NHDC)
WPI; 2000-499220/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-170914/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                    glycosides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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AAQ99928;

RESULT 11 AAQ99928

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Primer; polymerase chain reaction; PCR; amplification; Elbeta; human; multiple; tumour; suppressor; MTS1; cancer; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is primer for the PCR amplification of the human multiple tunnour suppressor gene 1 Elbeta (MTS1Elbeta), useful in cancer diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Multiple tumour suppressor; MTS; human; cancer; hybridisation; somatic mutation; gene therapy; PCR; primer; amplification; ss.
                                                                                                          Human multiple tumour suppressor gene 1 Elbeta reverse primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human mutant multiple tumour suppressor gene sequences - for production of recombinant mutant polypeptide(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63.0%; Score 12.6; DB 18;
78.9%; Pred. No. 1.2e+03;
Live 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 21 BP; 5 A; 3 C; 7 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cannon-Albright LA, Kamb A, Skolnick MH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 10; Columns 87-88; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleotide sequence of PCR primer 13.
 AAT72309 standard; DNA; 21 BP.
                                                                                                                                                                                                                                                                                                                                              95US-0474177.
94US-0214582.
94US-0215086.
94US-0215087.
94US-02515087.
                                                                                                                                                                                                                                                                                                               94US-0214582.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21
                                                                     10-SEP-1997 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 63.0
Best Local Similarity 78.9
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 ctagaggcgaattatctgt
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14-APR-1994;
01-JUN-1994;
17-MAR-1995;
                                                                                                                                                                                                                                                                                                             18-MAR-1994;
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                                                                                                                                                                                                                                                                                                                                                                 18-MAR-1994;
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                                                                                                                                                                                                                                                                         29-APR-1997
                                                                                                                                                                                                    Synthetic.
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                                     AAT72309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The cDNA sequences encoding several multiple tumour suppressor (MTS) polypeptides have been isolated and sequenced, using various sequencing and amplification primers such as the primer represented in this sequence. MTS polypeptide-encoding cDNAs and mutants of these are useful for the diagnosis or prognosis of human cancer. Germ-line mutations of MTS cDNAs can be used for diagnosing predisposition to melanoma, leukaemia, astrocytoma, glioblastoma, lymphoma, glioma, Hodgkin's lymphoma, CLL and cancers of the pancreas, thyroid, ovary, uterus, testis, kidney, stomach and rectum. The wild-type gene is useful for gene therapy and MTS polypeptides may also be used for protein replacement therapy. Also the polypeptides or cells contg. an altered MTS gene are useful for screening for potential cancer therapeutics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wild-type multiple tumour suppressor (MTS) gene and mutant sequences - useful in diagnosis, prognosis and therapy of human cancer, e.g. melanoma or leukaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                  Multiple tumour suppressor; El-alpha; diagnosis; cancer; leukaemia; astrocytoma; glioblastoma; Hodgkin's lymphoma; melanoma; glioma; gene therapy; chronic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 21 BP; 5 A; 3 C; 7 G; 6 T; 0 other;
                                                                                                                                                                                                Human MTS1E1-beta PCR amplification primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 10; Page 64; 156pp; English.
                                                                                         BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     940S-0251938.
940S-0214581.
940S-0215088.
940S-02259.
940S-0215086.
940S-0215086.
                                                                                      AAQ99928 standard; cDNA; 21
                                                                                                                                                                                                                                                                                                                                                                                                                     95WO-US03316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MYRI-) MYRIAD GENETICS INC.
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                                                                                                                                                                (first entry)
3 ctagaggcgaattatctgt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 78.9
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1995-344401/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-MAR-1994;
14-APR-1994;
18-MAR-1994;
                                                                                                                                                                                                                                                                                                                                              W09525429-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-1994;
18-MAR-1994;
18-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                     17-MAR-1995;
                                                                                                                                                              07-MAY-1996
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                                                                                                                                                                                                                                                                                                             Synthetic.
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Kamb A;

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Gaps

ó:

01-SEP-1998

Query Match

ò g RESULT 12 AAT72309

Length 21; Indels

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Primers AAV11267-V11269 are used in the isolation of the human multiple tumour suppression protein, MTS1E1-beta. The MTS gene locus is also referred to as the familial melanoma (MLM) gene locus, located on human chromosome 9921. Germ line mutations in MTS genes can be used in the diagnosis of predisposition to cancers, e.g. melanoma, leukaemia, astrocytoma, gliboblastoma, lymphoma, glioma, Hodgkin's lymphoma, CLL, and cancers of the pancreas, breast, thyroid, ovary, uterus, testis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; multiple tumour suppressor 1 gene; MTS1; cancer; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse multiple tumour suppressor gene segment - useful for primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63.0%; Score 12.6; DB 19; Length 21; 78.9%; Pred. No. 1.2e+03; ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                              DNA specific for Multiple Tumour Suppressor 1E1-beta gene useful for the diagnosis of cancers related to MTS1E1-beta mutation(s) and their treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reverse PCR primer used to amplify human MST1E1-beta gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 21 BP; 5 A; 3 C; 7 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                         Example 10; Column 87-88; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAV70613 standard; DNA; 21 BP.
               94US-0214582.
94US-0215086.
94US-0215087.
                                                                     94US-0227369.
94US-0251938.
95WO-US03316.
                                                                                                                                                (MYRI-) MYRIAD GENETICS INC.
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95US-0487033,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  kidney, stomach and rectum
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                                                                                                                                                                                                                          WPI; 1998-250421/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-044585/04.
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               18-MAR-1994;
18-MAR-1994;
18-MAR-1994;
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07-JUN-1995;
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17-MAR-1995;
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                                                                                                                                                                                      Kamb A;
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οy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  This is the nucleotide sequence of a PCR primer used for amplification in the method of the invention involving the use of the multiple tumour suppressor (MTS) gene, to diagnose and treat cancer. The MTS gene is useful in the diagnosis and prognosis of human cancer, e.g. by standard nucleic hybridisation techniques, of patient samples. The mutated sequences are those that are present in somatic mutations of the gene in cancers. The vectors can be used for gene therapy strategies to replace function of mutated to protein in patients. These can also be used to construct protein mimetics, also for therapeutic strategies. In addition the expression constructs can also be used for recombinant production of MTS. Recombinant MTS can be used to screen for drugs to be used for cancer therapy, and the protein itself may also be used to restore MTS function in a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WTS1E1-beta; multiple tumour suppressor; diagnosis; cancer; germ-line mutation; familial melanoma locus; MLM; predisposition; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                   Nucleic acids based on multiple tumour suppressor, MTS, sequences useful as hybridisation probes, primers and recombinant production Of MTS in the diagnosis and treatment of cancers related to MTS mutation(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63.0%; Score 12.6; DB 19; Length 21; 78.9%; Pred. No. 1.2e+03; Live 0; Mismatches 4; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 21 BP; 5 A; 3 C; 7 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                   Example 10; Column 87-88; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human MTS1E1-beta PCR primer #2.
                                                                   94US-0214582.
94US-0215086.
94US-0215087.
94US-0227369.
94US-0251938.
95WO-US03316.
               95US-0480810
                                                   95US-0480810
                                                                                                                                                                                                        (MYRI-) MYRIAD GENETICS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Best Local Similarity
Matches 15; Conserv
                                                                                   18-MAR-1994;
18-MAR-1994;
14-APR-1994;
01-JUN-1994;
17-MAR-1995;
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             07-JUN-1995;
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                                                                                                                                                                                                                                            Kamb A;
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AAV11268

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PCR primers AAV70612-14 were used to amplify nucleic acid encoding a human multiple tumour suppressor 1E1-beta (MTS1E1-beta) protein. Primers designed from the gene can be used to design primers to detect anormalities i.e. polymorphisms which may predispose towards malignancies such as melanoma, leukaemia, astrocytoma, lymphoma, glioma, as well as tumours of e.g. the breast, thyroid, pancreas, uterus and kidneys.
                                                                                                                                                                                                                                                                                                                                                                                            Example 11; Column 48; 80pp; English.
\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset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Sequence 21 BP; 5 A; 3 C; 7 G; 6 T; 0 other;

Query Match 63.0%; Score 12.6; DB 20; Length 21; Best Local Similarity 78.9%; Pred. No. 1.2e+03; Matches 15; Conservative 0; Mismatches 4; Indels (1 ctagatgctaggtatctgt 19 |||||| || |||||||| 3 ctagaggcgaattatctgt 21 ò g

Search completed: October 2, 2001, 16:18:38 Job time: 15482 sec

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Human gene single
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B-cell mRNA ribozy
NGF SELEX clone ha
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Bacteriophage 96 0
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Human gene signatu
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Brassica sp. polym
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ss circular oligo
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                                                                                                                                                                                                                        Human native inter
SELEX identified 1
                                                                            Human polymorphic
Human TUB gene 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antisense compounds for inhibiting focal adhesion kinase expression, especially useful for inhibiting retinal neovascularization, or for diagnosing and treating e.g. colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; focal adhesion kinase; FAK; signal transduction; cancer;
embryonic development disorder; angiogenic disorder; wound healing;
antisense; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human focal adhesion kinase antisense sequence #5.
                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
          AAZ30696
AAT42899
AAV50562
AAV50563
                                                                                   AAT96662
AAA94657
AAT25405
                                                                                                                                                                                                                      AAV64599
AAV14556
AAV79635
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AAT01299
                                                AAA68425
AAA68618
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AAT07685
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AAX19124
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                                                                                                                                                       AAF2224]
                                                                                                                                                                                                                                                                                                                                                                                                   BP.
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  AAC65539 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
  (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Monia BP, Gaarde WA;
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  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-AUG-1999;
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AAC65539;
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 RESULT
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Mismpla template s
Polymorphic fragme
MDV L1 cDNA primer
PCR primer for PG1
Human alpha-7 nico
PCR primer used to
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focal adhesi
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                                                                            (without alignments)
14.320 Million cell updates/sec
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                                                                 Search time 876.95 Seconds
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          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
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    nucleic search, using sw model

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AAC65559
AAV49869
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes new purified and isolated nucleic acids (i) encoding: (i) the A and B chains of a ricin-like toxin (II); and (ii) a heterologous linker, joining the two chains and including a cleavage recognition site for a disease-specific protease (III). Also described are: (I) plasmids or baculovirus transfer vectors that contain (I); and (2) recombinant protein (IV) consisting of the A and B chains of (III) joined by the specified linker. (IV), produced by expression of (I) in host cells, are used to inhibit or kill diseased cells that produce (III), particularly for treating cancers (e.g. leucocyte prodliferation; cancer of ovary, pancreas, breast or prostate; glioma) or infections caused by fungi, parasites (e.g. malaria) or viruses (e.g.
                     The present invention describes a number of phosphorothioate antisense sequences to the human focal adhesion kinase (FAK) protein. This protein is involved in integrin-mediated signal transduction, and is implicated
                                                           in cancer, particularly colon, breast and oral tumours, embryonic development disorders, angiogenic disorders and wound healing. The antisense sequences, including the one shown here, can be used in the
                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid encoding ricin-like toxin with an interchain linker
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e.g. killing selectively cancer or infected cells
                                                                                                                                                                                                                                                                                                                                                                                                         Ricin-like toxin; cancer; viral infection; parasitic infection; linker; B chain; A chain; protease; fungal infection: malaria; leucocyte proliferation; cytomegalovirus; herpes; hepatitis; rhinovirus; laryngeotracheitis; poliomyelitis; varicella zoster; cystic fibrosis; multiple sclerosis; ds.
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                                                                                                                                                               Score 20; DB 22; Length 20;
Pred. No. 0.68;
                                                                                                                                                                                                                                                                                                                                                                                  Human prostate-specific antigen linker regions of pAP-290.
                                                                                                                                                                                         0; Indels
                                                                                                                           Sequence 20 BP; 1 A; 7 C; 1 G; 11 T; 0 other;
                                                                                                                                                                                           Mismatches
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Claim 3; Column 23; 30pp; English.
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                                                                                                                                                                                                                                                                                                         AAX04289 standard; DNA; 36
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                                                                                                  treatment of all of these.
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Best Local Similarity 100.
Matches 20; Conservative
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30-APR-1997;
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cytomegalovirus (CMV), herpes, hepatitis, rhinovirus, laryngeotracheitis, poliomyelitis or varicella zoster), also cystic fibrosis and multiple sclerosis. Alternatively, (I) is used to express (IV) in vivo. (IV) is toxic specifically for (III)-expressing cells and does not depend for specificity on a cell-binding component. When used to treat virus-retrograde cells, transcytosis and cytotoxicity of (IV) are increased by retrograde translocation from endoplasmic reticulum to cytoplasm (which some viruses exploit to avoid immune detection), so selectivity and safety are further improved. (IV) are not toxic until chain A is released and this occurs only in target cells. The present sequence represents a nucleotide sequence from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a number of phosphorothioate antisense sequences to the human focal adhesion kinase (FAK) protein. This protein is involved in integrin-mediated signal transduction, and is implicated in cancer, particularly colon, breast and oral tumours, embryonic development disorders, anglogenic disorders and wound healing. The antisense sequences, including the one shown here, can be used in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; focal adhesion kinase; FAK; signal transduction; cancer; embryonic development disorder; angiogenic disorder; wound healing; antisense; phosphorothioate; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 15.2; DB 20;
Pred. No. 1.4e+02;
); Mismatches 3;
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Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 36 BP; 5 A; 9 C; 3 G; 19 T; 0 other;
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85.0%;
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Best Local Similarity
Matches 17; Conserv
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Matches

AAV49869 RESULT

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Enhanced LM609 grafted antibodies exhibiting selective binding affinity to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of angiogenesis, inflammatory diseases e.g. psoriasis, cancers and osteoporosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to enhanced LM609 grafted antibodies exhibiting selective binding affinity to alphavbeta_3 integrin or their functional fragments. The antibodies or their functional fragments can be used in the diagnosis and treatment of arginated diseases such as anglogenesis, inflammatory diseases (such as psociasis and chronic articular rheumatism), disorders associated with inappropriate or inopportune invasion of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ss; Ml3mp18; sequencing; target specificity; PCR; amplification; differential primer extension.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vessels (such as diabetic retinopathy, neovascular glaucome and cancer disorders such as tumours and Kaposi's sarcoma), retinal diseases (such as macular degeneration), restenosis and
                                                                                                                                                                                     LM609; grafted antibody; alphaVbeta_3 integrin; angiogenesis; inflammatory; cancer; retina; restenosis; osteoporosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 13.8; DB 22;
Pred. No. 6.5e+02;
); Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 33 BP; 4 A; 13 C; 2 G; 14 T; 0 other;
                                                                                                                                                 DNA encoding mutant VL CDR2 peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                           (MOLE-) APPLIED MOLECULAR EVOLUTION,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 42; 132pp; English.
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                                      AAF28225 standard; DNA; 33 BP.
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88.2%;
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                                                                                                             (first entry)
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                                                                                                                                                                                                                                           Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              osteoporosis
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Best Local 3
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                                                                                                                                                                                                                                                                                                              Vitaxin; antibody; variable region; heavy chain; light chain; integrin; LM609; inhibitor; integrin-mediated signal transduction; treatment; diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy; neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine; macular degeneration; osteoporosis; primer; V-L region; CDR; complementarity determining region; series
 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3 integrin - and related grafted antibodies based on murine monoclonal LM609, also related nucleic acid, used to treat, prevent or diagnose
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 Indels
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                                                                                                                                                                                                                                                                            LM609 grafted antibody V-L region CDR2 DNA fragment #2.
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Pred. No. 6.5e+02;
); Mismatches 2;
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 Mismatches
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88.2%;
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                                  Huse WD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-437472/37.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (IXSY-) IXSYS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAW76032.
                                                                                                                                                                                                                                       02-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9833919-A2.
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Best Local Simi
Matches 15;
15;
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                                                                                                                                                                                                       AAV49869;
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Length 33; Indels

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The invention provides polymorphic fragments of genes associated with hypertension. The nucleic acids including the polymorphic sites can be used as probes or primers for expressing variant proteins. Detection of the polymorphisms is useful in designing prophylactic and therapeutic regimes customized to underlying abnormalities. The polymorphisms can be used for association studies for hypertension, and in hypertension diagnostic assays. Where the polymorphisms have strong correlation with hypertension, within a gene, they are likely to have a causative role in hypertension. This information can be used to find the precise role of polymorphism in the disease, and this can be used to identify potential drugs which combat the disease. The polymorphisms can be tested for association with other disease e.g. agammaglobulinemia, diabetes inspidus, Lesch-Nyhan syndrome, muscullar dystrophy, wiskort-Aldrich syndrome, Fabrys disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrands disease, therefitery hemorrhagica telangiectasia, familial colonic polyposis, Ehers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria. The polymorphic forms can also be used in formatic polyposis.
                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acids containing polymorphisms used in the diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Marek's disease virus; MDV; vaccine; antisense; therapy; latency; tumor; primer; polymerase chain reaction; PCR; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 13.2; DB 21; Length 29;
Pred. No. 1.2e+03;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 29 BP; 11 A; 2 C; 12 G; 3 T; 1 other;
                                                                                                                                                                                                                                                            Chakravarti A, Haluska MK;
                                                                                                                                                           (AFFY-) AFFYMETRIX INC.
(UYCA-) UNIV CASE WESTERN RESERVE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 33; 53pp; English.
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75.0%;
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99EP-0250150
                                                                98US-0084641.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-DEC-1995 (first entry)
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Best Local Similarity 75.0
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                         WPI; 2000-107928/10
                                                                                                                                                                                                                                                                                                                                                                                                                           hypertension
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07-MAY-1999;
                                                            07-MAY-1998;
03-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9518860-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ97859;
                                                                                                                                                                                                                                                                Fan JB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ97859/c
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P X R B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B B X B X B B X B B X B B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The target nucleotide sequence was used to demonstrate a method for improving the priming specificity of a non-unique oligonucleotide primer. Preferably the oligonucleotide primer is modified by a radioactive element, a fluorescent modety or a blotin modety. The methods are used particularly for the sequencing of target DNA sequences. The methods using the priming specificity of a non-unique oligonucleotide primer by using differential extension of the primer with nucleotide primer by length discrimination against shorter extensions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome; Fabrys disease; familial hypercholesterolemia; hereditary spherocytosis; polycystic kidney disease; von Willebrands disease; forensic; human; tuberous sclerosis; hereditary hemorrhagica telangiectasia; familial colonic polyposis; osteogenesis imperfecta; porphyria; Ehlers-Danlos syndrome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Improving priming specificity of oligo:nucleotide primers - by using differential extension of the primer with nucleotide subsets and length discrimination against shorter extensions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                            a
"Unspecified amount of nucleotides not given
in specification"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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Pred. No. 1.1e+03;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 46 BP; 6 A; 19 C; 2 G; 19 T; 0 other;
                                                     Location/Qualifiers
20..21
/*tag= a
/note= "Unspecified a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mugasimangalam RC, Ulanovsky LE;
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Best Local Similarity 93.3%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                         97WO-US17305
                                                                                                                                                                                                                                                                                                                                                                                                                                                         96IL-0119342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (USAT ) US DEPT ENERGY
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Bacteriophage M13.
                                                                                          misc_feature
                                                                                                                                                                                                                                                            WO9814608-A1
                                                                                                                                                                                                                                                                                                                                                                                         30-SEP-1997;
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AAA04352/c RESULT

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The invention relates to a mammalian PGI gene and protein, and a set of PGI biallelic markers. The PGI polynucleotide and biallelic markers are used in a hybridisation assay, a sequencing assay, or in an allele-specific amplification assay for determining the identity of a nucleotide at a PGI-related biallelic marker. The methods can be used to detect and to assess the risk of developing cancer or prostate cancer. Barly-stage diagnosis of prostate cancer relies on prostate specific antigen (PSA) dosage. However, the effectiveness of this is limited due to its inability to discriminate between malignant and non-malignant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene; biallelic marker; PCR primer; PG1-related biallelic marker;
er; prostate cancer; diagnosis; therapy; prostate specific antigen;
                                                                        Marek's disease virus protein and its nucleotide sequence - used to protect chickens against Marek's disease and inhibit the establishment of latency and tumour cell development
                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                 The primers given in AAQ97859-60 were used for the PCR amplification of the upstream region of MDV L1 cDNA. The amplified fragment, Q2L1, was cloned into pBluescript KS+ for sequencing.
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                                                                                                                                                                                                                                                                            Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCR primer for PG1 biallelic markers 4-54-283 and 4-55-95.
                                                                                                                                                                                                                                                                                                         Indels
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Pred. No. 1.8e+03;
O; Mismatches 2;
                                                                                                                                                                                                                              Sequence 17 BP; 9 A; 2 C; 5 G; 1 T; 0 other;
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                Schat KA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 4; Page 354; 385pp; English.
                                                                                                                                    Example 1; Page 11; 42pp; English.
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                                                                                                                                                                                                                                                                         64.0%;
87.5%;
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Best Local Similarity 87.5
Matches 14; Conservative
              Ohashi K,
                                                                                                                                                                                                                                                                                                                                      5 cccttccgttattctt 20
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                                         WPI; 1995-255063/33.
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              O'Connell PH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer;
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The present invention describes an isolated nucleotide sequence (I) encoding at least a portion of the human alpha-7 neuronal nicotinic acctylcholine receptor (alpha7-hnAChR). Also described are: (1) a peptide encoded by (I); (2) a vector comprising (I); (3) a host cell transformed with a vector of (2); (4) a polynucleotide comprising at least 15 nucleotides which hybridises under stringent conditions to at least a portion of (I); (5) a method for detection of a polynucleotide encoding alpha 7-hnAChR in a biological sample; and (6) a method for amplification of nucleic acid from a sample suspected of containing nucleic acid encoding alpha 7-hnAChR. The primers and probes from the present invention can be used on brain tissue and blood samples of humans suspected of suffering from schizophrenia, small cell lung carcinoma, breast cancer and nicotine-dependent illness. This is particularly useful for diagnosis of schizophrenia. Other illnesses that can be studied/diagnosed are epilepsy (e.g. juvenile myocionic epilepsy) and prader-Willi and Angelman's syndromes.
affections of the organ. A need exists for both a reliable diagnostic procedure which would enable early-stage diagnosis, and for preventative and curative treatments of the disease. The PGI gene can be used for detection of prostate cancer, and the risk of developing it in the future, and can also be used to determine therapies for the disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; alpha-7 nicotinic receptor; neuronal; hybridisation; probe;
alpha-7 neuronal nicotinic acetylcholine receptor; schizophrenia;
small cell lung carcinoma; breast cancer; nicotine-dependent illness;
epilepsy; juvenile myoclonic epilepsy; Prader-Willi syndrome;
                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                         ö
                                                                                                                                                                    Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human alpha-7 nicotinic receptor PCR primer SEQ ID NO:14.
                                                                                                                                                                                                         Indels
                                                                                                                                                                64.0%; Score 12.8; DB 20;
87.5%; Pred. No. 1.8e+03;
ive 0; Mismatches 2;
                                                                                                            Sequence 18 BP; 6 A; 1 C; 8 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Angelman's syndrome; PCR primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                           BP.
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                                                                                                                                                                                                                                                                                                                                                                       AAX56167 standard; DNA; 21
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                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1999
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XLIS gene; human; detection; diagnosis; prenatal diagnosis; therapy; lissencephaly; LIS; agyria-pachygyria; subcortical laminar heterotopia; SCLH; cortical dysgenesis; cryptogenic epilepsy; neurological disorder; neurodegenerative disease; Alzheimer's disease; X-linked disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New gene and its gene product expressed in the brain, useful for diagnosing and treating disorders such as lissencephaly and subcortical laminar heterotopia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
                                                                                                                                                                                                                                                                                                  Human XLIS gene fragment PCR primer 6 F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               genetic counselling; PCR primer; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 9; Page 50; 71pp; English.
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2 tttcccatccgttatccct 20
                                                                                                                                                                                                                                             (first entry)
                                                                                                                                AAX36892 standard; DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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                                                                                                                                                                                     AAX36892;
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                                                                                                          AAX36892
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vaccine; eye disease; conventional trachoma; nonendemic trachoma; paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis; nongonococcal uretritis; epidymitis; cervicitis; salpingitis; PCR primer; bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ORFs) of the genome of Childran and Childra
                                                                                                                                                            Gaps
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                                                                                                                                                         ö
                                                                                                          Length 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCR primer used to amplify an ORF of Chlamydia trachomatis.
                                                                                                                                                         Indels
                                                                                                 Score 12.8; DB 20;
Pred. No. 1.9e+03;
0; Mismatches 2;
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                      BP; 9 A; 3 C; 8 G; 1 T; 0 other;
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                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome sequence of Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 1829; 1755pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                    AA206154 standard; DNA; 20 BP.
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97FR-0015041.
97FR-0016034.
                                                                                                    64.0%;
87.5%;
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                                                                                               Query Match
Best Local Similarity 87.5
Matches 14; Conservative
                                                                                                                                                                                                              2 tctcccttccgttatt 17
                                                                                                                                                                                                                                                                 18 TCTCCCTTGCGTTCTT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chlamydía trachomatis.
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17-DEC-1997;
                      Sequence 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
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                                                                                                                                                                                                                                                                                                                                                  RESULT 11
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Pinard J;

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This sequence is a primer for the human XIIS gene of the invention.

The XLIS fragments may be used to detect abnormalities in the expression of the XLIS gene transcripts or to compare their sequence with that of the XLIS transcripts from patients for in vitro especially prenatal diagnosis of lissencephaly (LIS) (or agyria-pachygyria), subcortical annuar heterotopia (SCLH), cortical dysgenesis, cryptogenic epilepsies or neurodegenerative diseases such as Alzaheimer's disease. These disorders mainly affect females as the XLIS gene is X-linked. The XLIS fragments may also be used to administer to patients to prevent or treat the above disorders and may be used to administer to patients to prevent or treat the above disorders and way be used to administer to patients to prevent or treat the above disorders. They may also be performed by amplifying XLIS connected the mRNA in the sample. Antibodies to XLIS may be used to detect XLIS in the intent the above disorders. They may also be administered to patients to prevent or treat the above disorders. They may also be administered to patients to prevent or treat the above disorders. They may also be administered to patients to prevent or treat the above disorders. They may also be administered to patients to prevent or treat the above neurological disorders. In addition XLIS may be used as a marker of neuronal cells at an early stage of development, its discovery increases understanding of both the neuronal movement which leads to the prain and of the fortical and an early stage of development is the leads to the property and the prain and of the prain and of the prain and the total and the prain and the total and the prain and the total and the leads and leads to the leads and leads to the leads and the leads and leads to the leads and the leads and leads the le
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Pred. No. 2.3e+03;
); Mismatches 4;
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78.9%;
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Best Local Similarity 78.99
Matches 15; Conservative
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Gaps

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tetecettecgttattett 20

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AAZ30696;

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The sequences given in AAT42898-901 are single stranded (ss) circular closed of the proliferation of myeloid leukaemia cells. These oligos are specifically targetted to a region in the bcr3/abl2 gene 385 conclideration of myeloid leukaemia cells. These oligos are specifically targetted to a region in the bcr3/abl2 gene 385 conclides 5 to the bcr/abl junction, abd towards the bcr2/abl2 cc nucleotides 5 to the bcr/abl junction, abd towards the bcr2/abl2 cc junction. These so circular oligonuclectides comprise a parablel cc binding (P) domain. The P and AP domains have sufficient complementarity to bind detectably to 1 strand of a defined nucleic acid target. The P domain is capable of binding in an anti-parallel manner to the target and the ends of the P and AP domains are separated by the loop domains. The sc circular oligonuclectides can be used to regulate the synthesis of DNA, RNA or protein (pref. by DNA replication, DNA reverse transcription, RNA splicing, RNA polyadenylation, RNA cranslocation or protein (pref. by DNA replication, Cc regulate the biosynthesis of DNA, RNA or protein in a targetted mammalian tumour cell in vivo, without substantially altering the blosynthesis of LNA, RNA or protein in a targett complex. The blosynthesis of LNA, RNA or protein in a targett complex conclication conclication and double stranded to detect a target nucleic acid by detecting an oligonuclectide-target complex. The circular oligonuclectide can bind both single and double stranded to linear forms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Single stranded circular oligo:nucleotide comprising parallel and anti-parallel binding domain - used to regulate biosynthesis of DNA, RNA or protein in targetted mammalian tumour cell in vivo
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                                                                                                                                                    /*tag= c
/note= "forms anti-parallel binding domain"
                                                                                                       "forms parallel binding domain"
                            a
"forms 5' > 3' bond with C34"
                                                                                                                                                                                                            /*tag= d
/note= "forms 3' > 5' bond with Tl"
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                                                                                                                                                                                                                                                                                                                                                                                                                                          (RESE ) RESEARCH CORP TECHNOLOGIES INC.
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78.9%;
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Best Local Similarity 78.9
Matches 15; Conservative
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                                               'note=
                                                                                                                             18..29
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      misc_feature
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                                                                                                                                                                                                                                                                                          Promoter; 40S ribosomal protein S28; genetic engineering; amplification; heterologous protein; gene expression; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This primer was used to PCR amplify the promoter sequence from the 40S ribosomal protein S28 gene (AAZ30685) from Aspergillus oryzae. The invention relates to novel gene promoters (AAZ30680-Z30685) isolated from Aspergillus oryzae which can be used in genetic engineering to express heterologous proteins in Aspergillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A new promoter derived from an Aspergillus genus microbe – useful for
producing exotic proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single stranded; circular; target sequence; parallel; detection; binding domain; anti-parallel; loop domain; complementarity; ss; synthesis; regulation; drug delivery; biosynthesis; tumour cell.
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                                                                                                                                                                                                                                               A. oryzae 40S ribosome protein S28 gene promoter primer.
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Pred. No. 2.4e+03;
0; Mismatches 4;
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                                                                                                                        AAZ30696 standard; DNA; 24 BP
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78.9%;
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Best Local Similarity 78.9°
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                        Synthetic.
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RESULT 15 AAV50562

Location/Qualifiers

Synthetic.

Key

AAT42899;

RESULT 14 AAT42899

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This DNA sequence is a region of a Brassica napus or Brassica oleracea genome which contains a polymorphic marker. This sequence can be used in the construction of allele-specific primers and probes for amplification or hybridisation, e.g. to determine common or disparate ancestry between 2 or more plants, to monitor the genetic contribution of an ancestral plant, to trace the progeny of proprietary plants, in certification of a hybrid plant or to identify the progeny of a back-crossed plant with an ancestral plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brassica species allele-specific oligonucleotide probes and primers - useful for plant breeding
                                                                                                                                                                                                                                                                                   Polymorphic marker; allele-specific; primer; probe; amplification; hybridisation; plant; hybrid certification; genetic contribution; progeny; back-cross; hybrid; ancestry; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sapolsky RJ;
                                                                                                                                                                                                                    Brassica sp. polymorphic marker N2/10B8/N3-2A DNA.
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/replace= "c"
/note= "polymorphism"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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AAV50562 standard; DNA; 41 BP
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96US-0032069.
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Best Local Similarity 78.9
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-333252/29
                                                                                                                                             21-DEC-1998
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02-DEC-1996;
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variation
                                                                  AAV50562;
A NAME OF COLOR OF STREET AND STR
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Gaps

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Search completed: October 2, 2001, 16:18:37 Job time: 15481 sec

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APPLICANT Monia, Brett P.
APPLICANT Monia, Brett P.
APPLICANT Gaarde, William A.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0389
CURRENT APPLICATION NUMBER: US/09/377,310B
CURRENT FILING DATE: 1999-08-19
SOFTWARE: Patentin Ver. 2.0
SECIL NO. 10 NOS: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                             US-09-377-310-6
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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Sequence 1, Appli
Sequence 148, App
Sequence 36, App
Sequence 36, Appl
Sequence 148, Appl
Sequence 7, Appli
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Sequence 13, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 4, Appl
Patent No. 5619127
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9.071 Million cell updates/sec
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                                                              Search time 417.38 Seconds
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Sequence 12,
Sequence 13,
Sequence 13,
Sequence 11,
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Sequence
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                                                                                                                                                                                                                                                                                   /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
        4.5
Compugen Ltd.
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US-08-288-405A-3
US-08-208-405A-3
US-08-700-186-12
US-08-914-981-12
US-08-915-13
US-08-116-115-13
US-08-748-415-1
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US-08-748-415-1
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US-08-235-35-31-1
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US-08-458-111-148
US-08-458-111-148
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US-08-458-111-148
US-08-458-111-148
US-08-488-705-57
US-08-488-705-57
US-08-488-705-57
US-08-488-705-57
                                                                                                                                                                                     Potal number of hits satisfying chosen parameters:
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US-08-738-381-44
                                                                                                                                                                    324599 seqs, 94655562 residues
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       GenCore version
Copyright (c) 1993 - 2000
                                                               2, 2001, 16:03:45
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Maximum Match 100%
Listing first 45 summaries

    nucleic search, using sw model

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                                                                                                US-09-757-100B-6
20
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Match Length
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                                                                                                            Perfect score:
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                                                  Sequence 1
Sequence 3
                             Sequence
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 Sequence
Sequence
Sequence
                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                     APPLICANT: Monia, Brett P.
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
FILE REFERENCE: 1SPH-0389
CURRENT APPLICATION NUMBER: US/09/377,310B
CURRENT FILING DATE: 1999-08-19
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 20;
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       US-08-180-2098-49
PCT-US94-02629-49
US-08-26-66
US-08-036-38-38
US-08-171-89-396
US-08-171-89-396
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US-08-173-396-396
US-08-475-228A-396
US-08-473-228A-396
US-08-473-228A-396
US-08-473-228A-396
US-08-473-328-396
US-08-473-352A-2
US-07-979-96-11
US-08-474-661-11
US-08-474-661-11
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Pred. No. 0.37;
Mismatches
                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                        ; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-377-310-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 26, Application US/09377310B; Patent No. 6133031; GENERAL INFORMATION:
                                                                                                                                                                                                                                                        ; Sequence 6, Application US/09377310B
; Patent No. 6133031
; GENERAL INFORMATION:
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ilarity 100.0%;
Conservative 0;
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           15004011065041
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 Query Match
Best Local Similarity
Matches 20; Conserv
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FEATURE:

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OPERATING SYSTEM:
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US-08-288-405A-3/C
Sequence 3, Application US/08288405A
Fatent No. 5559009
GENERAL INFORMATION:
APPLICANT: Chandy, Kanianthara G.
APPLICANT: Chandy, Grischa
APPLICANT: Gutman, George A.
TITLE OF INVENTION: A No. 5559009el Voltage-Gated Potassium Channel
TITLE OF INVENTION: Gene
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                                                                       75.0%; Score 15; DB 3; Length 15; 100.0%; Pred. No. 76; 0; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert,
ADDRESSEE: Attn: Walter H. Dreger
STREET: 4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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Pred. No. 3e+02;
); Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A-59844-1/WHD
; OTHER INFORMATION: antisense sequence US-09-377-310-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94111-4187
COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-591
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Attn: Walter STREET: 4 Embarcadero Cel CITY: San Francisco STATE: California COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 88.2
Matches 15; Conservative
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                                                                       Query Match 75.0
Best Local Similarity 100.
Matches 15; Conservative
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TYPE: nucleic acid
STRANDEDNESS: double
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US-08-288-405A-3
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                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/935,312
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
ATTOREY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68.0%; Score 13.6; DB 4;
80.0%; Pred. No. 4e+02;
Live 0; Mismatches 4;
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Sequence 12, Application US/08700186

Patent No. 5780266

GENERAL INFORMATION:
APPLICANT: Dillon, Patrick
APPLICANT: Vockley, Joseph
TILE OF INVENTION: ARGINASE II
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                       GENERAL INFORMATION:
APPLICANT CHANG, Lung-Ji
TITLE OF INVENTION: LENTIVIRAL VECTORS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: 624 Ninth Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: other nucleic acid
    DESCRIPTION: /desc = ""DNA""
US-08-935-312-15
Sequence 15, Application US/08935312 Patent No. 6207455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: COOPER, IVER P. REGISTRATION NUMBER: 28,005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: CH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42 GAAAGAGCAGAAGACAGTGA 23
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LENGTH: 42 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 gaaactgcagaaggcactga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 80.0°
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 202-737-3528 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
21P: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                            STREET: 624 Nint) CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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Sequence 13, Application US/07825959
Patent No. 5372929
GENERAL INFORMATION:
APPLICANT: Cimino, George C.
APPLICANT: Lin, Lilly
TITLE OF INVENTION: METHOD FOR MEASURING THE INACTIVATION OF
TITLE OF INVENTION: PATHOGENS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Limbach & Limbach
STREET: 2001 Ferry Building
                                                                                                                                                                                                                                                                                                                                           67.0%; Score 13.4; DB 2; Length 43; 93.3%; Pred. No. 5e+02; 1:ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67.0%; Score 13.4; DB 3; Length 43; 93.3%; Pred. No. 5e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-116-115-12/C
Sequence 12, Application US/09116115D
Patent No. 6054308
SEQUENCAL INFORMATION:
APPLICANT: DILLON, PATRICK J.
TITLE OF INVENTION: ARGINASE II
FILE REFERENCE: ATG-50004-3/D1
CURRENT APPLICATION NUMBER: US/09/116,115D
CURRENT PILING DATE: 1999-07-15
EARLIER PEPLICATION NUMBER: US 08/700,186
EARLIER PELLING DATE: 1997-08-20
EARLIER FILING DATE: 1997-08-20
EARLIER FILING DATE: 1996-08-30
EARLIER FILING DATE: 1966-08-30
EARLIER FILING DATE: 1966-08-30
SEARLIER FILING DATE: 1966-08-30
SARLIER FILING DATE: 1966-08-30
SARLIER FILING DATE: 1966-08-30
SARLIER FILING DATE: 1966-08-30
SARLIER FILING DATE: 1966-08-30
SOFTWARE: FASSEQ FOR WINGOWS VERSION 3.0
                   TELEX: 846169
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 43 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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  610-407-0701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: HOMO SAPIENS
                                                                                                                                                            MOLECULE TYPE: CDNA
                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                 ; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
US-08-914-981-12
                                                                                                                                                                                           HYPOTHETICAL:
                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-07-825-959-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 13.4;
Pred. No. 5e
                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Han, William T
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: ATG50004-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
TELEFRAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERNCE/DOCKET NUMBER: ATGS0004-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
                                         APPLICATION NUMBER: US/08/700,186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/914,981
FILING DATE: 20-AUGUST-1997
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-14-981-12/c
Sequence 12, Application US/08914981
Fatent No. 5912159
Fatent No. 5912159
APPLICANT: Dillon, Patrick
APPLICANT: Vockley, Joseph
TITLE OF INVENTION: ARGINASE II
NUMBER OF ERQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: RATHER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/700,186
FILING DATE: 20-AUGUST-1996
ATTORNEY/AGENT INFORMATION:
FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 67.0%;
Best Local Similarity 93.3%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                   CURRENT APPLICATION DATA
                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 ACTGCAGAAGGCAAT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; FRAGMENT TYPE:
; ORIGINAL SOURCE:
US-08-700-186-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL: NAMI-SENSE: NO
                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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ATTORNEY/AGENT INFORMATION:
NAME: Evans, Barry
REGISTRATION NUMBER: 22,802
REFERENE/DOCKET NUMBER: 370068-3580
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
   STER-1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: United States
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIALE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, N
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APPLICATION NUMBER: US/07/841,648
FILING DATE:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/250,934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
APPLICATION NUMBER: US/08/101,274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 1, Application US/08377495
; Patent No. 5631137
REFERENCE/DOCKET NUMBER: ST. TELECOMMUNICATION INFORMATION: TELEPHONE: (510) 603-9071
                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-131-324-13
                                                            TELEPHONE: (510) 603-9071
TELEFAX: (510) 603-9099
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISICS:
LENGTH: 27 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 aactgcagaaggcactga 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 83.3
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                  single
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STRANDEDNESS: single
                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New York
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US-08-377-495-1
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Patent No. 5565320
GENERAL INFORMATION:
APPLICANT: Cimino, George C.
APPLICANT: Lin, Lily
TITLE OF INVENTION: COMPOUNDS FOR THE PHOTODECONTAMINATION
TITLE OF INVENTION: OF PATHOGENS IN BLOOD
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Steritech, Inc.
STREET: 2525 Stanwell Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66.0%; Score 13.2; DB 1; Length 27; 83.3%; Pred. No. 5.7e+02; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/825,959

FILING DATE: 19920127

CLASSIFICATION: 436

ATTORNEY/AGENT INPORMATION:

NAME: Weseman, James C

REGISTRATION NUMBER: 30,507

REGISTRATION NUMBER: 30,507

RELEFANCE, (415) 433-4150

TELEFANCE, (415) 433-4150

TELEFAN: (415) 433-4150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: 2.25 SCHWELL DILVE
CTTY: CONCORD
STATE: California
CONTRY: United States of America
2.1P: 945.20
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPATE: PATENTIN Release #1.0, Version #1.25
SOFTWARE: PATENTIN NUMBER: US/08/131,324
FLING DATE: 28-190-1993
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/825,959
FLING DATE: 27-JAN-1992
ATTOMEY/AGERT INFORMATION:
ANDER APPLICATION PATES: ATTOMES TO THE APPLICATION NUMBER: US 07/825,959
FLING DATE: 27-JAN-1992
                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Carroll, Peter G. REGISTRATION NUMBER: 32,837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MoLECULE TYPE: DNA (genomic) FRAGMENT TYPE: internal US-07-825-959-13
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Best Local Similarity 83.3
Matches 15; Conservative
San Francisco
                                California
: USA
                                                                                                   94111
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Gaps
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APPLICANT: Martin, Mark T.
APPLICANT: Smith, Rodger G.
APPLICANT: Simpson, Michael J.
APPLICANT: Simpson, David
APPLICANT: Blackburn, Gary F.
TITLE OF INVENTION: REACTION-BASED SCREENING FOR EXPRESSION
TITLE OF INVENTION: OF AND CONCENTRATION OF CATALYTIC MOIETIES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                          .;
0
66.0%; Score 13.2; DB 1; Length 27; 83.3%; Pred. No. 5.7e+02; Live 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/377,495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Curtis, Morris & Safford, P.C.
STREET: 530 Fifth Avenue
CITY: New York
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APPLICANT: Martin, Mark T.
APPLICANT: Smith, Rodger G.
APPLICANT: Darsley, Michael J.
APPLICANT: Darsley, Michael J.
APPLICANT: Blackburn, David
APPLICANT: Blackburn, Gary F.
APPLICANT: Blackburn, Gary F.
TILLE OF INVENTION: REACTION-BASED SCREENING FOR EXPRESSION
TITLE OF INVENTION: Q AND CONCENTRATION OF CATALYTIC MOIETIES
CORRESPONDENCE ADDRESS: ADDRESSE CURTIS, MOTTIS & Safford, P.C.
STREET: 530 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 12.8; DB 3;
Pred. No. 8.6e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    370068-3580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/377,495
FILLING DATE:
RPLICATION NUMBER: US/08/250,934
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/747,654
FILING DATE: 13*NOV-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US/08/101,274
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; Sequence 1, Application US/09235353
; Patent No. 6177270
; GENERAL INFORMATION:
APPLICANT: Martin, Mark T.
                                                                                                      ; Sequence 1, Application US/08747654; Patent No. 6121007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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ATTORNEY/AGENT INFORMATION:
NAME: Evans, Barry
REGISTRATION NUMBER: 22,802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 37
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64.0%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: United States ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 22 base pairs
nucleic acid
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    5 GAAACTGCAGGAGTCA 20
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FILING DATE:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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Best Local Similarity
Matches 14; Conserv
                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             STREET: 530 Fift
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                               RESULT 12
US-08-747-654-1
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                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08748415
Patent No. 5891648
GENERAL INFORMATION:
APPLICANT: Martin, Mark T.
APPLICANT: Smith, Rodger G.
APPLICANT: Smith, Rodger G.
APPLICANT: Slmpson, David
APPLICANT: Blackburn, Gary F.
TITLE OF INVENTION: OF AND CONCENTRATION OF CATALYTIC MOIETIES
                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                             Length 22;
                                                           Score 12.8; DB 1; Length 2
Pred. No. 8.6e+02;
); Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZUMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,415
FILING DATE: 13-NOV-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Curtis, Morris & Safford, P.C.
STREET: 530 Fifth Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Evans, Barry
REGISTRATION NUMBER: 22,802
REFERENCE/DOCKET NUMBER: 370068-3580
TELECOMMUNICATION INFORMATION:
TELEPRAX: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/377,495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/250,934 FILING DATE: APPLICATION NUMBER: US/08/101,274
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APPLICATION NUMBER: US/07/841,648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
                                                             64.08;
87.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New York
: United States
                                                                                                      14; Conservative
                                                                                                                                              1 gaaactgcagaaggca 16
                                                                                                                                                                      5 GAACTGCAGGAGTCA 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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                                                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                     RESULT 11
US-08-748-415-1
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US-08-377-495-1
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Pred. No. 1.1e+03;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                    Length 35;
                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 1036
COUNTRY: USA
ZIP: 1036
COMPUTER READELE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/105,483
FILING APPLICATION: 424
PRIOR APPLICATION UMBER: US/08/105,483
APPLICATION NUMBER: US/08/105,483
FILING APPLICATION NUMBER: US/08/105,483
APPLICATION NUMBER: US/08/105,483
FILING DATE: 06-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Paoletti, Enzo
TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
TITLE OF INVENTION: STRAIN
NUMBER OF SEQUENCES: 462
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                  Score 12.8; DB 4;
Pred. No. 9.2e+02;
); Mismatches 2;
CURRENT FILING DATE: 1999-01-15
EARLIER APPLICATION NUMBER: PCT/FR97/01316
EARLIER FILING DATE: 1997-07-15
EARLIER FILING DATE: 1997-07-15
EARLIER FILING DATE: 1996-07-19
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
SLENGTH: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REPERENCE/DOCKET NUMBER: 454310-2400
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Curtis, Morris & Safford
ADDRESSEE: C/O William S. Frommer
STREET: 530 Fifth Avenue
CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
US-08-105-483-148
; Sequence 148, Application US/08105483
; Patent No. 5494807
                                                                                                                                                                                                                                       ; ORGANISM: Borrella burgdorferi
US-09-232-477-1
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TELEFAX: (212) 840-0712
INFORMATION FOR SEC ID NO: 148
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                  64.0%;
87.5%;
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Best Local Similarity 78.99
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                  Query Match 64.0
Best Local Similarity 87.5
Matches 14; Conservative
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STRANDEDNESS: single
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                                                                                                                                                                                                                 TYPE: DNA
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Sequence 1, Application US/09232477

Sequence 1, Application US/09232477

Sequence 1, Application US/09232477

GENERAL INFORMATION:

APPLICANT: AUDONNET, Jean-Christophe

APPLICANT: BOUCHARDON, Annabelle

APPLICANT: BOUCHARDON, Annabelle

APPLICANT: BOUCHARDON, POLYNOLE

TITLE OF INVENTION: PATHOLOGIES, IN PARTICULAR RESPIRATORY AND DIGESTIVE

TITLE OF INVENTION: PATHOLOGIES

TITLE OF INVENTION: PATHOLOGIES
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              APPLICANT: Darsley, Michael J.
APPLICANT: Simpson, David
APPLICANT: Slapson, David
APPLICANT: Blackburn, Gary F.
TITLE OF INVENTION: REACTION-BASED SCREENING FOR EXPRESSION
TITLE OF INVENTION: OF AND CONCENTRATION OF CATALYTIC MOIETIES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/235,353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 12.8; DB 4;
Pred. No. 8.6e+02;
); Mismatches 2;
                                                                                                                                                                                       ADDRESSEE: Curtis, Morris & Safford, P.C. STREET: 330 Fifth Avenue CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Evans, Barry
REGISTRATION NUMBER: 22,802
REFERENCE/DOCKET NUMBER: 370068-3580
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 454313-2240
CURRENT APPLICATION NUMBER: US/09/232,477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/748,415
FILING DATE: 13-NOV-1996
APPLICATION NUMBER: 05/08/37,495
FILING DATE:
APPLICATION NUMBER: US/08/250,934
FILING DATE:
APPLICATION NUMBER: US/08/101,274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (712) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64.0%;
87.5%;
       Smith, Rodger G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                               New York
: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 87.5
Matches 14; Conservative
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
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Search completed: October 2, 2001, 16:03:46 Job time: 14590 sec

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| Patent No. 6133031
| GBNERAL INFORMATION:
| APPLICANT: Monia, Brett P. |
| APPLICANT: Gaarde, William A. |
| TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase |
| TITLE OF INVENTION: Expression |
| TITLE OF INVENTION: Expression |
| FILE REFERENCE: ISPH-0389 |
| CURRENT APPLICATION NUMBER: US/09/377,310B |
| CURRENT FILING DATE: 1999-08-19 |
| NUMBER OF SEQ ID NOS: 43 |
| SEQ ID NO 4 |
| LENGTH: 20 |
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APPLICANT: Gaarde, William A.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0389
CURRENT APPLICATION NUMBER: US/09/377,310B
CURRENT APPLICATION NUMBER: 1999-08-19
NUMBER OF SEQ ID NOS: 1999-08-19
SOFTWARE: PatentIn Ver. 2.0
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PCT-US95-03032-7
US-08-015-770B-72
US-08-399-580B-11
US-08-413-338A-16
US-08-441-971-91
US-08-442-144A-91
US-08-570-155-8
PCT-US95-02861-8
US-07-841-662-21
US-08-69-695-21
US-08-69-695-21
US-08-69-685-21
US-08-669-685-21
US-08-689-685-21
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                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
COTHER INFORMATION: antisense sequence
US-09-377-310-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 24, Application US/09377310B
; Patent No. 6133031
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
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   Query Match
Best Local Similarity
Matches 20; Conserv
   US-09-377-310-24
                                                                                                                                                                                                                                                                                                                                                                                             RESULT 1
US-09-377-310-4
 SEQ ID NO 24
LENGTH: 15
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9.071 Million cell updates/sec
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                                                                                                                     Search time 417.38 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
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Sequence
Sequence
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Sequence 4
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Sequence 5
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/cgn2_6/ptodata/1/ina/5B_COMB.seg:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
                 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-377-310-4
US-09-377-310-24
US-08-4250-89-19
US-08-426-19
US-09-180-437-51
US-09-180-437-52
US-09-180-437-53
US-08-950-6
US-08-950-6
US-08-950-774-46
US-08-94-526-46
US-09-013-04-46
US-09-013-04-46
US-09-013-04-41
                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-280-799-185
PCT-US92-02977-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-517-584A-22
US-09-180-437-48
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                                                                                                                                                                                                                                                                                                        324599 seqs, 94655562 residues
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                                                                                                                   2001, 16:03:44
                                                                                                                                                                                                                                                                                                                                                                                                                                             Maximum Match 100%
Listing first 45 summaries
                                                                                   OM nucleic - nucleic search, using sw model
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                                                                                                                                                                               US-09-757-100B-4
20
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Match Length
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length: 50
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                                                                                                                                                                                                                                                      Scoring table:
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                                                                                                                                                                                                                        Sequence:
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GENERAL INFORMATION:
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US-08-434-474-19
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                                                                                                                                                                              STATE:
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Pred. No. 4e+02;
0; Mismatches 3; Indels
                                                                                             75.0%; Score 15; DB 3; Length 15; 100.0%; Pred. No. 54; 0; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                   Sequence 19, Application US/08250849
Patent No. 5567583
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: WETHOD FOR DETECTING A TARGET
TITLE OF INVENTION: WICLEIC ACID
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Mosson
STREET: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.

ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/250,849
FILING DATE: 05/26/94
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/808,463
FILING DATE: December 16, 1991
ATTORNEY AGENT INFORMATION:
NAME: Y. ROCKY TSAO
RECISTRATION NUMBER: 34,053
REFERENCE/DOCKET NUMBER: 06498/002001
           ; OTHER INFORMATION: antisense sequence US-09-377-310-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 19, Application US/0843474 Patent No. 5712386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (617) 542-5070
(617) 542-8906
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83.3%;
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                                                                                       Query Match 75.0
Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity 83.3
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                        3 cgccgtgaagcgaag 17
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STRANDEDNESS: sing]
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US-08-250-849-19
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FEATURE:
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Gaps
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Pred. No. 4e+02;
3; Mismatches 3; Indels
APPLICANT: Wang et al.
TITLE OF INVENTION: METHOD FOR DETECTING A TARGET
TITLE OF INVENTION: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: FUKUGAKO, Shioji
APPLICANT: FUKUGAKO, Shioji
APPLICANT: MORISAWA, YOShifuni
APPLICANT: WORISAWA, Takeshi
TITLE OF INVENTION: Antisense Compounds to CD14
FILE REFERENCE: 1110-209P
CURRENT APPLICATION NUMBER: US/09/180,437
CURRENT FILING DATE: 1998-11-06
EARLIER FILING DATE: 1998-03-09
EARLIER APPLICATION NUMBER: 09-053518 JAPAN
EARLIER FILING DATE: 1997-03-07
NUMBER OF SEQ ID NOS: 289
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 51
LENGTH: 20
                                                                                                                                                                                                                COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,474
FILING DATE: 05/04/95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/250,849
FILING DATE: 05/26/94
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06498/002002
                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 51, Application US/09180437; Patent No. 6251873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Y. ROCKY TSAO
REGIZTRATION NUMBER: 34,053
REFERENCE/DOCKET NUMBER: 0649
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66.0%;
83.3%;
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ORGANISM: Artificial Sequence
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Best Local Similarity 83.3
Matches 15; Conservative
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                              Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
                                                                      NUMBER OF SEQUENCES:
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Gaps
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  ; OTHER INFORMATION: Description of Artificial Sequence:other nucleic; OTHER INFORMATION: acid, synthetic DNA US-09-180-437-53
                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: JARVIS, THALE
APPLICANT: AGNIGGEN, JAMES A.
APPLICANT: MCSWIGGEN, JAMES A.
TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES
TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS OF C-FOS
TITLE OF INVENTION OR CONDITIONS RELATED TO LEVELS OF C-FOS
TITLE OF INVENTION OF CONDITIONS RELATED TO LEVELS OF C-FOS
CURRENT FILLING DATE: 1997-12-24
EARLIER APPLICATION NUMBER: 60/037,658
EARLIER PILING DATE: 1997-01-23
EARLIER PILING DATE: 1995-01-13
EARLIER PLING DATE: 1995-01-13
EARLIER PLING DATE: 1994-05-18
SEALIER PLING DATE: 1994-05-18
NUMBER OF SEQ ID NOS: 375
SOFTWARE: FASTSEQ for Windows Version 3.0
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                                                                                                              Length 20;
                                                                                                                                                         Indels
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COMPUTER: IBM PC compatible
COMPARE: DASSTEM: PC-DOSS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,077
                                                                                                            Score 12.8; DB 4;
Pred. No. 6.1e+02;
0; Mismatches 2;
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Pred. No. 1.2e+03;
0; Mismatches 3;
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APPLICANT: Quirk, Alan V
TITLE OF INVENTION: Yeast Strains
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Centeon LLC
                                                                                                                                                                                                                                                                                                                                               ; Sequence 6, Application US/08998099A; Patent No. 6103890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 4, Application US/08750077; Patent No. 5783423; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Centeon LLC
STREET: 1020 First Avenue
CITY: King of Prussia
COUNTRY: USA
                                                                                                              64.0%;
87.5%;
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                                                                                                            Query Match 64.0
Best Local Similarity 87.5
Matches 14; Conservative
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Best Local Similarity 82.4
Matches 14; Conservative
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COMPUTER READABLE FORM:
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; ORGANISM: Homo sapiens
US-08-998-099-6
                                                                                                                                                                                                                                                                                                                           ON-088-099-6/c
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US-08-750-077-4
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                                                                                       Length 20;
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Pred. No. 6.1e+02;
0; Mismatches 2; Indels
                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: FUKUSAKO, Shioji
APPLICANT: FUKUSAKO, Shioji
APPLICANT: MARLSAWA, YOShifumi
APPLICANT: KUSUYAWA, Takeshi
TITLE OF INVENTION: Antisense Compounds to CD14
FILE REFERENCE: 1110-209P
CURRENT APPLICATION NUMBER: US/09/180,437
CURRENT FILING DATE: 1998-11-06
EARLIER APPLICATION NUMBER: PCT/JP98/00953
EARLIER FILING DATE: 1998-03-09
EARLIER FILING DATE: 1997-03-07
NUMBER OF SEQ ID NOS: 289
                                                                                     Score 12.8; DB 4;
Pred. No. 6.1e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: FUNCASAKO, Shioji
APPLICANT: FUNCASAKO, Shioji
APPLICANT: FUNCASAKO, Takeshi
TITLE OE INVENTION: Antisense Compounds to CD14
FILE REFERENCE: 1110-209P
CURRENT APPLICATION NUMBER: US/09/180,437
CURRENT APPLICATION NUMBER: US/09/180,437
CURRENT APPLICATION NUMBER: PCT/JP98/00953
EARLIER APPLICATION NUMBER: PCT/JP98/00953
EARLIER PILING DATE: 1998-03-09
EARLIER FILING DATE: 1997-03-07
NUMBER OF SEQ ID NOS: 289
SOFTWARE: Patentin Ver. 2.0
; OTHER INFORMATION: acid, synthetic DNA US-09-180-437-51
                                                                                                                                                                                                                                                                                                                      Sequence 52, Application US/09180437 Patent No. 6251873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 53, Application US/09180437 Patent No. 6251873
                                                                                     64.0%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
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Best Local Similarity 87.5%;
Matches 14; Conservative
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SEQ ID NO 52
LENGTH: 20
                                                                                                                                                                      Best Local Similarity 87.8
Matches 14; Conservative
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                                                                                     Query Match
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COUNTRY: Canada
ZIP: M5G 1R7
           GENERAL INFORMATION:
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                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 15, Application US/08841267C
; Sequence 15, Application US/08841267C
; Patent No. 6007990
; GENERAL INFORMATION:
; APPLICANT: Levine, Robert A.
; APPLICANT: Wardlaw, Stephen C.
; TITLE OF INVENTION: Detection and Quantification of One or
; TITLE OF INVENTION: More Nucleotide Sequence Target Analytes in a Sample Using
; Patent No. 6007990
; TITLE OF INVENTION: Spatially Localized Target Analyte Replication
; FILE REFERENCE: UFB-001
; CURRENT APPLICATION NUMBER: US/08/841,267C
; CURRENT FILING DATE: 1997-04-29
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: 1..38
OTHER INFORMATION: /note= "Oligonucleotide for PCR
OTHER INFORMATION: amplification of the 3' end of the Hspl50 gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Pred. No. 1.2e+03;
0; Mismatches 3; Indels
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9411356.0
FILING DATE: 07-JUN-1994
PRIOR APPLICATION NUMBER: PCT/GB95/01317
APPLICATION NUMBER: PCT/GB95/01317
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MOOFE, SEEVEN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 878 4073
TELEPHONE: (610) 878 4221
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 base pairs
TYPE: NUCLEIC acid
STRANDONENCE: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
US-08-472-171-46
: Sequence 46, Application US/08472171
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82.4%;
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Best Local Similarity 82.4
Matches 14; Conservative
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Best Local Similarity 82.4
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: virus HBV
US-08-841-267-15
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Patent No. 5942418

GENERAL INFORMATION:
APPLICANT: LOOSMOTE, Sheena M
APPLICANT: Yacoob, Reza K
APPLICANT: Zealey, Gavin R
APPLICANT: Zealey, Gavin R
TITLE OF INVENTION: EXPRESSION OF GENE PRODUCTS FROM
TITLE OF INVENTION: GENETICALLY MANIPULATED STRAINS OF BORDETELLA
NUMBER OF SEQUENCES: 57
CORRESPONDENCES ADDRESSE:
ADDRESSEE: Sim & MCBurney
STREET: 6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
               APPLICANT: Taccob, Reza K.
APPLICANT: Zealey, Gavin R.
APPLICANT: Taccob, Michael R.
APPLICANT: Klein, Michael Expression Of Gene Products From
TITLE OF INVENTION: Genetically Manipulated Strains Of Bordetella
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                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,171
FILING DATE: 07-JUN-1995
CLASSIFICATION 1435
PRIOR APPLICATION NUMBER: US/08/393,334
FILING APPLICATION NUMBER: US/08/393,334
FILING APPLICATION NUMBER: US/08/393,334
FILING BAPLICATION NUMBER: US/08/393,334
FILING BATE: 23-FEB-1995
ATTORNEY/AGRATI NIFORMATION:
NAME: Stewart, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-507 MIS:V9
TELECOMMUNICATION INFORMATION:
TELEPHONE: 416-595-1163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 12.2; DB 2;
Pred. No. 1.2e+03;
0; Mismatches 3;
                                                                                                                                       NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & MCBurney
STREET: 330 University Avenue, Suite 701
STRATE: Toronto
STRATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
MSG 1R7
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Loosmore, Sheena M.
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82.4%;
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TELEX: 065-24567 Simbas
INFORMATION FOR SEQ ID NO: 4
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Best Local Similarity 82.4'
Matches 14; Conservative
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LENGTH: 50 base pairs
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STRANDEDNESS: single
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: LOSDONCE, Sheena M.
APPLICANT: Yacoob, Reza K.
APPLICANT: Zealey, Gavin R.
APPLICANT: Zealey, Gavin R.
APPLICANT: Standy Gavin R.
APPLICANT: Standy Gavin R.
APPLICANT: Standy Gavin R.
TITLE OF INVENTION: Expression Of Gene Products From
TITLE OF INVENTION: Genetically Manipulated Strains Of Bordetella NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 330 University Avenue, 6th Floor
CITY: Toronto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER REAABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CAUREMY APPLICATION DATA:
APPLICATION NUMBER: US/09/374,597
FILING DATE:
                                                                                                                                                                                                                                                                            Score 12.2; DB 2;
Pred. No. 1.2e+03;
0; Mismatches 3;
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Pred. No. 1.2e+03;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/393,334
FILING DATE: FEBRUARY 23, 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24973
REFERENCE/DOCKET NUMBER: 1038-964
TELECOMMUNICATION INFORMATION:
TELEPHONE: 416-595-1155
TELEFKX: 416-595-1163
TELEEXX: 416-595-1163
TELEEXX: 416-595-1163
TELEX: 065-24567 Simbas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 46, Application US/09374597; Patent No. 6140082; GENERAL INFORMATION:
                             TELEFAX: 416-595-1163
TELEX: 065-44567 Simbas
INFORMATION FOR SEQ ID NO: 46
SEQUENCE CHARATERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
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82.4%;
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Best Local Similarity 82.4%;
Matches 14; Conservative
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LENGTH: 50 base pairs
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Best Local Similarity 82.4
Matches 14; Conservative
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US-09-374-597-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: Canada
ZIP: M5G 1R7
                TELEPHONE:
                                                                                                                                                                                         ; TOPOLOGY:
US-09-013-047-46
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Sequence 46, Application US/09013047

Sequence 46, Application US/09013047

Sequence 46, Application US/09013047

Sequence 46, Application

GENERAL INFORMATION:

APPLICANT: Loosmore, Sheena M.

APPLICANT: Zealey, Gavin R.

APPLICANT: Zealey, Gavin R.

TITLE OF INVENTION: Expression Of Gene Products From

TITLE OF INVENTION: Genetically Manipulated Strains Of Bordetella

NUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sim & McBurney

STREET: 310 University Avenue, 6th Floor

CITY: Toronto

STATE: Ontario

COUNTRY: Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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COMPUTER READABLE FORM:

MEDULUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,526
FILING DATE: 01-DEC-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION UNMBER: 1038-724 MIS:jb
TELEPONE: (416) 595-1163
TELEPONE: (416) 595-1163
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: MICHAEL CALL
STRANDEDMESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/013,047
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 12.2; DB 2;
Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Stewart, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-507 MIS:vg
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/472,171
FILING DATE:
OR-UN-1995
APPLICATION DATA:
APPLICATION NUMBER: US 08/393,334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61.0%;
82.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 23-FEB-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 61.0°
Best Local Similarity 82.4°
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ggcgccgtgaagcgaag 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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US-08-894-526-46
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OY 19GCGCCGCGCAGG 39

RESULT 15

RESULT 15

Sequence 4, Application US/07678448A

TITLE OF INVERTION: Gencypling of Multiple Allele

TITLE OF INVERTION: Gencypling of Multiple Allele

TITLE OF INVERTION: Systems

NUMBERS OF SEQUENCES: 8

COMMERS OF SEQUENCES: 8

COMPUTER REDUCATION DATA:

APPLICATION NUMBER: US/07/678,448A

FILING DATE: 1000 DATA:

APPLICATION NUMBER: 10,431

PRICE PRICE COMMERS: 10,431

APPLICATION NUMBER: 10,431

RESISTANTION NUMBER: 10,531

RESISTANTION NUMBER: 10,531

RESISTANTION NUMBER: 10,531

RESISTANTION NUMBER: 10,531

TELERA: 40080 LM WH

TELERAM: 10080 MESS DE NO. 4:

SEQUENCE TYPE: NO. 5521301 APPLICABLE OF THE SECOND NUMBER: 10,531

TELERAM: 10080 MESS SYNTHACHIAL PEPARTER

NOUNCE: SYNTHACHICALLY NUMBER: NO. 5521301e

TELERAM: 10080 MESS SYNTHACHIAL PEPARTER

NOUNCE: SYNTHACHIAL NUMBER: NO. 5521301e

PRESTORE OF SYNTHACHIAL NUMBER: NO. 5521301e

PRESTORE OF SYNTHACHIAL NO. 5521301e
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Query Match 60.0%; Score 12; DB 1; Length 20; Best Local Similarity 75.0%; Pred. No. 1.5e+03; Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps

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Search completed: October 2, 2001, 16:03:45 Job time: 14589 sec

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c-fos target D3 ribozyme

Human IL4Ralpha ge

Primer #60.

Cyclin D3

Polymorphic fragme

NANBH PCR primer P Primer for amplify Primer for HBV pX Complementary stra Allele-specific PC

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Bacillus lichenifo Nucleotide sequenc Permutein linker e Probe for alkaline Alkaline protease Human GPC4 exon 1

Porphorymonas ging Oligonucleotide Kb HIF-lalpha gene am TnI gene forward p

Human PRO1434 (UNQ Forward primer for PCR primer 34387.t

Phanerochaete sord nodosus proteas

PCR primer for C. PRO240 probe #2.

HGF nucleic acid l Integrin alpha 6 s Oligo #5 for site-

Searched:

Database

4 5 7 7 10 11

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Sequence:

on O

Run

TnI gene forward p Human troponin I f Human troponin I g Mouse CGRP recepto

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New antisense compounds for inhibiting focal adhesion kinase expression, especially useful for inhibiting retinal neovascularization, or for diagnosing and treating e.g. colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, focal adhesion kinase; FAK; signal transduction; cancer; embryonic development disorder; angiogenic disorder; wound healing; antisense; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human focal adhesion kinase antisense sequence #2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAV32360
AAX25907
                                           AAF69762
AAA04651
AAQ25255
AAT07272
                                                                                                                                                                                                                                                    AAF73589
AAA21515
                                                                                                                                                                                                                                                                                              AAC58525
AAA51273
                                                                                                                                                                                                                                                                                                                                           AAF60392
AAA60931
AAZ43239
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AAT30041
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AAV07603
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AAT34327
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AAZ00590
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 99US-0377310.
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 (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaarde WA;
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Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-AUG-1999;
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Monia BP,
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 RESULT
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Human gene single
Mass spectrometric
Oligonucleotide SC
Nucleotide Scquenc
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Human AML-1 limiti
Human leukaemia br
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Human focal adhesi
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                                                                                                  Search time 876.95 Seconds (without alignments)
14.320 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                                                                                                                                                                                                                                                                                                                                          // SIDSB/gcgdata/geneseq_geneseq_n/Na1980.DAT:*
// SIDSB/gcgdata/geneseq_geneseq_n/Na1981.DAT:*
// SIDSB/gcgdata/geneseq_geneseq_n/Na1981.DAT:*
// SIDSB/gcgdata/geneseq_geneseq_n/Na1981.DAT:*
// SIDSB/gcgdata/geneseq_geneseq_n/Na1984.DAT:*
// SIDSB/gcgdata/geneseq_geneseq_n/Na1984.DAT:*
// SIDSB/gcgdata/geneseq_geneseq_n/Na1984.DAT:*
// SIDSB/gcgdata/geneseq_geneseq_n/Na1986.DAT:*
// SIDSB/gcgdata/geneseq_geneseq_n/Na1986.DAT:*
// SIDSB/gcgdata/geneseq_geneseq_n/Na1980.DAT:*
// SIDSB/gcgdata/geneseq_geneseq_n/Na1981.DAT:*
// SIDSB/gcgdata/geneseq_geneseq_n/Na1981.DAT:*
// SIDSB/gcgdata/geneseq_geneseq_n/Na1981.DAT:*
// SIDSB/gcgdata/geneseq_geneseq_n/Na1991.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /SIDS8/gcgdata/geneseq/geneseqn/NA2001.DAT:*
            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                 730101 seqs, 313950809 residues
                                                                                                     ٠.
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                                                                                                  2001, 16:18:33
                                                                                                                                                                                                                                                                                                                                                                                                    Listing first 45 summaries
                                                                      OM nucleic - nucleic search, using sw model
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AAT87201
AAT09720
AAT09720
AAV09361
AAF95308
AAF95308
AAF95308
AAF9608
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AAC65556
                                                                                                                                                                                                                      IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                          ggcgccgtgaagcgaaggca
                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0% Maximum Match 100%
                                                                                                                                                        US-09-757-100B-4
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                                                                                                    October
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IL-4 2'F/NH2 RNA ligand, nitrocellulose filter binding clone #21.
                                                                                                                                                           AAT87270 standard; RNA; 40 BP.
                                                                                                                                                                                                                                               16-NOV-1997 (first entry)
      3 cgccgtgaagcgaag 17
                             AAT87270;
                                                                                                                                  AAT87270
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                                         The present invention describes a number of phosphorothioate antisense sequences to the human focal adhesion kinase (FAK) protein. This protein is involved in integrin-mediated signal transduction, and is implicated in cancer, particularly colon, breast and oral tumours, embryonic development disorders, anglogenic disorders and wound healing. The antisense sequences, including the one shown here, can be used in the treatment of all of these.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a number of phosphorothicate antisense sequences to the human focal adhesion kinase (FAK) protein. This protein is involved in integrin-mediated signal transduction, and is implicated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antisense compounds for inhibiting focal adhesion kinase expression, especially useful for inhibiting retinal neovascularization, or for diagnosing and treating e.g. colon cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in cancer, particularly colon, breast and oral tumours, embryonic development disorders, anglogenic disorders and wound healing. The antisense sequences, including the one shown here, can be used in the treatment of all of these.
                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, focal adhesion kinase; FAK; signal transduction, cancer;
embryonic development disorder; angiogenic disorder; wound healing;
antisense; phosphorothioate; ss.
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                                                                                                                                                                                                                                                                                      DB 22; Length 20; 0.66;
                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human focal adhesion kinase antisense sequence #22.
                                                                                                                                                                                                                         Sequence 20 BP; 5 A; 5 C; 9 G; 1 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 15 BP; 4 A; 4 C; 6 G; 1 T; 0 other;
                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                         100.0%; Score 20; 100.0%; Pred. No.
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Claim 3; Column 23; 30pp; English.
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                                                                                                                                                                                                                                                                                                                                                                               1 ggcgccgtgaagcgaaggca 20
                                                                                                                                                                                                                                                                                                                                                                                                      1 ggcgccgtgaagcgaaggca 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC65556 standard; DNA; 15
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                                                                                                                                                                                                                                                                                                                                    20; Conservative
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                                                                                                                                                                                                                                                                                                               Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-AUG-1999;
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AAT87178-276 are interleukin (IL)-4 RNA ligands obtained after 17 rounds of SELEX (Systematic Evolution of Ligands by Exponential enrichment). The sequences were analysed for conserved sequences and aligned by this criterion. The 2'F sequences fell into a single group with 12 orphan sequences. 2'NH2 sequences fell into 2 distinct groups. Group 1 were shown to bind to IL-4 and the other group were shown to bind to on itrocellulose filters and were identified by the presence of a direct repeat of the sequence GGAGG. A single orphan 2'NH2 sequence was also found to nitrocellulose filters. Nucleic acid (NA) ligands to a cytokine on the case fell into 3 groups, of which one group bound to nitrocellulose filters. Nucleic acid (NA) ligands to a cytokine can be identified using SELEX. A candidate mixture of NA's are contacted with a cytokine where the NA's having an increased affinity to the rest of the mixture. The NA's having an increased affinity to the rest of the mixture of NA's enriched for the NA sequences and relatively higher affinity and selectivity for binding to the cytokine. The NA ligands are useful in diagnostic and therapeutic applications especially to prevent or treat diseases or medical conditions in human patients, coprevent or treat diseases or medical conditions in human patients, copress mediated by IFN gamma or interleukin-4, septic shock, corrections and relatives or praft-version mediated by tumour necrosis
high affinity ligand; cytokine; interferon-gamma; IFN-gamma; RANTES; interleukin-4; IL-4; tumour necrosis factor-alpha; TNF-alpha; Systematic Evolution of Ligands by Exponential enrichment; SELEX; diagnosis; inflammatory response; septic shock; arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= a
/note= "all U's are 2'-NH2 modified and all C's are
2'-F modified"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identification of nucleic acid ligands that bind cytokine(s) partitioning the ligands from a nucleic acid mixture, using ?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tasset D;
                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 20; Page 69; 175pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96WO-US09537
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                                                                                                                                                                         graft-vs-host reaction; ss
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/*tag=
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                                                                                                                                                                                                                                                                                                                                     Key
modified_base
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Gaps

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0; Indels

0; Mismatches

Conservative

Best Local Similarity Matches 15; Conserva

Query Match

75.0%; Score 15; DB 22; Length 15; 100.0%; Pred. No. 1.6e+02;

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to prevent or treat diseases or medical conditions in human patients, e.g. associated with excessive cytokine production such as inflammatory responses mediated by IFW-agamma or interleukin-4, septic shock, arthritis or graft-vs-host reactions mediated by tumour necrosis
                                                                                                                        Sequence 40 BP; 12 A; 5 C; 18 G; 5 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 21 BP; 2 A; 6 C; 11 G; 2 T; 0 other;
                                                                                   factor-alpha
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                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                       high affinity ligand; cytokine; interferon-gamma; IFN-gamma; RANTES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         interleukin-4; IL-4; tumour necrosis factor-alpha; TNF-alpha; Systematic Evolution of Ligands by Exponential enrichment; SELEX; diagnosis; inflammatory response; septic shock; arthritis; graft-vs-host reaction; ss.
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partitioning the ligands from a nucleic acid mixture, using SELEX
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0
                                                              Length 40;
                                                                                                    Indels
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/note= "all pyrimidines are 2'-F"
                                                       Score 14.2; DB 18;
Pred. No. 4.1e+02;
1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                             Interleukin-4 2'F RNA ligand, orphan clone #21.
G; 5 U; 0 other;
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Sequence 40 BP; 12 A; 5 C; 18
                                                                                                                                                                                                                                                                                    AAT87201 standard; RNA; 40 BP.
                                                         71.0%;
78.9%;
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                                                                                                  Conservative
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/*tag=
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                                                       Query Match
Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                             AAT87201;
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                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polymerase chain reaction; amplification; non-specific priming; blocking oligonucleotide; donor; acceptor; fluorophore; energy transfer; ligation; AML-1; acute myeloid leukaemia; breakpoint related sequence; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amplification process could be monitored using either a primer;
blocking oligonucleotide duplex or a universal detection duplex
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Detecting target nucleic acid by amplification - with primer-blocking oligo:nucleotide duplex(es) labelled with donor and acceptor fluorophore(s), to reduce non-specific priming
      Length 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human AML-1 limiting primer, for asymmetric amplification.
                                                                Indels
71.0%; Score 14.2; DB 18; 78.9%; Pred. No. 4.1e+02; ive 1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 4; Page 23; 41pp; English.
                                                                                                                                                                                                                                                                                                                                             AAT09720 standard; DNA; 21 BP
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                                                                                                                              2 gcgccgtgaagcgaaggca 20
                                                                                                                                                                                     5 gcgccaugaagcaaaggga 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1996-020598/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to a primer.
Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9532306-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-NOV-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                          AAT09720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wang CJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            coupled
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66.0%; Score 13.2; DB 17; Length 21;

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Target; DNA duplex; donor; acceptor; fluorescent label; fluorophore;
energy transfer; polymerase; primer; acute myeloid leukaemia; AML-1; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kits for detecting target nucleic acids - and DNA duplexes with donor and acceptor fluorescent labels
                                                                                                          Limiting primer used for detecting target nucleic acid AML-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 4; Column 12; 17pp; English.
               AAV09361 standard; DNA; 21 BP.
                                                                          15-MAY-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                      (BIOT -) BIOFRONICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-120033/11.
                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                         16-DEC-1991;
04-MAY-1995;
                                                                                                                                                                                                                                                                                              04-MAY-1995;
                                                                                                                                                                                                                                                                                                                             26-MAY-1994;
                                                                                                                                                                                                                                  US5712386-A.
                                                                                                                                                                                                                                                                27-JAN-1998
                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                   Wang CJ,
               ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the human acute myeloid leukaemia breakpoint related sequence (AMP-1), and the human x chromosome specific ameloginen (AMG-X) were used as amplification tragets. The sequences of the primers used for AML-1 and AMG-X respectively were AAT45479 and AAT45480, the duplex comprised AAT45481 and AAT45482 and the sequences of excess and limiting primers for AML-1 and AMG-X respectively were AAT45483 and AAT45484, and AAT45485 and AAT45486. Male human genomic DNA sequences were asymmetrically amplified with excess primer for the addition of the primer duplex. The results compiled from detection at cycle 30 demonstrated the quantitative
                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid detection by amplification - in presence of primer-complementary oligo:nucleotide to block non-specific priming
                                                                                                                                                                                                                                                                                          Detection duplex, asymmetric amplification; human; acute; myeloid; leukaemla; breakpoint; related sequence; AMP-1; X chromosome; specific ameloginen; AMG-X; primer; excess; limiting; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             In an example to demonstrate the application of a detection duplex to monitor the asymmetric amplification of target nucleic acids,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              resolution and detection sensitivity by the duplex. The decrease in fluorescence intensity reflected the initial target doses.
                              ö
                                                                                                                                                                                                                                                             Human leukaemia breakpoint related sequence, limiting primer.
                              Indels
Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 21 BP; 2 A; 6 C; 11 G; 2 T; 0 other;
                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 4; Column 12; 17pp; English
                                                                                                                                                                       BP.
              83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                               91US-0808463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94US-0250849
91US-0808463
                                                                                                                                                                    AAT45484 standard; DNA; 21
                                                          2 gcgccgtgaagcgaaggc 19
                                                                            (first entry)
              Best Local Similarity 83.3
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BIOT-) BIOTRONICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-010704/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wu K;
                                                                                                                                                                                                                                02-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                              16-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                   US5567583-A.
                                                                                                                                                                                                                                                                                                                                                                                                                 22-OCT-1996
                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                  AAT45484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wang CJ,
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94US-0250849. 91US-0808463. 95US-0434474.

95US-0434474

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This is a limiting primer used in a kit for detecting a target nucleic acid of human acute myeloid leukaemia breakpoint related sequence (admi-1). The kit is a DNA duplex which comprises a first oligonucleotide of acting as a primer, with or without a segment noncontiguous to its priming sequence, for use with a polymerase in the amplification of a target nucleic acid, a second oligonucleotide bairings, with the first oligonucleotide, the second oligonucleotide pairings, with the first oligonucleotide, the second oligonucleotide pairings, with the first oligonucleotide, the second oligonucleotide and a second fluorophore covalently attached to the first oligonucleotide, with one of the two fluorophores of acting as a primer for the polymerase, and a first fluorophore covalently attached to the second oligonucleotide, with one of the two fluorophores of being a donor fluorophore and the other being an acceptor fluorophores of that when the two fluorophores are in close proximity resonance energy transfer between them is allowed. Each of the first oligonucleotide contains 10-50 nucleotides. Another kit claimed comprises a first and second primer both optionally having a sepment non-contiguous to a first or second primin sequence, respectively, which are used with a polymerase for the amplification of the first primer. Each of the first primer is along an oligonucleotide with is incapable of acting as a primer for the polymerase and has at least 5 consecutive nucleotides contains 10-50 nucleotides with a first fluorophore covalently attached to it, and second containing 10-50 nucleotides with a first fluorophore covalently attached to it, and a second oligonucleotide being incapable of containing 5-30 nucleotides with a second oligonucleotide and the second containing a second oligonucleotide with a second containing 5-30 nucleotides with a second oligonucleotide such the first oligonucleotide and the first oligonucleotide is and of the second containing 5-30 mucleotides with a second oligonucleotide such the firs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleotides, and the first and second fluorophores, one of which is adonor fluorophore and the other an acceptor fluorophore are in close
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proximity when the first oligonucleotide hybridises to the second oligonucleotide to allow resonance energy transfer between them. The kits are used in homogeneous assays in which the target nucleic acid sequence is amplified and the amplified target is detected without
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Gaps

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66.0%; Score 13.2; DB 18; Length 21; 83.3%; Pred. No. 1.2e+03; Live 0; Mismatches 3; Indels (

1 geggegtgaageggegge 18

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RESULT AAV09361

2 gcgccgtgaagcgaaggc 19

Conservative

Query Match Best Local Similarity Matches 15; Conserv

.; 0

Gaps

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Length 21;

Score 12.8; DB 22; Pred. No. 1.9e+03;

64.0%; 87.5%;

Conservative

Similarity

Pred. No. 1.96; Mismatches

BP.

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AAZ43694 standard; DNA; 33
                                                                                                                                     5 ccgtgaagcgaaggca 20
                                                                                                                                                                             ccgtgaagcgaatgaa 17
                                            Query Match
Best Local Simi
Matches 14;
                                                                                                                                                                                                                                                                                                                                       AAZ43694;
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                                                                                                                                                                                                                                                                     AAZ43694
                                                                                                                                                                                                                                                RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disease, stroke, peripheral vascular diseases, venous thromboembolism and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also useful in forensics, paternity testing, genetic analysis and phenotype correlations to diseases. The present sequence is an example of one of the human gene SNPS shown in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; variant thrombospondin 1; variant thrombospondin 4; SNP; polymorphism; vascular disease; coronary artery disease; forensics; myocardial infarction; atherosclerosis; stroke; venous thromboembolism; pulmonary embolism; paternity test; ds.
                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              McCarthy JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids comprising single nucleotide polymorphisms, useful in applications such as forensics, paternity testing, medicine, genetic analysis and phenotype correlations to diseases such as diabetes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /standard_name= "single nucleotide polymorphism"
                                                                                                                                                       ;
0
                                                                                                             Length 21;
                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Daley GQ,
                                                                                                           Score 13.2; DB 19;
Pred. No. 1.2e+03;
); Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human gene single nucleotide polymorphism #69.
                                          Sequence 21 BP; 2 A; 6 C; 11 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bolk S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 21 BP; 7 A; 5 C; 5 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (WHED ) WHITEHEAD INST BIOMEDICAL RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ireland JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
replace(11,A)
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Examples; Page 51; 242pp; English.
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                                                                                                                                                                                                                                                                                                                                                            BP.
conducting a separation step.
                                                                                                         66.0%;
ilarity 83.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0153357.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0220947.
2000US-0225724.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-SEP-2000; 2000WO-US24503
                                                                                                                                                                                                                                                                                                                                                          AAF95308 standard; DNA; 21
                                                                                                                                                                                                  2 gcgccgtgaagcgaaggc 19
                                                                                                                                                                                                                                            1 gcggcgtgaagcggcggc 18
                                                                                                                                                                                                                                                                                                                                                                                                                                              06-JUN-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-226749/23.
                                                                                                           Query Match
Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
Variation
                                                                                                                                                                                                                                                                                                                                                                                                      AAF95308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lander
                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                  AAF95308
                                                                                                                                                                                                                                                                                                           RESULT
SXS
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known genetic mutations, using modified mucleoside triphosphates to improve the performance. The method comprises: (1) amplifying a DNA sequence by polymersae chain reaction (PCR) using primers selected to sequence by polymersae chain reaction (PCR) using primers selected to of modified nucleoside triphosphates (NPPS) to effect limited extension of already present or newly added primers, where: (a) the extension of cartion stops at the next occurrence of a particular base in the DNA strand being copied; (b) the extension reaction proceeds up to or past the mutation site, so that wild-type amplification products will have a different molecular weight from mutant amplification of the DNA chains during ionization of the NTPs results in stabilization of the DNA chains during ionization yields and/or a change in the mass of the DNA chains; (3) performing the limited primer extension using an enzyme that generates the complement of the DNA strand being copied; (4) performing at least partial primer degradation and optionally further modification of the maplification products; and (5) determining the mass of the DNA chains; (3) performing the limited primer products; and (5) determining the mass of the considered of the maplification products; and (5) determining the mass of the considered of the maplification products; and (5) determining the mass of the considered of the maplification and optionally further modification and the mass of the considered of the maplification and optionally further modification and the mass of the considered of the maplification and optionally further modification and the mass of the considered of the maplification and performing the mass of the considered of the maplification and optionally further modification and the mass of the considered of the maplification and optionally further modification and the mass of the considered of the maplification and optionally further modification and the mass of the considered of the mass of the considered of the mass of the considered of the mass o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes a method for mass-spectrometric analysis of
                                                                                                                                                                                                                              Primer; mass-spectrometry; genetic mutation; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mass-spectrometric analysis of known gene mutations
                                                                                                               Mass spectrometric mutation analysis primer 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 33 BP; 6 A; 11 C; 11 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example; Page 8; 16pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BRUK-) BRUKER DALTONIK GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98DE-1024280.
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-073581/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                DE19824280-A1.
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23-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-DEC-1999.
                                                                                                                                                                                                                                                                                                                                             Synthetic.
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Coupled polymerase chain reaction-restriction endonuclease digestion-ligase detection reaction to identify low abundance sequences differing by single-base changes, insertion or deletion from high

Bergstrom DE;

Barany F, Day JP, Hammer RP,

WPI; 2000-638269/61.

(CORR) CORNÉLL RES FOUND INC (LOUU) UNIV LOUISIANA STATE. (PURD) PURDUE RES FOUND.

17-MAR-2000; 2000WO-US07133.

WO200056929-A2

28-SEP-2000

99US-0125251.

19-MAR-1999;

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                                                                                                                                                                                                                                                                                                                                                               The specification describes a new regulatory sequence for Trichoderma viride derived cellulase cbhi gene and the establishment of a system for mass producing cellulase in moulds such as T. viride. As the regulatory sequence of cbhi genes originating in T. viride can highly express objective proteins, proteins such as cellulase can be expressed. An expression vector containing the regulatory sequence and Hunicola insolens derived endo-glucanase NCE4 DNA was produced, and used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Coupled polymerase chain reaction; PCR; ligase detection reaction; LDR; restriction endonuclease digestion; RED; infectious disease; cancer; waste water purification; ds.
                                                                                                                                                                                                                                                                                                                                                      Oligonucleotides AAV36074-75 are used in the course of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                       cory sequence for Trichoderma viride derived cellulase cbhl for producing Humicola insolens derived endo-glucanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63.0%; Score 12.6; DB 19; Length 36; 78.9%; Pred. No. 2.4e+03; ive 0; Mismatches 4; Indels
                                                                                                                 Regulatory sequence; cellulase cbhl gene; mass production;
Humicola insolens; endo-glucanase NCE4; ss.
                                                                                                                                                                                                                                                                 Ξ
                                                                                                                                                                                                                                                                 Watanabe
                                                                                             Oligonucleotide SCE3-Stu of the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 36 BP; 4 A; 11 C; 12 G; 9 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleotide sequence of a synthetic duplex DNA.
                                                                                                                                                                                                                                                                Sumida N,
                                                                                                                                                                                                                                                                                                                                                                                                                                   endo-glucanase at 15 grams per litre.
                                                                                                                                                                                                                                                                                                                                  Example 11; Page 29; 92pp; Japanese
                                                                                                                                                                                                                                                                 Moriya T, Murakami T,
                                                                                                                                                                                                                                            (MEIJ ) MEIJI SEIKA KAISHA LTD.
                                     AAV36074 standard; DNA; 36 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA96608 standard; DNA; 50 BP
                                                                                                                                                                                                       97WO-JP03268.
                                                                                                                                                                                                                          96JP-0243695.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ggcgccgtgaagcgaaggc 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 GGAGCCATGATGCGCAGGC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                   WPI; 1998-250959/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                WO9811239-A1
                                                                                                                                                                                                      16-SEP-1997;
                                                                                                                                                                                                                          13-SEP-1996;
                                                                          02-SEP-1998
                                                                                                                                                                                  19-MAR-1998
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                                                                                                                                                                                                                                                                                                       Regulatory
                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                Aoyagi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                      AAV36074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA96608;
                                                                                                                                                                                                                                                                                                                 gene -
                         AAV36074/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
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                 RESULT
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The specification describes the use of coupled polymerase chain reaction (PCR), restriction endonuclease digestion (RED) and ligase detection reaction (LDR) to identify one or more low abundance sequences differing by one or more single base changes, inserts or deletions, from a high abundance sequence, in several target nucleotide sequences. The method involves 3 PCR reaction phases, a RED phase and an LDR phase. The method is used to identify one or more low abundance sequences. The method is also useful for detecting a wide variety of infectious diseases caused by acterial, viral, parasite and fungal infectious agent. Cancers can also be detected by this method. The method is also used for detection, identification and monitoring of pathogenic and indigenous municipal waste water purification system and water reservoirs or in polluted areas undergoing bioremediation and to detect plasmids containing genes that can metabolise xenoblotics, to monitor specific target microorganisms in population dynamic studies, or either to detect. Indentify, or monitor specific target microorganisms in the environment and in industrial plants. The presents sequence represents a synthetic duplex DNA template, used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; c-fos; hammerhead ribozyme; hairpin ribozyme; target site;
cancer; oncogene; leukaemla; neuroblastoma; diagnosis; genetic drift;
mutation; diseased cell; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human c-fos target sequence nucleotide position 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 12.6; DB 21;
Pred. No. 2.4e+03;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 50 BP; 11 A; 18 C; 12 G; 9 T; 0 other;
abundance sequence in target sequences
                                                                   Example 7; Fig 6A; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63.0%;
78.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the course of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gcggcatgaaccggaggc 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAV95266/c
ID AAV95266 standard; RNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 78.9
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAV95266;
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English.

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cyclin or cell-cycle dependent kinase other than CDK1,
                          Disclosure; Page 76; 109pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Duda A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-123317/13
                                                                                                                                                                    Query Match
Best Local Similarity
RNA encoding a cycl
PCNA and Cyclin B1
                                                                                                                                                                                                                                                                                                                                                                                                            WO200109161-A1.
                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JUL-1999;
                                                                                                                                                                                                                                                                                                                     30-APR-2001
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                                                                                                                                                                                                                                                                                                                                          Primer #60.
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                                                                                                                                                                                                                                                                                                AAF74126;
                                                                                                                                                                                        Matches
δλ
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                                                                                                                                                                                     The present invention describes an enzymatic nucleic acid molecule which specifically cleaves RNA derived from a c-fos gene. AAV95401 to AAV95540 and AAV95541 to AAV95584 represent hammerhead ribozymes and hairpin
                                                                                                                                                                                                                 ribozymes, respectively, which specifically cleave human c-fos. AAV95261 to AAV95400 and AAV95385 to AAV95628 represent human c-fos target sequences. The enzymatic nucleic acid molecules can be used for treating cancer associated with elevated levels of c-fos oncogene, especially leukaemias, neuroblastomas and lung, breast and colon cancers. The ribozymes may also be used as diagnostic tools to examine genetic drift and multiplications within diseased cells, or to detect the presence of c-fos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                           Enzymatic nucleic acid molecules which specifically cleave RNA derived from a c-fos gene - useful for treating conditions related to levels of c-fos, especially cancer
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0
                                                                                                                                                                                                                                                                                                                                         Length 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ribozyme; hairpin; hammerhead; gene therapy; vasotropic;
                                                                                                                                                                                                                                                                                                                                        Score 12.2; DB 19;
Pred. No. 3.6e+03;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                          Sequence 17 BP; 2 A; 8 C; 3 G; 4 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Robbins JM;
                                                                                      McSwiggen JA, Stinchcomb DT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cyclin D3 ribozyme binding site #1.
                                                                                                                                                                   English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Barber JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP.
                                                                                                                                                                                                                                                                                                                                        61.0%;
82.4%;
                           98WO-US01017
                                              97US-0037658
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0110954
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA84390 standard; DNA; 19
                                                                  (RIBO-) RIBOZYME PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 82.45
                                                                                                                                                                                                                                                                                                                                                                               1 ggcgccgtgaagcgaag 17
                                                                                                                                                                                                                                                                                                                                                                                                 17 GGCGCTGTGAAGCAGAG 1
                                                                                                                                                                   Claim 2; Page 50; 72pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (IMMU-) IMMUSOL INC.
                                                                                                         WPI; 1998-427942/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Welch PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-412314/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          restenosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200032765-A2.
                                                                                                                                                                                                                                                                                        RNA in a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-DEC-1998;
                           20-JAN-1998;
                                               23-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-JUN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-DEC-2000
        30-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAA84390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tritz R,
                                                                                      Jarvis
                                                                                                                                                                                                                                                                                                                                                                                                                                13
                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA84390
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The present invention relates to a hairpin or hammerhead ribozyme, designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase other than cell-cycle dependent kinases CDK1. PCNA and Cyclin B1.
Representative examples of ribozyme recognition sites are given in AAA8415 to AAA86787. The ribozyme of the invention is useful for Inhibiting restenosis by introduction of the ribozyme into cells. The ribozyme is resistant to endonuclease activity and hence is efficient in restenosis treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention is used in producing a recombinant organism that can be used to express SLGGA4 for protein structure analysis and binding studies. A composition comprising a genotyping oligonucleotide is used to detect a polymorphism in the SLC6A4 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide comprising a polymorphic variant for the solute carrier family 6 neurotransmitter transporter, serotonin member 4 gene for identifying drugs for treating disorders related to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to a polymorphic variant of a reference sequence for the solute carrier family 6 neurotransmitter transporter, serotonin member 4 (SLC6A4) gene or a fragment of it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sectonin 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                   Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stephens JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Solute carrier family 6 neurotransmiter transporter; SLC6A4; genotyping; allele specific oligonucleotide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or a sequence complementary to the first sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                       21;
                                                                                                                                                                                                                                                                                                                                                                                                                Score 12.2; DB 21.
Pred. No. 3.6e+03;
); Mismatches 33
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                                                                                                                                                                                                                                                                                                             Sequence 19 BP; 3 A; 4 C; 7 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20 BP; 2 A; 8 C; 3 G; 7 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 37; 152pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GENA-) GENAISSANCE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                   61.0%;
82.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0146290.
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ID AAF74126 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 gccgtgaagcgaaggca 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 gctgtgttgcgaaggca 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14; Conservative
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                                  Gaps
                                  ö
                                                                                                                                                                                                                                                                                                                  Polymorphism; human; interleukin 4 receptor-alpha; IL4R-alpha; allergic disease; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide useful for the identification of therapeutics in allergic diseases is new -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 12.2; DB 22; Length 22; Pred. No. 3.7e+03; 0; Mismatches 3; Indels (
 Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chew A, Denton RR, Duda A, Nandabalan K, Stephens JC;
Windemuth AK;
                                Indels
Score 12.2; DB 22;
Pred. No. 3.6e+03;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 22 BP; 9 A; 2 C; 10 G; 1 T; 0 other;
                                                                                                                                                                                                                                                                                   Human IL4Ralpha gene PCR primer #98.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 65; 188pp; English.
                                                                                                                                                                                  AAF69762 standard; DNA; 22 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GENA-) GENAISSANCE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61.0%;
82.4%;
Query Match 61.0%;
Best Local Similarity 82.4%;
Matches 14; Conservative
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                                                                                                                                                                                                                                                    (first entry)
                                                                 4 gccgtgaagcgaaggca 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 61.0
Best Local Similarity 82.4
Matches 14; Conservative
                                                                                                19 GCGGTGAAATGAAGGCA 3
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                                                                                                                                                                                                                                                                                                                                                                                                 WO200104270-A1.
                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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4 gccgtgaagcgaaggca 20 gcagggaagagaaggca 21 ò g

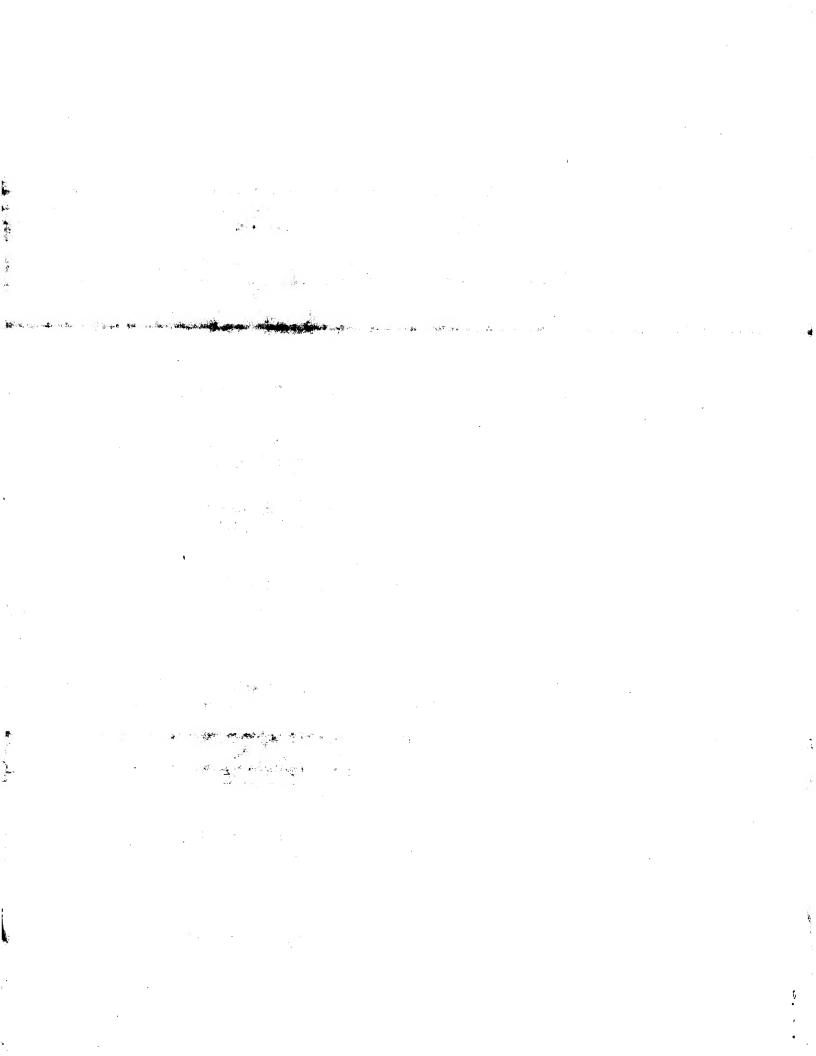
Search completed: October 2, 2001, 16:18:35 Job time: 15479 sec

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Gaps

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Sense primer for m Probe for human PG Human Ets-2 phosph Primer V-beta-3 fo PCR primer for the Primer murf3.

Syn

Primer murF4.

PCR primer used to Anabaena variabili

PCR primer for DNA Arabidopsis thalia Yeast acyltransfer Arabidopsis thalia

Yeast acyltransfer PCR primer for DNA

Liposome membrane-chicken 1gG light Arabidopsis thalia cels dockerin gene Arabidopsis thalia M. tuberculosis 16 Human NKC2 gene e PCR primer used to M. tuberculosis 16 Mycobacterium genu

oę

Potal number

Database

Searched:

Perfect score:

Run on:

Sequence:

Scoring table:

bovis 16S rRNA smegmatis 16S r

M. intracellulare Mycobacteria 16S 1

tuberculosis 16

Mycobacterium 16S M. tuberculosis 16

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New antisense compounds for inhibiting focal adhesion kinase expression, especially useful for inhibiting retinal neovascularization, or for diagnosing and treating e.g. colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; focal adhesion kinase; FAK; signal transduction; cancer; embryonic development disorder; angiogenic disorder; wound healing; antisense; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human focal adhesion kinase antisense sequence #1.
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                                                                              AAT63364
AAX86099
AAT63369
AAX86104
 AAZ35374
AAZ01125
                                               AAA29338
AAZ10873
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AAA37487
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AAX36171
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AAT92997
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                                  AAA38381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Monia BP, Gaarde WA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-006141/01.
   Homo sapiens
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AAC65535;
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Maximum DB seq length: 50
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The present invention describes a number of phosphorothioate antisense sequences to the human focal adhesion kinase (FAK) protein. This protein is involved in integrin-mediated signal transduction, and is implicated in cancer, particularly colon, breast and oral tumours, embryonic development disorders, angiogenic disorders and wound healing. The antisense sequences, including the one shown here, can be used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a number of phosphorothioate antisense sequences to the human focal adhesion kinase (FAK) protein. This protein is involved in integrin-mediated signal transduction, and is implicated in cancer, particularly colon, breast and oral tumours, embryonic development disorders, anglogenic disorders and wound healing. The antisense sequences, including the one shown here, can be used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antisense compounds for inhibiting focal adhesion kinase expression, especially useful for inhibiting retinal neovascularization, or for diagnosing and treating e.g. colon cancer
                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; focal adhesion kinase; FAK; signal transduction; cancer;
embryonic development disorder; angiogenic disorder; wound healing;
antisense; phosphorothioate; ss.
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                                                                                                                                                                                                                        DB 22; Length 20;
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                                                                                                                                                                                                                      100.0%; Score 20; DB 22 100.0%; Pred. No. 0.55;
                                                                                                                                                                      Sequence 20 BP; 2 A; 7 C; 8 G; 3 T; 0 other;
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Claim 3; Column 23; 30pp; English.
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                                                                                                                                    treatment of all of these.
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Matches 20; Conserv
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Acyl-CoA:cholesterol acyltransferase; ACAT; ACAT-like protein; sterol; ester; triacylglycerol; fatty acyl-CoA; lipid composition; plant cell; diacylglycerol acyltransferase; DAGAT; triglyceride; cancer; diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a translational reporter vector selected from p2luc and p2luci. The vectors have a polylinker interposed between a renilla luciferase gene and a firefly luciferase gene, which are out-of-frame with respect to each other but are co-expressed upon recoding. The translational reporter vector is useful for assaying translational recoding in vitro or in vivo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Translational reporter vector for quantification of translation recoding in vivo and in vitro, comprises renilla luciferase gene, polylinker for insertion of selected DNA and an out-of-frame firefly
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                                                                                                                                                                                                      vector; renilla luciferase;
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                                                                                                                                                                                                                                                                                                                                                                                                          Gesteland RF;
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Best Local Similarity
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Gaps

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Length 15;

75.0%; Score 15; DB 22; I 100.0%; Pred. No. 1.5e+02; Conservative 0; Mismatches 0;

Query Match Best Local Similarity Matches 15; Conserv

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The invention provides polymorphic fragments of genes associated with hypertension. The nucleic acids including the polymorphic sites can be used as probes or primers for expressing variant proteins. Detection of the polymorphisms is useful in designing prophylactic and therapeutic regimes customized to underlying abnormalities. The polymorphisms can be used for association studies for hypertension, and in hypertension of diagnostic assays. Where the polymorphisms have strong correlation with hypertension, within a gene, they are likely to have a causative role in hypertension. This information can be used to find the precise role of a polymorphism in the disease, and this can be used to identify potential cutys which combat the disease. The polymorphisms can be tested for association with other diseases. The polymorphisms can be tested for association with other diseases. G. agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabrys disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrands disease, tuberous sclerosis, hereditary hemorrhagica telangiectasia, familial
    Fabrys disease; familial hypercholesterolemia; hereditary spherocytosis; polycystic kidney disease; von Willebrands disease; forensic; human; tuberous sclerosis; hereditary hemorrhagica telangiectasia; familial colonic polyposis; osteogenesis imperfecta; porphyria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                colonic polyposis, Ehlers-Danios syndrome, osteogenesis imperfecta, and acute intermittent porphyria. The polymorphic forms can also be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acids containing polymorphisms used in the diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Retroviral vector; gene delivery vehicle; expression; PCR primer; non-immunogenic selectable marker; gene therapy; activation;
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                                                                                Ehlers-Danlos syndrome; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 75.0°
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                    (AFFY-) AFFYMETRIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-107928/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypertension
                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                   07-MAY-1999;
                                                                                                                                                                                                                                                                         07-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-0CT-1998
                                                                                                                                                                                                                                                                                              03-MAY-1999;
                                                                                                                                                                                                 10-NOV-1999.
                                                                                                                                                           EP955382-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAV42721;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAV42721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              per primers AA245392-93 were used to amplify rat acyl-CoA:cholesterol acyltransferase (ACAT)-like gene. The ACAT-like protein is active in the formation of a sterol, ester and/or triacylglycerol from a fatty acyl-CoA and sterol and/or diacylglycerol substrate. The DNA can be used for modifying the lipid composition of plant cells. The ACAT-like protein has diacylglycerol acyltransferase (DAGAT) activity, and so the synthesis of triglycerides can be suppressed or increased using the DNA. The protein can be used to produce plant oils with a modified triglyceride content. The products can also be used to identify antagonists and agonists of DAGAT activity. Such agonists and antagonists are particularly useful in treating or ameliorating diseases associated with DAGAT activity, including concentration or PKC activity, including cancer, diabetes, concentration or PKC activity, including cancer, diabetes, cardiopulmonary diseases e.g. heart failure, atherosclerosis, adisorders, obesity, diseases associated with abnormal lipid metabolism, and diseases associated with abnormal fat absorption,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel polynucleotides used for modifying plant oil composition and for developing products for treating e.g. cancer, diabetes, cardiopulmonary disease or metabolic disorders
cardiopulmonary disease; heart failure; atherosclerosis; adipocytosis; leukaemia; skin carcinoma; fibroblastoma; metabolic disorder; obesity; abnormal lipid metabolism; abnormal fat absorption; lipoprotein secretion; adipogenesis; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus; Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polymorphic fragment of hypertension associated gene GSY1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68.0%; Score 13.6; DB 21;
80.0%; Pred. No. 7.2e+02;
ive 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 41 BP; 7 A; 13 C; 19 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lipoprotein secretion and adipogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Page 30; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA04346 standard; DNA; 29 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ccgcgggctcacagtggtcg 20
                                                                                                                                                                                                                                   99WO-US12541.
                                                                                                                                                                                                                                                                       98US-0088143
98US-0108389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 ccgcggccgcacaatgggcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 80.0 es 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                      Ruezinsky
                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-105701/09.
                                                                                                                                                                                                                                                                                                                                  (CALJ ) CALGENE LLC.
                                                                                                                                                       WO9963096-A2
                                                                                                                                                                                                                                   04-JUN-1999;
                                                                                                                                                                                                                                                                     05-JUN-1998;
12-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                        Lassner MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-MAY-2000
                                                                                                                                                                                             09-DEC-1999
                                                                                                                    Rattus sp.
                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA04346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'n
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Matches
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Gaps

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Indels

membrane

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The invention relates to nucleic acids encoding novel plant acyltransferase-like proteins (AAA37343-A37445) which comprise one of a conserved acyltransferase motifs (AAY9944-Y99481). Acyltransferases catalyse the transfer of acyl groups from a donor to a variety of substrates such as glycerides, sterols, stanols and phosphatides.

Such enzymes play a key role in lipid synthesis, and thereby affect the characteristics of the plant. For example, cold-hardened plants have different lipid concentrations in the cell membrane compared to non-hardened plants, which makes the membrane more fluid and the plant mon-hardened plants, which makes the membrane sequences of the rowention can be used as probes or for expressing acyltransferase-like proteins in host cells e.g., for recombinant protein production. They may be expressed in plant cells to alter the lipid composition of the production of chill-resistant plants, or for altering the composition of plant oils. Sequences AAA33473-AA344 represent PCR primers used in an exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNAs (AAA37331-A37342) for cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prenyltransferase; ATPT1; ATPT2; ATPT4; ATPT4; ATPT5; ATPT6; ATPT7; ATPF8 ATPT9; ATPT8; ATPT9; ATPT11; ATPT12; tocopherol; homogentisic acid; phytylpyrophosphate; 2-methyl-6phytylbenzoquinol; antioxidant; nutritional supplement; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCR primer for DNA encoding a prenyltransferase designated ATPT8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 13.2; DB 21; Length 39;
Pred. No. 1.1e+03;
0; Mismatches 3; Indels (
                                                                                                                                                                       Novel acyltransferase related proteins useful for altering fluidity in plant cells e.g. to induce chill tolerance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Weiss JD, Post-Beittenmiller D;
                                                                                     Van Eenennaam A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       into plant and baculovirus expression constructs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 39 BP; 11 A; 9 C; 12 G; 7 T; 0 other;
                                                                                     Ruezinsky DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana acyltransferase
                                                                                                                                                                                                                                  Example 7; Page 31; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66.0%;
83.3%;
  98US-0101939.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0129899.
99US-0146461.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-APR-2000; 2000WO-US10368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ccgcgggctcacagtggt 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ccgcggccgcacaatggt 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAC61924 standard; DNA; 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity 83.3
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lassner MW,
                                                                                     Emig RA,
                                                                                                                               WPI; 2000-303447/26.
                                           (CALJ ) CALGENE LLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CALJ ) CALGENE LLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200063391-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis sp.
  25-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JUL-1999;
                                                                                     Lassner MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Savidge B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAC61924;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC61924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
  δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the markers and a heterologous sequence are useful in gene therapy. The vectors can be used to deliver a molecule into a target area where it may cause the activation of a previously inactive substance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCR primers AAV42720-21 were used to amplify human furin cDNA (see AAV42731). The amplified product is used in the retroviral vector of the invention to encode a cell bound prodrug convertase for ablation therapy. The specification describes encode a cell specification describes expression of a non-immunogenic selectable marker or molecule which is capable of activating a previously inactive compound. Vectors expressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana acyltransferase ATAT7 PCR primer, SEQ ID NO:173.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Non:immunogenic pro:drug activating enzyme(s) and selectable marker(s) - are used in gene therapy for the treatment of a wide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66.0%; Score 13.2; DB 19; Length 31; larity 83.3%; Pred. No. 1.1e+03; Conservative 0; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Acyltransferase; lipid synthesis; recombinant expression; membrane fluidity; cold resistance; transgenic plant; baculovirus expression; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 31 BP; 5 A; 12 C; 10 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 8; Page 53; 121pp; English
human; furin; ablation therapy; ss
                                                                                                                                                                                                                                                                                                                                                                                                       Moore MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP.
                                                                                                                                                                                                                                                 97US-0038473.
                                                                                                                                                                                          98WO-US00715
                                                                                                                                                                                                                                    98US-0038339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US22231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 giggotcacagaggeg 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA37483 standard; DNA; 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           variety of disorder(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                     Chada S, Jolly DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-399153/34
                                                                                                                                                                                                                                                                                                                   (JOLL/) JOLLY D J. (MOOR/) MOORE M D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200018889-A2
                                                                                                                                                                                                                                13-JAN-1998;
14-JAN-1997;
27-FEB-1997;
                                                             Homo sapiens
                                                                                                       WO9830709-A2
                                                                                                                                                                                        14-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-AUG-2000
                                                                                                                                                 16-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-APR-2000
                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAA37483;
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AAA37483 RESULT

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Gaps

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Oligonucleotides can be used to alter the profile of the blood factor without significantly altering its activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immunodeficiency virus type 1.
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                                                                                                                                                                                                                                                                                                                                                                                                       AAA72106 standard; DNA; 44 BP.
                                                                                                                                         64.0%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-JAN-1999; 99US-0115404.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-JAN-2000; 2000WO-US00456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                         Query Match 64.0
Best Local Similarity 87.5
Matches 14; Conservative
                                                                                                                                                                                                                                       2 cgcgggctcacagtgg 17
                                                                                                                                                                                                                                                                                 19 egegtgeteagagtgg 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-465959/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Weiss CD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (WILD/) WILD C T.
(WEIS/) WEISS C D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200040616-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 - NOV - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAA72106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wild CT,
                                                                                                                                                                                                                                                                                                                                                           10
                                                                                                                                                                                                                                                                                                                                                                              AAA72106
                                                                                                                                                                                                                                                                                                                                                           RESULT
  SS \times S
                                                                                                                                                                                                                                                                                 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                            PCR primers AAC61924-25 were used to amplify DNA encoding a perplicansferase. The specification describes premyltransferases designated APPI, APPI, ATPI, AT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                       Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Factor VIII analogue is sufficiently mutated from the original gene that it is not recognised by blood Abs of the patient. The analogue is composed of human FVIII but carries the B-domain of human FV in place of the FVIII B-domain.
                                                                    sequence encoding prenyltransferase used increase the production of tocopherols -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oligonucleotide carrying mutation for factor VIII gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New hybrid DNA encoding hybrid procoagulant proteins - prepd. by modifying DNA encoding human factor VIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 13.2; DB 21;
Pred. No. 1.1e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 50 BP; 9 A; 16 C; 14 G; 11 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 1.16
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                         Example 2; Page 26; 114pp; English.
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83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human factor VIII analogue;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAQ04938 standard; DNA; 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ccgcgggctcacagtggt 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cegeggeegeacaatggt 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; ; pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GENE-) GENETICS INST INC.
                                                                  An isolated nucleic acid
transform plant cells to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag=
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                      WPI; 2000-647519/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-NOV-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-NOV-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Simi
Matches 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQ04938;
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The invention relates to raising a neutralising antibody response to a broad spectrum of HIV (human immunodeficiency virus) strains and isolates, comprising the administration of a peptide which corresponds to or mimics highly conserved portions of the gp41 envelope glycoprotein which are important in mediating the process of viral entry into host cells. Such peptides can correspond to or mimic the coiled coil solution structure of the N-helical domain (the heptad repeat region), or can correspond or mimic the C-helical domain (the transmembrane-proximal amphipathic alpha-helical domain (the pp41 core 6-helix bundle, which is formed by the interaction of the N- and C-helical domains of three gp41 proteins. The peptides can be administered either singly or as a combination (particularly multimerised. For example, N- and C-helical domain peptides can be alternately linked together to form a peptide which mimics the core alternately linked together to form a peptide (s) generates a humoral response, with the production of antibodies against gp41 structures involved in viral entry. As these portions of gp41 are well conserved,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Raising neutralizing antibody response to human immunodeficiency virus, comprises administering a polypeptide capable of forming a stable coiled-coil solution structure
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                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                           ;
0
                                                                                                                                               Length 39;
                                                                                                                                                                                                                                           Indels
                                                                                                                                          Score 12.8; DB 11;
Pred. No. 1.8e+03;
0; Mismatches 2;
Sequence 39 BP; 9 A; 11 C; 11 G; 8 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HIV-1 gp41 C-helical domain 5' PCR primer.
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Pred. No. 2.2e+03;

78.98;

Best Local Similarity

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Ribonucleotide reductase R1; tumourigenicity modulation; therapy; neoplastic cell; tumour growth; tumour regression; PCR primer; mouse; ss.
such antibodies may be effective against a broad range of HIV strains and isolates. The peptide compositions may be administered as a prophylactic or therapeutic vaccine to generate antibodies which reduce or inhibit the ability of HIV to infect uninfected cells. A composition comprising polyclonal or monoclonal antibodies can be administered to reduce HIV infection of uninfected cells. Antibodies raised against entry relevant gp41 structures may also be used therapeutically and as tools to further elucidate the mechanism of HIV cell entry. Sequences AAA72104-A72107 represent PCR primers used in an exemplification of the invention to construct DNA (AAA72102) encoding a protein construct (AAB14603) comprising the N- and C-helical domains of HIV-1 gp41 separated by a short peptide linker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents a PCR primer for the mouse ribonucleotide reductase R1 (RRR1) gene. The gene and the protein it encodes can be used in the methods of the invention for modulating tumourigenicity of neoplastic cells in a mammal. The RRR1 can slow tumour growth and cause tumour regression and reduction of tumourigenicity and metastatic
                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Use of ribonucleotide reductase R - for modulating the tumourigenicity and metastatic potential of neoplastic cells in a mammal, particularly for inhibiting tumour growth
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                                                                                                                                                                                                                                                                                     Length 44;
                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Primer for ribonucleotide reductase R1 coding sequence.
                                                                                                                                                                                                                                                                                 Score 12.8; DB 21;
Pred. No. 1.8e+03;
                                                                                                                                                                                                                                Sequence 44 BP; 13 A; 10 C; 15 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 29 BP; 3 A; 11 C; 7 G; 8 T; 0 other;
                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example; Page 21; 56pp; English.
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Best Local Similarity 87.5%;
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                        cgcgggctcacagtgg 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wright JA, Young AH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-520956/44.
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19-MAR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAV59089;
                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
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Score 12.6; DB 19; Length 29;

63.0%;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for cancer causitively associated
   Gaps
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                                                                                                                                                                                                                                                           Sense primer for methylthioadenosine phosphorylase gene exons 5-8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sense primer is designed for the PCR amplification of exons
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                                                                                                                                                                                                                                                                                          Chromosome 9p21; human; cancer; tumour; diagnosis; prognosis; methylthicadenosine phosphorylase; MTAP; glioma; metanoma; primary lymphoid malignancy; non-small cell lung cancer; head and neck cancer; ovarian cancer; bladder cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 32;
 Indels
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Pred. No. 2.2e+03;
); Mismatches 4;
 . 7
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bladder cancer or a chondrosarcoma (claimed).
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 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Diagnosing and determining prognosis with derangements of chromosome 9p21
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0
                                                                                                                                                                                                                                                                                                                                                                  chondrosarcoma; PCR primer; ss.
                                                                                                                                                        BP
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78.9%;
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                                                                  2 cctcgagctgacagtcgtc 20
                                                                                                                                                     AAZ35374 standard; DNA; 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ccgcgggctcacagtggtc 19
                                                                                                                                                                                                                         27-MAR-2000 (first entry)
                                  1 ccgcgggctcacagtggtc
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Best Local Similarity 78.9°
Matches 15; Conservative
15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schmid M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-126650/11.
                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9967634-A1.
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 Matches
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Ets-2; human; transcription factor; chromosome 21q22.3; cancer; invasion; metastasis; skeletal abnormality; Down's syndrome; expression inhibition; phosphorothioate; antisense; ss.
                                                       Human Ets-2 phosphorothioate antisense oligonucleotide, SEQ ID NO:40.
                    21-AUG-2000 (first entry)
                                                                                                                                                              Homo sapiens
                                                                                                                                                                                               US6054316-A
                                                                                                                                                                                                                                  25-APR-2000
     The invention relates to a mammalian PGI gene and protein, and a set of PGI ballelic markers. The PGI polynucleotide and biallelic markers are used in a hybridisation assay, a sequencing assay, or in an a lale-specific amplification assay for determining the identity of a nucleotide at a PGI-related biallelic marker. The methods can be used to detect and to assess the risk of developing cancer or prostate cancer. Early-stage diagnosis of prostate cancer relies on prostate specific antigen (PSA) dosage. However, the effectiveness of this is limited due to its inability to discriminate between malignant and non-malignant affections of the organ. A need exists for both a reliable diagnostic procedure which would enable early-stage diagnosis, and for preventative cand curative treatments of the disease. The PGI gene can be used for detection of prostate cancer, and the risk of developing it in the cuture, and can also be used to determine therapies for the disease.
                                                                                                                                                                                                                                              PG1 gene; biallelic marker; PCR primer; PG1-related biallelic marker; cancer; prostate cancer; diagnosis; therapy; prostate specific antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Use of a prostate cancer associated gene and biallelic markers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 47;
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Pred. No. 2.2e+03;
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                                                                                                                                                                                                              Probe for human PG1 biallelic marker 4-50-293.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chumakov I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; Page 328; 385pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bougueleret L,
                                                                                                   AAZ01125 standard; DNA; 47 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                             98WO-IB02133
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19 CTGAGGTCTCATAGTGGTC 1
                                                                                                                                                                           27-SEP-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 63.0
Best Local Similarity 78.9
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            derived from it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Blumenfeld M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                       WO9932644-A2
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22-DEC-1997;
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                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                        AAZ01125;
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Sequences AAA38349-A3838 represent antisense oligonucleotides targetted to the human Ets-2 gene, which inhibit its expression. The antisense oligonucleotides were designed to target different regions of the human Ets-2 RNA, and were designed to target different regions of the human Ets-2 RNA, and were analysed for their effect on Ets-2 RNA levels by quantitative real-time PCR. The Ets-domain transcription factors are a family of proteins which are involved in controlling key cellular events such as proliferation, differentiation and development. The Ets domain is a DNA-binding domain shared by all members of this family. Through this motif, Ets family members bind to the promoter regions of various genes at a GCA consensus sequence, thereby acting as either repressors or activators of the gene. All but one Ets family protein bind to DNA as monomer. Ets-2 has been implicated in the regulation of cellular proliferation and differentiation. The Ets-2 gene is located at chromosome 21q22.3, which is within a region known to undergo translocations associated with malignancies. Ets-2 has been found to be upregulated in several cancers, including lymphoblastic leukaemia. It may also play a role in the cancer phenotype, as it activates the urokinase plasminogen activator to epidermal growth factor (EGF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      stimulation. High levels of uPA and metalloproteinases are associated with tumour invasion and metastasis in breast cancers. As the Ets-2 gene is located on chromosome 21, which is triplicated in Down's syndrome, it is also thought to be responsible for the skeletal abnormalities present in this condition. The antisense oligonucleotides of the invention are useful for the treatment or prophylaxis of conditions associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   Antisense compound, 8-30 nucleobases in length, inhibiting the expression Ets-2 is useful for treating cancer and detecting Ets-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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Pred. No. 3.4e+03;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ets-2 expression, especially cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Column 40; 31pp; English.
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    99US-0344579.
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Best Local Similarity 82.4
Matches 14; Conservative
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                                                                                                                                                          (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                         Cowsert LM;
                                                                                                                                                                                                                                                                                                                    WPI; 2000-338495/29.
25-JUN-1999;
                                                                           25-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expression
                                                                                                                                                                                                                                         Baker BF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAA29338/c
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Gaps

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1 ccgcgggctcacagtggtc 19 | | ||||| ||||||| | 10 cagggggctgacagtggac 28

ò a AAA38381 standard; DNA; 18 BP.

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AAA38381 RESULT

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AAA38381

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AAA29335-38 are oligonuclectide primers used to synthesize the alpha and beta chain cDNA for a MAGE-1 specific T cell receptor from the CD8 positive cytotoxic T lymphocyte (CTL) clone 82/30. Novel immune cells with predefined specificity, are produced by either complexing the cells with an antigen specific MHC-restricted TCR or transfecting the cells on thigher specific MHC-restricted chimaric TCR gene. The antigen-specific MHC-restricted chimaric TCR gene. The antigen-specific MHC-restricted chimaric TCR gene can be transfected with lymphocytic cells for treatment of a tumour. Alternatively, the autologous climents of the transfected with an antigen associated with the tumour and a segment encoding a single chain TCR (scFv-TCR) which binds to an antigen associated with the tumour and a segment encoding a signal transducing element of an immune cell. Compositions comprising the manner cells may be used for the treatment of cancer (especially melanomas, if the TCR binds to the MAGE-1 antigen), infectious diseases, cutoimmune disease and/or graft rejection.
                                                                                                                                   human leukocyte antigen; HLA-A1; melanoma; neoplastic; MAGE-1; TCR; MHC; soluble; major histocompatability complex; antigen; T cell receptor; lymphocyte; tumour; cytostatic; anti-microbial; immunosuppressive; primer; alpha chain; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immune cells with predefined specificities useful for treating melanoma
                                                                                              Primer V-beta-3 for MAGE-1 specific TCR-alpha chain cloning.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 29; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                      (YEDA ) YEDA RES & DEV CO LTD (BOLH/) BOLHUIS R L H.
                                                                                                                                                                                                                                                                                                                                                            99WO-IL00622
                                                                                                                                                                                                                                                                                                                                                                                                 98IL-0127142
                                                     12-SEP-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-451678/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and immune diseases
                                                                                                                                                                                                                                                                           WO200031239-A1
                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                            18-NOV-1999;
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                                                                                                                                                                                                                                                                                                                     02-JUN-2000
                  AAA29338;
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Gaps ö Query Match 61.0%; Score 12.2; DB 21; Length 29; Best Local Similarity 82.4%; Pred. No. 3.4e+03; Matches 14; Conservative 0; Mismatches 3; Indels (

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Search completed: October 2, 2001, 16:18:33 Job time: 15477 sec

Ar. Appl 4, Appl 14, Appl 11, Appl 51, Appl 6 13, Appl

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Sequence:

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Sequence 14, Sequence 14, Sequence 14, Sequence 14, Sequence 11, Patent No. 516 Sequence 13, Sequence 5, Applications of the sequence 6, Appli
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Fatent No. 6133031
GENERAL INFORMATION:
FAPLICANT: Monia, Brett P.
FILE OF INVENTION: Expression
FILE REFERENCE: ISPH-0389
CURRENT APPLICATION NUMBER: US/09/377,310B
CURRENT PAPLICATION NUMBER: US/09/377,310B
SOFTWARR: PatentIn Ver. 2.0
SEQ ID NOS: 43
LENGTH 15
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US-08-467-023-105
US-08-198-431-14
US-08-158-431-14
US-08-15-14
US-08-15-14
US-09-10-14
US-09-09-11-14
US-09-099-11-14
US-09-099-11-14
US-08-099-11-14
US-08-18-18-13
US-08-18-13
US-08-13-13
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Mismatches
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APPLICANT: Monia, Brett P.
APPLICANT: Gaarde, William A.
ITLE OF INVENTION: Antisense Modulation of For TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0389
CURRENT APPLICATION NUMBER: US/09/377,310B
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-377-310-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 13, Application US/09377310B
; Patent No. 6133031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 15; Conserv
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US-09-377-310-33
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US-09-377-310-13
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     SEQ ID NO 13
LENGTH: 20
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6.804 Million cell updates/sec
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                                                                                                                               Search time 417.38 Seconds
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
                   GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-377-310-13
US-08-462-467B-28
US-08-399-411-11
US-08-399-411-11
US-08-397-211-39
US-09-087-231-39
US-09-116-498-16
US-09-116-498-16
US-07-885-971-10
US-08-185-971-10
US-08-195-10-9
US-08-435-501-9
US-08-435-501-9
US-08-435-764-9
US-08-194-087-10
PCT-US93-04648-10
PCT-US93-04648-10
US-08-271-9468-10
US-08-271-94-087-10
US-08-271-94-08-10
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PCT-US95-08604-7
PCT-US95-08606-7
US-08-716-190-14
US-08-951-083-272
US-08-832-985-49
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                                                                                                                                                                                                                                                                                                                                     324599 seqs, 94655562 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                             2001, 16:03:55
                                                                                            OM nucleic - nucleic search, using sw model
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15
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                                                                                                                             2,
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Match
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Score 12.4; DB 1; Length 27; Pred. No. 1.3e+02;
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Patent No. 5831008
GENERAL INFORMATION
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
TITLE OF INVENTION: Zinc Finger Proteins
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
  Retinoblastoma Protein - Interacting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,568
FILING DATE: 02-JUN-1995
CLASSIFICATION: 514
PRIOR ADDITON: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALLALO
OPERATUR PSTERM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
                                      NUMBER OF SEQUENCES: 93
CORRESPONDER ADDRESS:
CARRESEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                       Zinc Finger Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Campbell, Cathryn A.
REGISCRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1264
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-901
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/399,411
FILING DATE: 06-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/399,411
FILING DATE: 06-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82.7%;
92.9%;
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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Best Local Similarity 92.9
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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MEDIUM TYPE: Floppy
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STREET: 43.0 _
CITY: San Diego
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TITLE OF INVENTION:
                                                                                                                         CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
US-08-399-411-11/c
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                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-459-568-11
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US-08-4678-28/C
Sequence 28, Application US/08462467B
Sequence 28, Application US/08462467B
Sequence 28, Application US/08462467B
Setent No. 6210899
Tare 06 INVENTION: The Use of a BMP Protein Receptor
TILE OF INVENTION: Complex for Screening Bone Metabolism Actives and Cells
TITLE OF INVENTION: BMP Receptor
TITLE OF INVENTION: BMP Receptor
TITLE OF INVENTION: BMP Receptor
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSE: The Procter & Gamble Company
STREET: 11810 East Miami River Road
CITY: Ross
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                      100.0%; Score 15; DB 3; Length 20; 100.0%; Pred. No. 4.1;
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                                                                                                                                               0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,467B
                                                                                                                                               0; Mismatches
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    ; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-377-310-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNET/AGENT INFORMATION:
NAME: Hersko, Bart S.
REGISTRATION NUMBER: 32,572
REFERENCE/DOCKET NUMBER: 5474R
TELECOMMUNICATION INFORMATION:
TELEPHONE: (513) 627-0633
TELEFANE: (513) 627-0630
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARATERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 11, Application US/08459568; Patent No. 5811304; GENERAL INFORMATION:
APPLICANT: Huang, Shi
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100.0%; Pre-
0;
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US-08-462-467B-28
                                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 86.7
Best Local Similarity 100.
Matches 13; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                       1 tggcttatcttcagt 15
                                                                                                                                                                                                           3 tggcttatcttcagt 17
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 tggcttatcttca 13
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US-08-459-568-11/c
  FEATURE:
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0; Gaps

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Sequence 2, Application US/09087232A
Patent No. 6153431
GENERAL INFORMATION:
APPLICANT: QUILLENT Et al.
TITLE OF INVENTION: HUMAN IMMUNOBEFICIENCY VIRUS CO-RECEPTOR
TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole
STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
               Gaps
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               Indels
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                                                                                                                                                                                                                                                                                                           APPLICANT: Dale, James B.
APPLICANT: Lederer, James W.
APPLICANT: Lederer, James W.
TITLE OF INVENTION: RECOMBINANT MULTIVALENT M PROTEIN
TITLE OF INVENTION: VACCINE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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Pred. No. 1.3e+02;
0; Mismatches 1;
               Mismatches
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REGISTRATION UNBER: 43,058
REFERENCE/DOCKET NUMBER: 481112.405C1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/937,271
FILING DATE: 15-SEP-1997
CLASSIFICATION: 424
                                                                                                                                                                                                                                   Sequence 39, Application US/08937271
Patent No. 6063386
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
^^MDITTER: IBM PC compatible
PC PASS/MS
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TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 39.
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92.98;
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NAME: Rosenman, Stephen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 82.7
Best Local Similarity 92.9
Matches 13; Conservative
             13; Conservative
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                                                               1 tggcttatcttcag 14
                                                                                          10 TGGCTTATCTTCTG 23
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STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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US-09-087-232A-2/C
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COUNTRY:
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             Matches
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Fatent No. 606931
GENERAL INFORMATION:
INFORMATION: Retinoblastoma Protein - Interacting
TITLE OF INVENTION: Retinoblastoma Proteins
ITLE OF INVENTION: Retinoblastoma Proteins
OFRESSONDENCE ADDRESS:
ADDRESSE: ADDRESS:
ADDRESSE:
ADD
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Pred. No. 1.3e+02;
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Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
NAME: Campbell, Cathryn A.
REGISTRATION HUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1264
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 555-9001
TELEPHONE: (619) 555-9001
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                     82.7%;
92.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82.7%;
92.9%;
                                                                                                                                                                                                                                                                                                                                                                                        Query Match 82.7
Best Local Similarity 92.9
Matches 13; Conservative
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Best Local Similarity
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US-08-516-859A-11
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Sequence 10, Application US/07884811
Patent No. 5316921
CENERAL INFORMATION:
TITLE OF INVENTION: SINGLE-CHAIN HEPATOCYTE GROWTH FACTOR VARIANTS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STRATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTKI: ....
ZIP: 94080
COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/884,811
**TING DATE: 19920518
                                                                                                                                                                                                                                                                                                                                                                         Score 11.8; DB 4;
Pred. No. 2.7e+02;
0; Mismatches 2;
                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "Oligonucleotides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 11.8; DB 1;
Pred. No. 2.8e+02;
REFERENCE/DOCKET NUMBER: 1049-1-009
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SED ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                         ; SEQUENCE DESCRIPTION: SEQ ID NO: 16: US-09-116-498-16
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
                                                                                                                                    LENGTH: 22 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33,055
                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                            78.78;
86.78;
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86.78;
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NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,0
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                            Query Match 78.7
Best Local Similarity 86.7
Matches 13; Conservative
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CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 tggcttatcttcagt 15
                                                                                                                                                                                                                                                                  HYPOTHETICAL: NO
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Best Local Similarity
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US-07-884-811-10
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Ramani, Vineet N.K.
TITLE OF INVENTION: NOVEL ALTERNATIVE G-COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
                                                                                CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/087,232A
FILING DATE: 28 MAY 1998
CLASSIFICATION A135
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/048,057
FILING DATE: 30 MAY 1997
ATTORNEY/AGENT INFORMATION:
NAME: KOLE, LISA B.
REGISTRATION NUMBER: 35,225
REFERENCE/DOCKET NUMBER: 35,225
REFERENCE/DOCKET NUMBER: 35,225
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAX: (212) 765-2519
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80.0%; Score 12; DB 3; Length 21; 100.0%; Pred. No. 2.1e+02; ive 0; Mismatches 0; Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/116,498
FILING DATE: 16-Jul-1998
CLASSIFICATION: CURROWN>
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NAME: Jackson Esq., David A.
        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMEUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc - "PRIMER"
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Patent No. 6251582
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 21 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: sing
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Best Local Similarity
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US-09-116-498-16
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Sequence 10, Application US/08194088B
Patent No. 5580963
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
SINGLE-CHAIN HEPATOCYTE GROWTH FACTOR VARIANTS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Generacch, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 11.8; DB 1;
Pred. No. 2.8e+02;
0; Mismatches 2;
                                                                  COMPUTER: 1.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                           CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

CURSING APPLICATION DATA:

FILING DATE:

RELIGHOR DATE:

PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/885971

FILING DATE: 18-MAY-92

ATORNEY AGENT INFORMATION:

NAME: MARSCHANG, DIANG L.

REGISTRATION NUMBER: 35,600

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-5416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: patin (Generatech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/194,088B
FILLIG DATE: 09-FEB-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 09-FEB-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/884811
FILING DATE: 18-MAY-1992
ATTORNEY/AGGNT INFORMATION:
NAME: GAllegos, R. Thomas
REGISTRATION NUMBER: 32,692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 78.7
Best Local Similarity 86.7
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 30 base pairs
Nucleic Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 tggcttatcttcagt 15
                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY:
US-08-087-783A-10
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     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
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                                                                                                                                                                                                                                Sequence 10, Application US/07885971
Fatent No. 5328837
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: HEATOCYTE GROWTH FACTOR PROTEASE DOMAIN VARIANTS
NUMBER OF SEQUENCES: 21
CORRESPONDESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
COMPUTER: IBM PC COMPATIBLE
COMPUTER: CALIFA: CA
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  Gaps
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Pred. No. 2.8e+02;
0; Mismatches 2;
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/885,971
FILING DATE: 19920518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 779
TELECOMUNICATION INFORMATION:
TELEPHONE: 415/25-3216
TELERA: 910/31-716
ILELRA: 910/31-716
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
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ilarity 86.7%;
Conservative
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ATTORNEY/AGENT INFORMATION:
13; Conservative
                                                   LENGTH: 30 bases
TYPE: NUCLEIC ACID
STRANDEDNESS: single
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 tggcttatcttcagt 15
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Best Local Similarity
Matches 13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY:
US-07-885-971-10
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0
Score 11.8; DB 1; Length 30;
Pred. No. 2.8e+02;
0; Mismatches 2; Indels
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Pred. No. 2.8e+02;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                      Sequence 9, Application US/08435764
Fatent No. 5763584
GENERAL INFORMATION:
TITLE OF INVENTION: Receptor Activation
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
PRICATION NUMBER: 05/06/453,77
FILING DATE:
PRICATION 135
PRICATION NUMBER: 07/884811
FILING DATE: 18-MAY-1992
PRICR APPLICATION DATA:
APPLICATION NUMBER: 07/885911
FILING DATE: 18-MAY-1992
PRICR APPLICATION DATA:
FILING DATE: 18-MAY-1992
PRICR APPLICATION NUMBER: 07/950572
FILING DATE: 21-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: DESCRIPTION CANAGED TO THE CANAGED
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REFERENCE/DOCKET NUMBER: 775
TELECOMMUNICATION INFORMATION:
   78.78;
86.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELERA: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                Best Local Similarity 86.7
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 78.7
Best Local Similarity 86.7
Matches 13; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                             1 tggcttatcttcagt 15
                                                                                                                                                              7 TGACATATCTTCAGT 21
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                                                                                                                                                                                                                                                                                  RESULT 15
US-08-435-764-9
      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5.4 Application US/08435501

Patent No. 5684136

GENERAL INFORMATION:

APPLICANT: Genentech, Inc., Paul J. Godowski;

TITLE OF INVENTION: Receptor Activation

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STAFE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFRWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/84811
FILING DATE: 18-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/865971
FILING DATE: 18-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/950572
FILING DATE: 21-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   773P1
                                                                             TELERAX: 415/952-9881
TELEX: 910/371-7168
INPORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 bases
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: 773
                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-2614
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELERAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
US-08-435-501-9
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94080
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US-08-194-088B-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-435-501-9
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G-alpha protein GP Yeast alpha factor Bacillus thuringie Mutagenic PCR prim Primer used to int

Juniperus Cryj I Sequence of PCR pr Mutagenic PCR prim Primer used to int Probe for the nove

Antibody heavy cha

Dog genomic marker Primer deltaK3 huH

Retinoblastoma gen Streptococcus pneu

primer for N-terminal primer Primer used to PCR 5' primer f

STE2 gene 3' PCR p ATM region b (nt 5 Antisense PCR prim Microsatellite rep Primer pair 14A W Human beta-lactogl

Mouse ssH2B PCR pr Oligonucleotide pr Primer for amplify HPV-16 target sequ

PCR primer used to Ribonucleotide red

Antisense oligonuc Ribonucleotide red

Perfect score:

Sequence:

OM nucleic

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Run

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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New antisense compounds for inhibiting focal adhesion kinase expression, especially useful for inhibiting retinal neovascularization, or for diagnosing and treating e.g. colon cancer
                                                                                                                                                                                                                                                                               embryonic development disorder; angiogenic disorder; wound healing; antisense; phosphorothioate; ss.
                                                                                                                                                                                                                                                                          Human; focal adhesion kinase; FAK; signal transduction; cancer
                                                                                                                                                                                                                                                               Human focal adhesion kinase antisense sequence #31.
                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                         AAX59982
AAA47518
AAQ52566
AAV08563
AAX07298
AAA66237
                                                                      AAV54903
AAQ26930
                                                                                                                             AAQ32816
AAQ57839
AAQ76318
                          AAT12845
AAT11444
                                                                                     AAT62465
AAT49593
                                                                                                                                             AAV22500
AAV12309
                                      AAT00441
                                                           AAQ29005
                                                                                 AAT62463
                                                                                                 AAT73031
                                                                                                       AAV54902
                                                                                                            AAT62479
                                                                                                                  AAV00716
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                                           AAV27
AAV84
AAQ55
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 99US-0377310.
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                                                                                                                                                                                                                              AAC65565 standard; DNA; 15
                                                                                                                                                                                                                                                     entry)
 (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                   Monia BP, Gaarde WA;
                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-006141/01.
                                                                                                                                                                                                                                                    (first
Homo sapiens
                                                                                                                                                                                                                                                                                                                                 19-AUG-1999;
                                                                                                                                                                                                                                                                                                                                            19-AUG-1999;
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RESULT
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PCR primer for Cel
Human focal adhesi
PCR primer for mou
Antisense primer f
PCR primer used to
Human gene single
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Streptococcus pyog
CCR5/CCR2b PCR pri
                                           (without alignments)
10.740 Million cell updates/sec
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                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                    Search time 876.95 Seconds
                                                                                                                                                                                                                                                                                                                                       Description
                                                                                                                                                                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                730101 seqs, 313950809 residues
                                     ٠.
                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                    2, 2001, 16:18:48
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Maximum Match 100%
Listing first 45 summaries
                          - nucleic search, using sw model
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AAX94668
AAF95414
AAA60107
AAA57918
AAF76114
AAV84128
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AAV08375
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                                                                                                                                                                                                       Homo sapiens
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Matches 15;
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                   The present invention describes a number of phosphorothioate antisense sequences to the human focal adhesion kinase (FAK) protein. This protein is involved in integrin-mediated signal transduction, and is implicated in cancer, particularly colon, breast and oral tumours, embryonic development discreters, angiogenic discreters and wound healing. The antisense sequences, including the one shown here, can be used in the treatment of all of these.
                                                                                                                                                                      Gaps
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Pred. No. 22;
Mismatches 0; Indels
                                                                                                                                              22; Length 15;
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                                                                                                                                                                                                                                                                                                                                        PCR primer for Cellulose synthase coding sequence.
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                                                                                                             Sequence 15 BP; 2 A; 3 C; 3 G; 7 T; 0 other;
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                                                                                                                                                        22;
                                                                                                                                                                                                                                                                                                                                                             Cellulose synthase; cotton; PCR primer; ss.
                                                                                                                                                                    0; Mismatches
                                                                                                                                              Score 15;
Pred. No.
 Claim 15; Column 25; 30pp; English.
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Matches 15; Conservative
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Matches 15; Conservative
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Gossypium hirsutum.
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The present invention describes a number of phosphorothioate antisense sequences to the human focal adhesion kinase (FAK) protein. This protein is involved in integrin-mediated signal transduction, and is implicated in cancer, particularly colon, breast and oral tumours, embryonic development disorders, angiogenic disorders and wound healing. The antisense sequences, including the one shown here, can be used in the treatment of all of these.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antisense compounds for inhibiting focal adhesion kinase expression, especially useful for inhibiting retinal neovascularization, or for diagnosing and treating e.g. colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                      Human; focal adhesion kinase; FAK; signal transduction; cancer; embryonic development disorder; angiogenic disorder; wound healing;
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                                                                                                                                                    Human focal adhesion kinase antisense sequence #11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20 BP; 5 A; 3 C; 4 G; 8 T; 0 other;
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                                                                                                                                                                                                                                                        antisense; phosphorothioate; ss.
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AAC65545 standard; DNA; 20
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ID AAT28037 standard; DNA; 21
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This primer corresponds to the sequence of plasmid pSPORTI/N89-5, and is the reverse complement of nucleotides 968-948 in a gene encoding mouse bone morphogenetic protein (BMP) receptor type-II kinase-3 (BRK-3), which induces cellular differentiation in response to BMP. The primer may be used with anchor primer AAT27231 in 5'-rapid amplification of CDNA ends (5'-RACE), to isolate 600 bp at the 5'-end of the BKR-3 gene, by PCR amplification of NIB3T3 mouse embryo fibroblast (ATCC CRL 1658) cDNA. To reduce background, a 2nd round of PCR is performed using nested primer AAT27232 with the anchor primer. This results in isolation of 600 bp from the 5'-end of the gene, which may be used to assemble a full-length clone (AAT27225) by PCR using primers AAT2723-4 and cloning in phage Bluescript-II-SK(-) in Escherichia coll DH5-alpha. The receptor and antibodies against the may be used in diagnostic assays for BMP disorders, or in the angle of the book of the coll DH5-alpha. The receptor and antibodies against the may be used in diagnostic assays for BMP disorders, or in the angle of the coll DH5-alpha. The receptor and antibodies against the angle be used to assays for BMP disorders, or in the coll DH5-alpha.
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                                                     nsed to
                                                                                                                                                                                                                                                                                                                                                                                            therapy to bind or scavenge BMPs. In addition, expression of the BMR: 3 gene along with a reporter gene under the control of a hormone-responsive element in a cell culture may be used to screen compounds for BRK-agonist or -antagonist activity, by monitoring
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86.7%; Score 13; DB 17; Length 21; 100.0%; Pred. No. 2.8e+02;
                                                Isolated bone morphogenic protein receptor kinase protein determine if a test cpd. is capable of binding to, or is (ant)agonist of BMP receptor kinase protein transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCR primer used to amplify an ORF of Chlamydia pneumoniae.
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                                                                                                                    Example 9; Page 30; 87pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   reporter gene expression.
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Best Local Similarity 100.
Matches 13; Conservative
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Chlamydia pneumoniae.
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                 WPI; 1996-251762/25
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AAX94668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                        A PCR primer (AAT28037) Includes the reverse complement of a partial cDNA clone isolated from NIBT3 mouse embryonic fibroblasts. It was used with an anchor primer (AAT28038) to amplify the 5' end of mouse bone morphogenetic protein (BMP) type receptor kinase protein-3 (BRK-3) cDNA. Following further PCR amplification and cloning into pUT6, a cDNA clone (AAT28020) coding for full-length murine BRK-3 (AR855224) was obtd. The PCR primer is the reverse complement of nucleotides 968-948 of this clone.
                                                                                                                                                                                                                                                                         Assays for bone morphogenetic protein activities - using complex of BMP type I receptor kinase protein and BMP receptor kinase protein BKR-3
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                                                                                                  95WO-US14027
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94US-0334178
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Matches 13; Conservative
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                                                                                                                                                                                                                      Rosenbaum JS;
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                                WO9614579-A1
                                                                                                  30-OCT-1995;
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Synthetic.
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                                                    frames and other nucleic acid sequences from the genome of Chlamydia pneumoniae (see AAX91990). C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be contributing factor in heart disease, sarcoidosis, sinusitis, purulent otits media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAX3684-AAX36879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as
                                                                                                                                                                                                                                                                                                                                                                                                                         Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
polymorphism; vascular disease; coronary artery disease; forensics;
myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
pulmonary embolism; paternity test; ds.
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                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids comprising single nucleotide polymorphisms, useful in applications such as forensics, paternity testing, medicine, genetic analysis and phenotype correlations to diseases such as diabetes and
                                           AAX91991-X97517 represent PCR primers used to amplify open reading
                                                                                                                                              immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= a
/standard_name= "single nucleotide polymorphism"
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                                                                                                                                                                                                              Length 20;
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Pred. No. 6e+02;
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                                                                                                                                                                              Sequence 20 BP; 3 A; 4 C; 6 G; 7 T; 0 other;
Genome sequence of Chlamydia pneumoniae
                       Page 1688; Disclosure; 1912pp; English.
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92.98;
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2000US-0225724
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                                                                                                                                                                                                             Query Match 82.7
Best Local Similarity 92.9
Matches 13; Conservative
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                                                                                                                                                                                                                                                         2 ggcttatcttcagt 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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16-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Variation
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The present invention provides a method of diagnosing a vascular disease in an individual, involving determining the sequence at various polymorphic sites within the human thrombospondin 1 and thrombospondin 4 genes. The sequences at a number of polymorphic sites are also provided in the specification. In particular, the method can be used in the diagnosis of atherosclerosis, myocardial infarction, coronary heart disease, stroke, peripheral vascular diseases, venous thromboembolism and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also useful in forensize, paternity testing, genetic analysis and phenotype correlations to diseases. The present sequence is an example of one of the human gene SNPS shown in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New PR domain peptides comprising amino acid sequences from, for example retinoblastoma-interacting zinc finger, or egl-43 proteins, for regulating gene transcription and controlling cell proliferation and differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rb) interacting zinc finger (RIZ) protein (AAB12028). RIZ is a nuclear phosphoprotein that acts as a cell differentiation factor. RIZ can modulate cell growth by binding to Rb protein, which is involved in regulating cell proliferation. In addition, RIZ can act to regulate transcription. RIZ functions to maintain cells in the Gl phase of the cell cycle, by interacting with Rb through the cr2 domain of RIZ. RIZ protein is a PR domain protein and is present primarily in the cell
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transcription regulator; breast cancer; gene therapy; melanoma;
neuroblastoma; leukaemia; Parkinson's disease; Huntingdon's disease;
Alzheimer's disease; paralysis; motor neurone disorder; PCR primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rb-interacting zinc finger; RIZ; retinoblastoma; heart disease; rat;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 12.4; DB 22;
Pred. No. 6.1e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 21 BP; 3 A; 6 C; 4 G; 8 T; 0 other;
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92.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rat RIZ PCR primer # 1.
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nes 13; Conserv
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Best Local Si
Matches 13;
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serotypes of group A streptococci, and may therefore be used as vaccines to protect against and control infection by type A streptococci. Type A streptococci are not only responsible for streptococcal pharyqitis (strep throat), forms of pneumonia and a condition resembling toxic shock, but are also involved in the development of acute rheumatic fewer (ARF) and rheumatic heart disease. In a patient with ARF, antibodies formed during a group A streptococcal infection are also cross-reactive with heart tissue, which indicates that the streptococci and host tissue contain similar antigenic motifs. The new multivalent various serotypes of group A streptococci antibodies against various serotypes of tissue, sequences AAA57903-A57904 and AAA579919 represent PCR primers used in the generation of DNA (AAA57893-A57912) encoding multivalent thybrid Streptococcus pyogenes M proteins (AAB03113-B03117, and a part of the generation of DNA (AAA57893-A57902) encoding

AAB03119-B03121, AAB03123-B03124)

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nucleus. RIZ gene mutations may be implicated in various cancers such as melanoma, neuroblastoma, leukaemia and breast cancer, and so the RIZ gene may be used in gene therapy for these disorders. Since RIZ protein is implicated in cell cycle arrest, inhibition of RIZ activity may be useful in neurodegenerative disorder therapy e.g. for Parkinson's, Huntingdon's or Alzheimer's disease, paralysis or motor neurone disorders, or cardiac disorders e.g. heart disease, where the ability to induce neural, cardiac tissue proliferation would be useful. The present sequence was used in the construction of vectors which were used to clone
                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Multivalent hybrid M protein; group A streptococcus; serotype; immunogenic; sero-specific antibody; streptococcal infection; cross reactivity; vaccine; acute rheumatic fever; ARF; rheumatic heart disease; streptococcal pharyngitis; strep throat;
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Pred. No. 6.2e+02;
0; Mismatches 1; Indels (
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                                                                                                                                                      Sequence 27 BP; 9 A; 7 C; 9 G; 2 T; 0 other;
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                                                                                                                        mammalian RIZ coding sequences.
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92.9%;
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                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus pyogenes.
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Matches 13; Conserv
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The invention relates to a method of surveying the CC (beta) chemokine receptor (CCR) genotypes in a population. The method is particularly applied to the human CCRS and CCR2 genes located on chromosome 3p21-22, which encode co-receptors for HIV-1. The method involves obtaining genomic DNA samples from a representative number of individuals within a population; combining each sample with experimental and control primer combinations to produce primer-annealed DNA; amplifying the DNA to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Surveying CC beta chemokine receptor (CCR) genotypes in population, involves amplifying genomic DNA of individuals with experimental and control primer combinations, size-separating amplicons and determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCR5/CCR2b PCR primer, SEQ ID:18, used to genotype HIV susceptibility.
                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC chemokine receptor; beta chemokine receptor; CCR; human; CCR5; CCR2, polymorphism; genotyping; HtV1 transmission; infection susceptibility; AIDS; acquired immunodeficiency syndrome; disease progression; chromosome 3p21-22; PCR primer; ss.
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Pred. No. 6.3e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                   Sequence 30 BP; 3 A; 6 C; 12 G; 9 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           AAF76114 standard; DNA; 19 BP.
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92.9%;
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Best Local Similarity 92.9
Matches 13; Conservative
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streptococcal M proteins comprising N-terminal peptide fragments of M proteins that elicit opsonic antibodies against multiple serotypes of group A streptococci (e.g., Streptococcus pyogenes). The antibodies generated using the hybrid proteins are against one or more M protein serotypes, where at least one of the serotypes is MJ, MJ8 or MJ9. The invention also encompasses a recombinant DNA molecule comprising a nucleotide sequence that encodes a multivalent hybrid M protein; and a method for immunisteng a mammal against streptococcal infections, comprising administering an immunogenic multivalent hybrid M protein to the mammal. The multivalent hybrid M protein to spesonic or protective antibodies to the M proteins of different

New immunogenic recombinant hybrid M protein comprising amino-terminal peptide fragments of streptococcal M protein useful as vaccine against rheumatic fever and infections leading to rheumatic fever $\,$

WPI; 2000-364475/31.

invention relates to multivalent immunogenic hybrid group A

Disclosure; Column 13-14; 62pp; English.

variant allele show resistance to HIV-1 infection. The detection of CCR5 variants may be used to identify individuals at lower risk of infection relative to the general population who, if infected, may exhibit slower progression to AIDS.

to the wild-type allele.

BP; 7 A; 6 C; 5 G; 3 T; 0 other;

Sequence 21

88888888

Individuals homozygous for the IIV-1 infection. The detection

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produce amplicons; separating the amplicons by size; determining the genotype based upon the presence of CCR alleles; and compiling the genotypes determined. The method is particularly applied to the human CCRS and CCRS and CCRS are associated with a variation in the susceptibility of an individual to infection by HIV-1, or with a variation in the disease c progression of AIDS after infection. The invention specifically claims the experimental PCR primers AAF76112, and the control PCR primers AAF76114 for surveying CCRS and CCR2b genotypes. The method of the invention fulfils a longstanding need for the development of a rapid and informative genotyping strategy that can readily applied to analyse CCRS, CCR2 and related genetic variants, and disease progression. The present sequence repersents a human and disease progression. The present sequence represents a human and disease progression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 19 BP; 6 A; 4 C; 5 G; 4 T; 0 other;
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0; Indels Query Match 80.0%; Score 12; DB 22; Best Local Similarity 100.0%; Pred. No. 1e+03; Matches 12; Conservative 0; Mismatches 0 2 gecttatcttca 13

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Gaps

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Length 19;

AAV84128 standard; DNA; 21 BP. 15-MAR-1999 (first entry) 15 GGCTTATCTTCA 4 AAV84128; 셤 ö

HIV-1; CCR5; CCR5-delta32; co-receptor; infection; diagnosis; AIDS; gene therapy; human; PCR; primer; ss. HIV-1 co-receptor CCR5-delta32 variant PCR primer delta-32 inv. 98WO-EP03437. Homo sapiens. WO9854317-A1 29-MAY-1998; 03-DEC-1998 Synthetic

(MOND-) FOND MONDIALE RECH & PREVENTION SIDA. 97US-0048057 30-MAY-1997;

Braun J, Quillent C; Beretta A, Arenzana Siesdedos F, WPI; 1999-059835/05. New CCR5 variant protein of the HIV-1 co-receptor - useful in developing resistance of CCR5-expressing cells to HIV-1 infection Claim 7; Page 8; 55pp; English.

This is the nucleotide sequence of a claimed DNA primer, designated delta-32 inv. which can be used for the amplification of HIV-1 CCRS co-receptor nucleic acids. It corresponds to nucleotide 955 of wild-type CCRS cDNA (see AAV84126). 4 Pairs of primers (see AAV84127-34) are provided. These can be used in claimed methods for detecting and identifying the presence of a CCRS variant in a sample. Primer pair delta-31 inv and delta-32 sens (see AAV84127) are particularly useful in detecting the presence of variant CCRS-delta32 (see AAV84159) that contains a 32 bp deletion when

ö TATA-box binding protein; epitope-tagged TBP; transcription complex; TAF; TBP associated factor; TAF-interaction factor; gene expression regulator; Transgenic animal expressing epitope-tagged TATA-box binding protein - for isolating higher-order transcription complexes and specific factors that associate with the protein, useful as potential Gaps ; 0 80.0%; Score 12; DB 20; Length 21; Ilarity 100.0%; Pred. No. 1e+03; Conservative 0; Mismatches 0; Indels ö Polites Primer for Transgene for epitope tagged TBP protein. Meisterernst M, Example 4; Page 11; 38pp; English. BP 98EP-0109516. 97EP-0108433 Berglund E, Kirschbaum B, AAV08563 standard; DNA; 21 2 ggcttatcttca 13 13 GCCTTATCTTCA 2 WPI; 1999-001394/01. (FARH) HOECHST AG. Local Similarity nes 12; Conserv therapeutic agents PCR primer; ss Homo sapiens. 12-FEB-1999 26-MAY-1998; 26-MAY-1997; EP881288-A1. 02-DEC-1998. Synthetic. Query Match Best Local Si Matches 12; AAV08563; RESULT 12 AAV08563/ ò qq

This sequence is a PCR primer for DNA encoding an epitope-tagged TATA-box binding protein (TBP) that is expressed by the transgenic non-human animals of the invention. The animals are used to produce TBP. TBP is used to isolate and characterise higher-order transcription complexes (from different tissue and cell types, optionally at different developmental stages). It is also used to identify new and/or specific. TBP associated factors (TAFs, e.g. transcription factors, activators or inhibitors) and TAF-interaction factors, and to raise antibodies against TBP. The TAFs may be useful for regulating gene expression.

C. e.g. disease-related genes, so are potential pharmaceuticals, also for identifying human analogues for use in drug screening. The antibodies are used for affinity purification of TBP and its complexes. TBP can isolate transcription complexes from a wide variety of different tissues and calls (contrast known methods that are limited to isolation from a

Sequence 21 BP; 6 A; 4 C; 8 G; 3 T; 0 other;

4 tggcttatcatcaat 18

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RESULT 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This primer corresponds to a region 550 bp downstream of the ATG initiation codon of human Bob (see AAX0792), a new HIV/SIV traslocation promoter agent which acts with CD4 to serve as a receptor for retroviral entry. It was used with an upstream primer (see AAX07297) in the RT-PCR amplification of lymphocyte RNA. Bob mRNA was detected in PHA-stimulated peripheral blood monounclear cells (PMBC), purified T cells, and weakly in monounclear cells (PMBC), purified T cells, and weakly in monoucytes and B cells. Human, African green monkey and pig-tailed macaque genes (see AAX072894) encoding 2 receptors, termed Bonzo and Bob (see AAW9778-88), that are associated with retroviral entry into cells have been identified. Diagnostic and therapeutic uses of these novel translocation promoting agents are provided, and unitidial agents for treatment
                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid encoding the human translocation promoter Bonzo used to screen for potential agents for treating acquired immune deficiency syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                         SIV receptor; HIV receptor; Bob; translocation promoting agent;
                                                ;
0
Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bonzo; G protein coupled receptor; chemokine receptor; AIDS, infection; virus transmission; PCR; primer; ss.
                                                Indels
Score 11.8; DB 20;
Pred. No. 1.3e+03;
); Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                              Human SIV/HIV receptor Bob downstream PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unutmaz D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 22 BP; 6 A; 5 C; 4 G; 7 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kewalramani VN, Littman DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 51; 97pp; English.
                                             0;
                                                                                                                                                                                                                                                          BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIV- and HIV-induced AIDS.
78.78;
86.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYNY ) UNIV NEW YORK STATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97US-0896155
                                                                                                                                                                                                                                                     AAX07298 standard; DNA; 22
                                                                                                                                                                                                                                                                                                                                                (first entry)
                                             Conservative
                                                                                           1 tggcttatcttcagt 15.
                                                                                                                     19 TGGCCTAACTICAGT 5
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Best Local Similarity
`~hes 13; Conserva
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                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9903888-A1
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Query Match
Best Local Simi
Matches 13;
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                                                                                                                                                                                                                                                                                                     AAX07298;
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The present invention describes a radiation hybrid map of the dog (Canine familiaris) genome comprising the genome location of a marker selected from AAA6619 to AAA6692. The radiation hybrid map is useful for identifying and localising dog genes, since it covers approximately 80 % of the dog genome and provides a dense map integrating different types (i.e. Types I and Type II) of markers. The map and the dog genome markers (or complementary sequences) are especially useful to identify genes responsible for phenotypic and behavioural traits in dogs, to identify morbid genes, to analyse diseases and identify implicated genes in such diseases and their alleles, and to study dog pedigrees. They may also be useful for isolating corresponding human gene sequences e.g. genes involved in genetic diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New radiation hybrid map of the dog, Canine familiaris, genome, useful for e.g. identifying genes implicated in phenotypic and behavioral traits or in genetic diseases and for studying dog pedigrees
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                           Dog; genome; genomic marker; radiation hybrid map; identification; chromosome location; gene marker; polymorphic microsatellite marker; phenotype; behaviour; pedigree; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                           Dog genomic marker oligonucleotide sequence SEQ ID NO:99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78.7%; Score 11.8; DB 21;
86.7%; Pred. No. 1.3e+03;
ive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 23 BP; 10 A; 6 C; 5 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 57; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CNRS ) CNRS CENT NAT RECH SCI.
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   ВР
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AAA66237 standard; DNA; 23
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                                                                                                               (first entry)
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Best Local Similarity 86.7°
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Galibert F, Andre C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primer deltaK3 huHGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-387821/33.
                                                                                                                                                                                                                                                                                                                                                Canis familiaris.
                                                                                                                                                                                                                                                                                                                                                                                                    WO200029615-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-NOV-1999;
                                                                                                               09-0CT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAY-2000
                                                         AAA66237;
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78.7%; Score 11.8; DB 20; 86.7%; Pred. No. 1.3e+03; tive 0; Mismatches 2;

Conservative

1 tggcttatcttcagt 15

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Length 22;

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Polymerase chain reaction; PCR; amplify; primer; PRK 5.1 huHGF; human hepatocyte growth factor; huHGF; varient; E. coli; human; fetal; kidney 293 cells; hepatocyte; ligand; receptor; activation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequences given in AAO52616-28 are primers which were used in the generation of pRK 5.1 human hepatocyte growth factor (huHGF) varient molecules. The amplification products from these reactions were cloned in E. coil cells and were then used to transfect human fetal kidney 293 cells. The expressed proteins were used to study the ability of huHGF to induce DNA synthesis of hepatocytes in primary culture. The expressed proteins may be used as first and/or second ligands in a conjugate for receptor activation. These conjugates may be used to activate the respective receptors and thereby mimic the biological activity of the corresponding native ligand.
                                                                                                                                                                                                                                                                                                                                                                                                  Activation of receptors, partic. of growth factors - using conjugate of two ligands capable of binding to receptors, for mimicking biological activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 30 BP; 7 A; 7 C; 4 G; 12 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 49; 103pp; English.
                                                                                                                                                                                                                        92US-0884811.
92US-0885971.
92US-0950572.
                                                                                                                                                                                       93WO-US04717.
                                                                                                                                                                                                                                                                                              (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                   WPI; 1993-386581/48.
                                                                                                                                                                                       17-MAY-1993;
                                                                                                                                                                                                                                            18-MAY-1992;
22-SEP-1992;
                                                                                                                                                                                                                         18-MAY-1992;
                                                                                                                  W09323550-A.
                                                                                                                                                      25-NOV-1993.
                                                                                                                                                                                                                                                                                                                                 Godowski PJ;
                                                                                 Synthetic.
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Search completed: October 2, 2001, 16:18:49 Job time: 15493 sec

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Gaps

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Ouery Match

78.7%; Score 11.8; DB 14; Length 30;

Best Local Similarity 86.7%; Pred. No. 1.3e+03;

Matches 13; Conservative 0; Mismatches 2; Indels

100, App 68, Appl

Sequence Sequence Sequence

Sequence

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sednence sed

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GENERAL INFORMATION:
APPLICANT: Wonia, Brett P.
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0389
CURRENT APPLICATION NUMBER: US/09/377,310B
CURRENT APPLICATION NUMBER: US/09/377,310B
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence II, Application US/09377310B
; Retent No. 6133031
; GENERAL INFORMATION:
APPLICANT: Monia, Brett P.
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Appression
FILE REFERENCE: ISPH-0389
US-08-487-113D-87
US-08-473-503-87
US-08-473-503-87
US-08-720-420A-87
US-08-715-680-87
US-08-475-680-87
US-08-906-517-69
US-08-906-517-69
US-08-482-882-100
US-08-483-389-100
US-08-483-393-100
US-08-483-393-100
US-08-473-503-100
US-08-720-420A-100
US-08-775-680-100
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US-08-775-680-100
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Mismatches
                                                                                                                                                                                               ALIGNMENTS
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CURRENT FILING DATE: 1999-08-19
NUMBER OF EGG ID NOS: 43
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                              CTHER INFORMATION: antisense sequence US-09-377-310-31
                                                                                                                                                                                                                                             ; Sequence 31, Application US/09377310B
; Patent No. 6133031
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                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 15; Conserv
 RESULT 2
US-09-377-310-11
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 SEQ ID NO 31
LENGTH: 15
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LENGTH: 20
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6.804 Million cell updates/sec
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                                                                 ; Search time 417.38 Seconds
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Sequence 6
Sequence 6
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/cgn2_6/ptodata/l/ina/5B_COMB.seq:*
/cgn2_6/ptodata/l/ina/6A_COMB.seq:*
/cgn2_6/ptodata/l/ina/6B_COMB.seq:*
/cgn2_6/ptodata/l/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/l/ina/PcTUS_COMB.seq:*
          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-377-310-31

US-09-377-310-11

US-08-137-310-11

US-08-117-952-668

US-09-101-886B-71

US-08-988-718-15

US-09-237-510-6

US-09-488-571-119

US-09-015-876-20

US-08-015-876-20

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US-08-477-8778-79
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US-08-477-989B-78
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US-08-483-389-87
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Maximum Match 100%
Listing first 45 summaries
                                              OM nucleic - nucleic search, using sw model
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15
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                                                                 October 2,
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Match
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                                                                                                                                             Scoring table:
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Length 15; Indels

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 US-08-117-952-668/c
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US-08-117-952-668
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Pred. No. 1.3e+02;
0; Mismatches 1; Indels
                                                                                DB 3; Length 20;
                                                                                                                                                                                                                                                                                                     APPLICANT: HOKE, Glenn D
APPLICANT: BRADLEY, Matthews O
APPLICANT: BLIAMS,
APPLICANT: LEE, Che-Hung
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES DIRECTED
TITLE OF INVENTION: AGAINST HUMAN ICAM-1
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: 8901 Wisconsin Ave.
                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/136,118
                                                                                                              Mismatches
                                                                              Score 15;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Spevack, A. David
REGISTRATION NUMBER: 24,743
REFERENCE/DOCKET NUMBER: N.C. 75,776
TELECOMMUNICATION INFORMATION:
          OTHER INFORMATION: antisense sequence US-09-377-310-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/918,259
FILING DATE: 24-UL-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                        Sequence 7, Application US/08136118
Patent No. 5580969
GENERAL INFORMATION:
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92.9%;
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TELEFAX: (202) 295-1022
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                            Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                             1 tacccaggtgagtc 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Bethesus
STATE: Maryland
COUNTRY: USA
ZIP: 20889-5606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                           US-08-136-118-7/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ANTI-SENSE:
US-08-136-118-7
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FEATURE:
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Gaps
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US-09-101-886B-71
Sequence 71, Application US/09101886B
SEQUENCE THOMAS
APPLICANT: DILERENUD, OLE K
APPLICANT: NILSSEN, OIVIND
TITLE OF INVENTION: GENETIC TEST FOR ALPHA-MANNOSIDOSIS
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
Sequence 668, Application US/08117952
Patent No. 5851760
GENERAL INFORMATION:
APPLICANT: Evans, Glen A.
APPLICANT: Smith, Michael W.
TITLE OF INVENTION: METHOD FOR GENERATION OF SEQUENCE
TITLE OF INVENTION: SAMPLED MAPS OF COMPLEX GENOMES
                                                                                                                                                           NUMBER OF SEQUENCES: 797
CORRESPONDENCE ADDRESS:
ADDRESSE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                            SOFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,952
FILING DATE: 07-SEP-1993
CLASSIFICATION: 435
RIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/471
FILING DATE: 15-JUN-1993
ATTORREY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 12.4; DB 2;
Pred. No. 1.3e+02;
); Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUITE 701E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: Oligonucleotide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: BARBARA G. ERNST
STREET: 555 13TH STREET, NW
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-4737
TELEFAX: 619-546-9392
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92.9%;
                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 92.9
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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RESULT

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: R. J. Rodrick, Becton Dickinson and Company STREET: 1 Becton Drive CITY: Franklin Lakes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/08865675
Patent No. 5928869
GENERAL INFORMATION:
APPLICANT: Nadeau, James G.
APPLICANT: Pitner, James B.
APPLICANT: Carl P.
APPLICANT: Schram, James L.
TITLE OF INVENTION: PLORESCENCE QUENCHING
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/865,675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 11.8; DB 2;
Pred. No. 3e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 6, Application US/09237510 ; Patent No. 5958700
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NAME: Fugit, Donna R.
REGESTRATION NUMBER: 32,13:
REFERENCE/DOCKET NUMBER: P.
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-988-128-15
                                                                                                                                                                                                                   78.7%;
86.7%;
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86.78;
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Best Local Similarity 86.7
Matches 13; Conservative
                                                                                                                                                                                                                 Query Match 78.7
Best Local Similarity 86.7
Matches 13; Conservative
                        SEQUENCE CHARACTERISTICS:
                                              LENGTH: 34 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                            16 TACCCAGCTGTGTCT 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: NJ
COUNTRY: US
ZIP: 07417
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US-09-237-510-6/c
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US-08-865-675-6
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Patent No. 5994505
GENERAL INFORMATION:
APPLICANT: Ting, Jenny Pan-Yung
APPLICANT: Chin, Keh-Chin
TITLE OF INVENTION: No. 5994505el Forms of Class II MHC
TITLE OF INVENTION: Transactivator (CIITA)
TUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Myers Bigel Sibley & Sajovec, P.A.
STREET: P.O. Box 37428
CITY: Releigh
STATE: No. 5994505th Carolina
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 11.8; DB 4; Length 20;
Pred. No. 2.8e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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COMPUTER: IBM PC COMPATIBLE
OPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988,128
FILING DATE: 10-DEC-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: B194AS, SOF03111 J.
REGISTRATION NUMBER: 39,111
REFERENCE/POCKET NUMBER: 5470-136
TELECOMMUNICATION INFORMATION:
MEDIUM TOWN OF ALCOME.
                                                                           SOPTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                        APPLICATION NUMBER: US/09/101,886B
FILING DATE: 29-JANUARY-1998
CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB97/00109
FILING DATE: 12-JAN-1997
ATTONNEY/AGENT INFORMATION:
NAME: ERNST, BARBARA G
REGISTRATION NUMBER: 30,377
REDERENCE/DOCKET NUMBER: .1181-240
TELECOMMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION 180640
                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 202-783-6031
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78.78;
86.78;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (919) 854-1401
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Best Local Similarity 86.7
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 tacccaggtgagtct 15
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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US-09-101-886B-71
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SEQUENCE CHARACTERISTICS: LENGTH: 30 base pairs
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Best Local Similarity 92.3
Matches 12; Conservative
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ADDRESSEE: Patrea L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
3 cccaggtgagtct 15
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                                     15 CCAAGGTGAGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30309-3450
                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Atlanta
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US-09-015-876-20
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Patent No. 6187545
Batent No. 6187545
BAPLICANT: NFORMATION:
APPLICANT: Madeline M. Butler
APPLICANT: Jax M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF PEPCK-CYTOSOLIC EXPRESSION
FILE REFERENCE: RTS-0123
CURRENT FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 177
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              APPLICANT: Nadeau, James G.
APPLICANT: Pitner, James B.
APPLICANT: Linn, Carl P.
APPLICANT: Schram, James L.
APPLICANT: NVENTION: FIUORESCENCE QUENCHING
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: R. J. Rodrick, Becton Dickinson and Company
STREET: 1 Becton Divive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/237,510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 11.8; DB 2
Pred. No. 3e+02;
); Mismatches
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ZIP: 07417
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
POUNTRER: IBM PC COMPATIBLE
PC-DOS/MS-DV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Fugit, Donna R.
REGISTRATION NUMBER: 32,135
REFERENCE/DOCKET NUMBER: P-:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78.78;
86.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 78.7
Best Local Similarity 86.7
Matches 13; Conservative
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US-09-237-510-6
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Best Local Similarity
Matches 12; Conserva
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-488-671-119/c
                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
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                                                                                                                                                                                                                                 STATE: N. COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 119
LENGTH: 20
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PESTUR 10

19:08-133-702-34

Sequence 34, Application US/0813702

PERMILLANY COMMUNICATION

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APPLICANT: MARMANDE, TANEAGED
APPLICANT: MARMANDE, MASATO
TITLE OF INVENTION: AN ISOLATED NUCLEIC ACID MOLECULE ENCODING HUMAN
TITLE OF INVENTION: AN ISOLATED NUCLEIC GLIQUITIN-CONJUGATING ENZYME
FILE REFERENCE: 0-53599
CURRENT APPLICATION NUMBER: US/09/273,565A
CURRENT FILING DATE: 1999-03-22
EARLIER APPLICATION NUMBER: 09/055,699
EARLIER PILING DATE: 1998-04-07
EARLIER PILING DATE: 1997-03-19
EARLIER PLING DATE: 1997-03-19
EARLIER PILING DATE: 1996-03-19
EARLIER FILING DATE: 1997-03-05
SAPTHARE: PLING DATE: 1997-03-05
SOFTWARE: PALCATION NUMBER: JP 69163/1997
EARLIER FILING DATE: 1997-03-05
SOFTWARE: PALCATION VORDER: JP 69163/1997
SEQ ID NO 86
LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence: C1 Primer US-09-273-565-86
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                                                                                                                                                                                         1064/41979CP4
APPLICATION NUMBER: US 08/469,427
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569,063
FILING DATE: 06-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, JOSEPH D
RGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/41979C;
TELECHONE: (202) 628-8800
TELEPHONE: (202) 628-8804
INFORMATION FOR SEQ ID NO: 53:
SEGUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 86, Application US/09273565A Patent No. 6166190
                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: DNA (genomic) US-08-609-443B-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: FUJIWARA, TSUTOMU
APPLICANT: WATANABE, TAKESHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 73.3
Best Local Similarity 100.
Matches 11; Conservative
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Best Local Similarity 100.
Matches 11; Conservative
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US-09-273-565-86/c
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Patent No. 5840693
GENERAL INFORMATION:
APPLICANT: ERIKSSON, Ulf
APPLICANT: ALITALO, Kari
APPLICANT: ALITALO, Kari
APPLICANT: ALITALO, Kari
ITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
TITLE OF INVENTION: DAA CODING THEREFOR
NUMBER OF SEQUENCES: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
STREET: 1200 G Street, N.W., Suite 700
STREE: DC
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73.3%; Score 11; DB 1; Length 20; 100.0%; Pred. No. 8.1e+02; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
ADDRESSEE: AKZO NOBEL PATENT DEPT.
STREET: 1300 PICCARD DRIVE, SUITE 206
CITY: ROCKVILLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DAYA:
APPLICATION NUMBER: US/08/609,443B
FILING DATE: 01-MAR-1996
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/397,651
FILING DAYE: 01-MAR-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: KLESNER, SHARON N
REGISTRATION NUMBER: 36,335
REFERENCE/DOCKET NUMBER: T/98353
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-948-7400
TELEPANTION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/015,876
                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear; MOLECULE TYPE: DNA US-09-015-876-20
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                                                                      MARYLAND
                                                                                                                                                                                                                                                                                              FILING DATE:
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UTSD:406/KIT

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Query Match 73.3%; Score 11; DB 2; Length 28; Best Local Similarity 100.0%; Pred. No. 8.3e+02; Matches 11; Conservative 0; Mismatches 0; Indels
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                   FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/456,103
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: KItchell, Barbara S.
REGISTRATION NUMBER: 33,928
REGISTRATION NUMBER: 33,928
REGISTRATION NUMBER: 33,928
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ 10 NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
WOLECULE TYPE: other nucleic acid
US-09-067-908-4
APPLICATION NUMBER: US/09/067,908
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          Sequence 4, Application US/08456103
Sequence 4, Application US/08456103
Sequence 4, Application US/08456103
Sequence 100 Statage
GENERAL INFORMATION:
APPLICANT: MUNICAL RECOMBINANT GENE
TITLE OF INVENTION: INFLAMMATION-INDUCED EXPRESSION OF A
TITLE OF INVENTION: RECOMBINANT GENE
NUMBER OF SEQUENCES:
COMPRESSE: Annold, White & Durkee
STREET: P.O. Box 4433
COMPTRY: United States of America
STATE: Texas
COMPTRY: United States of America
SIP: 77210-4433
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
FILING DATE: Submitted Herewith
CURSSIFICATION NUMBER: US/08456,103
FILING DATE: Submitted Herewith
COMPANY/ACENT INDAMATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/09067908

Patent No. 5851822

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: INFLAMMATION-INDUCED EXPRESSION OF A TITLE OF INVENTION: RECOMBINANT GENE
NUMBER OF SEQUENCES:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
COUNTRY: United States of America
STATE: Texas
COUNTRY: United States of America
STATE: Texas
COUNTRY: United States of America
STATE: FRAMABLE FORM:
MEDIDIM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 73.3%; Score 11; DB 1; Length 28; Best Local Similarity 100.0%; Pred. No. 8.3e+02; Matches 11; Conservative 0; Mismatches 0; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REGISTRATION NUMBER: 33,928
REFERENCE/POCKET NUMBER: UTSD:406/KIT
TELECOMMUTCATION INFORMATION:
TELEFHONE: (512) 418-3000
TELEFRAX: (713) 789-2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELES: ('...'
TELES: 79-0924
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERSTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
TYPE: ...ecq: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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Human Notch3 mutan Human Notch3 mutan Humanised antibody Humanised LO-CD2a Humanised LO-CD2a PCR primer used to PCR primer used to HIV-1 LTR (long te Human ICAM-R CDNA Humanised ICR-1.1 PCR primer 8 used
        Oligonucleotide ca
VEGF-B186 exon 5 b
VEGF-B167 exon 5 b
Human VEGF-B186 ex
Human eukaryotic i
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Human hAPO8 RACE p
PCR primer FOGIVHF
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Primer for antibod
Chimeric ICR-1,1 a
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GATA-1 locus splic
Primer used to amp
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Bacillus thuringie
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Human vascular end
Humanised 340 Vh a
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Humanised murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antisense compounds for inhibiting focal adhesion kinase expression, especially useful for inhibiting retinal neovascularization, or for diagnosing and treating e.g. colon cancer
                                                                                                                                                                                                                                                                                                              Human ICAM-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; focal adhesion kinase; FAK; signal transduction; cancer; embryonic development disorder; angiogenic disorder; wound healing; antisense; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human focal adhesion kinase antisense seguence #29.
                                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                 AAV22892
AAZ10191
                                                                                                                                                                                                       AAA08308
AAZ24334
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AAT44073
                                                                                                                                                                                                                                                                                                                       AAV54868
AAX21887
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                                                                                AAV22641
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AAC65563 standard; DNA; 15
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 (ISIS-) ISIS PHARM INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-AUG-1999;
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                                                                                         AAC65563;
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RESULT
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ICAM-1 antisense o
Human ICAM-1, E-se
Chromosome 11 (loc
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Target oligonucleo
Mouse PEPCK-cytoso
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Blackcurrant rever
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Human focal adhesi
                                                                  Search time 876.95 Seconds (without alignments)
10.740 Million cell updates/sec
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/SIDSB/gcgdata/geneseq/geneseqn/Na1990.DAT:
/SIDSB/gcgdata/geneseq/geneseqn/Na1990.DAT:
/SIDSB/gcgdata/geneseq/geneseqn/Na1991.DAT:
/SIDSB/gcgdata/geneseq/geneseqn/Na1993.DAT:
/SIDSB/gcgdata/geneseq/geneseqn/Na1993.DAT:
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/SIDSB/gcgdata/geneseq/geneseqn/Na1998.DAT:
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                                                                                                                                                                                                                                                                                                            /SIDS8/gcgdata/geneseq/geneseqn/NA1980.DAT:*/SIDS8/gcgdata/geneseq/geneseqn/NA1981.DAT:*/SIDS8/gcgdata/geneseq/geneseqn/NA1982.DAT:*
         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                      hits satisfying chosen parameters:
                                                                                                                                                                                  730101 seqs, 313950809 residues
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                                                                   2, 2001, 16:18:48
                                                                                                                                                                                                                                                        Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                - nucleic search, using sw model
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AAV38613
AAQ82668
AAF98212
AAV28523
AAT15506
AAV15506
AAV82665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAC65563
                                                                                                                                                    IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                1 tacccaggtgagtct 15
                                                                                                         US-09-757-100B-31
15
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Match Length
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Maximum DB seq length: 50
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Score

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Total number of

Searched:

Scoring table:

Perfect score:

Title:

Sequence:

OM nucleic

Run on:

CDNA

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Antisense; pre-mRNA; mature mRNA; vascular defect; tissue defect; human intercellular adhesion molecule-1; ICAM-1; inflammation; adult respiratory distress syndrome; multiple organ failure; GM1594;
                                                                                                                                                                    ICAM-1 antisense oligonucleotide #7
                                                                                                                                                                                                                                                                                                                                                                93US-0136118.
92US-0918259.
                                                                                                                                                                                                                                                                                                                                         92US-0918259
                                                              RESULT 3
AAT58077/c
ID AAT58077 standard; DNA; 21
                                                                                                                                           (first entry)
 1 tacccaggtgagtct 15
             (USNA ) US SEC OF NAVY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-033603/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTCCCAGGTGAGTC
                                                                                                                                                                                                                                   septic shock; ss
                                                                                                                                           18-MAR-1997
                                                                                                                                                                                                                                                                                                                                        24-JUL-1992;
                                                                                                                                                                                                                                                                                                                                                                 12-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                            24-JUL-1992;
                                                                                                                                                                                                                                                                                     US5580969-A.
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                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                 AAT58077;
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ID AAV386
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                      The present invention describes a number of phosphorothioate antisense sequences to the human focal adhesion kinase (FAK) protein. This protein is involved in integrin-mediated signal transduction, and is implicated in cancer, particularly colon, breast and oral tumours, embryonic autisense taisorders, angiogenic disorders and wound healing. The antisense sequences, including the one shown here, can be used in the treatment of all of these.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a number of phosphorothioate antisense sequences to the human focal adhesion kinase (FAK) protein. This protein is involved in integrin-mediated signal transduction, and is implicated in cancer, particularly colon, breast and oral tumours, embryonic development disorders, anglogenic disorders and wound healing. The antisense sequences, including the one shown here, can be used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antisense compounds for inhibiting focal adhesion kinase expression, especially useful for inhibiting retinal neovascularization, or for diagnosing and treating e.g. colon cancer -
                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                Human; focal adhesion kinase; FAK; signal transduction; cancer;
embryonic development disorder; angiogenic disorder; wound healing;
                                                                                                                                                                                            .;
0
                                                                                                                                                                    22; Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 15; DB 22; Length 20; 100.0%; Pred. No. 16; 0; Mismatches 0; Indels
                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                         Human focal adhesion kinase antisense sequence #9.
                                                                                                                                                                                           0;
                                                                                                                                                                   DB
15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 other;
                                                                                                                           Sequence 15 BP; 3 A; 4 C; 4 G; 4 T; 0 other;
                                                                                                                                                                                           Mismatches
                                                                                                                                                                   Score 15;
Pred. No.
Claim 15; Column 25; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 15; Column 23; 30pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                          antisense; phosphorothioate; ss.
                                                                                                                                                                                           .;
0
                                                                                                                                                                  100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                             BP.
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                                                                                                                                                                                                                                                                                                            AAC65543 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antisense sequences, inclu
treatment of all of these.
                                                                                                                                                                Ouery Match 100.
Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                     1 tacccaggtgagtct 15
                                                                                                                                                                                                                                  (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Monia BP, Gaarde WA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-006141/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                               12-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US6133031-A.
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                                                                                                                                                                                                                                                                                                                                      AAC65543;
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                                                                                                                                                                                                                                                                             The sequences given in AAT58071-85 represent oligonucleotides which are
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                                                                                                                                                                                                                                                                                                                                                          These oligonucleotides may be used for treating septic shock and the manifestations of septic shock, e.g. inflammation, and vascular and tissue defects. They are also useful in the treatment of septic shock associated diseases, e.g. adult respiratory distress syndrome,
                                                                                                       Anti-sense oligo:nucleotide(s) for blocking ICAM-1 mRNA translation - for treating septic shock, adult respiratory distress syndrome
                                                                                                                                                                                                                                                                                                    antisense to sequences contained in the pre-mRNA or mature mRNA transcript of human intercellular adhesion molecule-1 (ICAM-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human ICAM-1, E-selectin, VCAM-1 antisense oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 12.4; DB 18;
Pred. No. 4.7e+02;
); Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 21 BP; 5 A; 9 C; 5 G; 2 T; 0 other;
Williams TJ;
                                                                                                                                                                                                                     Claim 1; Column 21; 16pp; English.
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Bradley MO, Hoke GD, Lee C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82.7%;
92.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             multiple organ failure etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAV38613 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 82.7
Best Local Similarity 92.9
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 tacccaggtgagtc 14
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Gaps

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Sequences were determined from the ends of chromosome 11-specific cosmids by automated sequencing without intermediate subcloning.
A sample of 371 DNA sequence fragments were determined and of these, 277 were suitable for STS primer prediction by computer these, 277 were mapped by in situ hybridisation, somatic cell hybrid analysis (using the "primer" program available from E.Lander, MIT).
The STSS and cosmids were mapped by in situ hybridisation, somatic cell hybrid analysis to both. Using this method, 370 STSS specific for human chromosome 11 were generated and most of them were regionally mapped. This procedure illustrates a novel method for sequencing complex genomes, designated "sequence sampled mapping method is useful for the completion of high density sequence—based maps, and ultimately, for the complete sequencing of genomic DNA directly from cosmid clones.
See AAQ82001-Q82706 and AAQ91325-Q91358 for STS primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pathogen; yeast; intergenic spacer region; IGS1; PCR primer; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel assemblage useful for discriminating among pathogenic yeasts,
                                                                                                                                                                Sequencing complex genomes, present as fragments in a cosmid
library - by sequencing end-specific nucleotides of each clone
then correlating with spatial relationship of cosmid, esp. for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 12.4; DB 16;
Pred. No. 4.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C neoformans strain discrimination probe #30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 22 BP; 8 A; 5 C; 4 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                          (SALK ) SALK INST BIOLOGICAL STUDIES.
                                                                                                                                                                                                                                                                   Example 4; Page 92; 128pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82.7%;
92.9%;
93US-0117952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-SEP-2000; 2000WO-US26758
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GENE-) GENETIC VECTORS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    McCabe M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 82.7
Best Local Similarity 92.9
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cryptococcus neoformans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 acccaggtgagtct 15
                                                                                                                                                                                                                                mammalian chromosomes.
                                                                                   Smith MW;
                                                                                                                          WPI; 1995-036508/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 ATCCAGGTGAGTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (FELL/) FELL J.
(DIAZ/) DIAZ M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200123616-A2
07-SEP-1993;
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                                                                                   Evans GA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence is that of an antisense oligonucleotide which is substantially complementary to at least a portion of the preor mature RNA transcript of human intracellular adhesion molecule (ICAM). E-selectin or vascular cell adhesion molecule (VCAM). It can be used to inhibit expression of these proteins. Inhibition of these proteins forms the basis for treatment of conditions and diseases that have an inflammatory component, e.g. acne, psoriasis, arthritis, organ rejection, wounds, burns, septic shock or
                                    vascular cell adhesion molecule-1; antisense; inflammatory; disease; treatment; septic shock; psoriasis; wounds; burns; acne; arthritis; organ rejection; inhibition; expression; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                   ICAM-1; intracellular adhesion molecule-; E-selectin; VCAM-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antisense oligonucleotides to ICAM-1, E-selectin or VCAM-1 for treating diseases having an inflammatory component, e.g. psoriasis, wounds and septic shock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 21;
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92.9%; Pred. No. 4.7e+02;
ive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chromosome 11 (locus LDHC) STS primer LDHC-Z.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inflammatory complications of septic shock.
                                                                                                                                                                                                                                                                                                                                                                                         Williams TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 8; Page 40; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                           Lee C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ82668 standard; DNA; 22 BP.
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Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                  (DYAD-) DYAD PHARM CORP.
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                                                                                                                                                                                                                                                                                                                                                                                         Bradley MO, Hoke GD,
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                                                                                                                                                                                   WO9824797-A1
                                                                                                                                                                                                                                                              02-DEC-1996;
                                                                                                                                                                                                                                                                                                         02-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUN-1994;
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                                                                                                                       Synthetic.
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Query Match

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RESULT 5 AAQ82668/c

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Gaps

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Length 22; Indels

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                                                                                The present invention describes an assemblage comprising two primers, each of which can be used to amplify the intergenic spacer region IGS1 from one of various strains of the yeast Cryptococcus neoformans. A number of primers and probes are provided, as are the sequences of the IGS1 for 91 C. neoformans strains. This is useful in the discrimination of pathogenic yeasts, and the sequences can be used to construct a database having the same purpose. The present sequence is a probe or
comprises two universal primers adapted for nucleic acid amplification
                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Primer 5 and primer 6 (see AAV28524) are designed to amplify a 481 nucleotide DNA fragment initiating 265 nucleotides upstream of the polyA tail of RNA2 of a blackcurrant reversion virus (BRV) Finnish isolate genome (see AAV28525). They were used with primer 1,2 (see AAV28521-22), designed to amplify a 210 nucleotide fragment, to detect different isolates of BRV originating from widely different geographic locations. Primer pair 1,2 amplified the expected virus-specific fragments from all tested virus isolates, and the primer pair 5,6 amplified the expected virus isolates, and the nearly all the tested virus isolates, indicating that the viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Blackcurrant reversion disease; BRV; rna2; diagnosis; Ribes; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Blackcurrant reversion virus RNA2 3' proximal fragment primer 5.
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                                                                                                                                                                                                                                                                                           Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Diagnosing blackcurrant reversion disease in plants e.g. blackcurrant - using reverse transcriptase-PCR with primers amplifying cDNA fragment complementary to fragment of new
                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                          Score 12.4; DB 22;
Pred. No. 4.8e+02;
); Mismatches 1;
                                                                                                                                                                                                                                           Sequence 33 BP; 7 A; 6 C; 13 G; 7 T; 0 other;
                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sus1 P;
                                                                                                                                                                                                         primer described in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 2; Page 27; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lehto K, Lemmetty A,
                                                  Claim 6; Page 18; 88pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAV28523 standard; DNA; 20 BP.
                                                                                                                                                                                                                                                                                           82.7%;
92.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Blackcurrant reversion virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          blackcurrant reversion virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97WO-FI00507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96FI-0003474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                           Query Match 82.7
Best Local Similarity 92.9
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ABOA-) ABOATECH OY AB.
                                                                                                                                                                                                                                                                                                                                                                2 acccaggtgagtct 15
                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-193642/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9810100-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-AUG-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Latvala S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV28523;
                 protocol
                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
AAV28523
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claimed PCR primers (see AAT99462-T99531) hybridise to sequences that rencode the extracellular domain of human heat-stable toxin (ST) receptor protein (see AAW37371), a highly specific marker for metastasised colorectal cancer cells. PCR using these primers provides specific and sensitive detection of human ST receptor expression. A specific primer pair comprises the primers given in AAT99528 and AAT9952. Claimer pair comprises the primers given in AAT99529. Claimed in vitro methods for determining whether or not (i) an individual has metastasised colorectal cancer cells, or (ii) a tumour cells far a colorectal cancer cell comprise the steps of examining a sample of extraintestinal tissue and/or body fluids or tumour cells from an individual to determine whether ST Expression is determined by immunoassay or by PCR using primers that selectively amplify ST receptor CDNA or mRNA (see also
                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Determining whether an individual has metastasised colorectal cancer cells and origin of tumour cells - by detecting presence of heat-stable toxin receptor on cells in a sample
sequences detecting by these primer pairs are well conserved in all 1solates, including the common (E) and strong (R) forms of the reversion disease. The invention provides methods and kits for the diagnosis of blackcurrant reversion disease using RT-PCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; heat stable toxin receptor; colorectal cancer; tumour; diagnosis; human; PCR; primer; ss.
                                                                                                                                                                   ;
0
                                                                                                                                    Length 20;
                                                                                                                                                                   Indels
                                                                                                                                     DB 19; L
7.9e+02;
                                                                                  Sequence 20 BP; 7 A; 5 C; 6 G; 2 T; 0 other;
                                                                                                                                                                     Mismatches
                                                                                                                                  80.0%; Score 12;
100.0%; Pred. No.
tive 0; Mismatci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 14; Page 54; 62pp; English.
                                                                                                                                                                                                                                                                                                                         AAT99528 standard; DNA; 32 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYJE-) UNIV JEFFERSON THOMAS
                                                                                                                                                                                                                                                                                                                                                                                                                            Human ST receptor PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96US-0016564.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Waldman SA;
                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                    Query Match 80.0
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                        2 acccaggtgagt 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-008454/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ST receptor; heat
metastasis; diagno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carrithers SL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9742506-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                          21-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-NOV-1997.
                                                                                                                                                                                                                                                                                                                                                           AAT99528;
                                                                                                                                                                                                                                                                                                         AAT99528
 SSSSSXS
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DB 19; Length 32;

80.0%; Score 12;

Query Match

Sequence 32 BP; 6 A; 11 C; 9 G; 6 T; 0 other;

(first entry)

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Detector oligonucleotide; hairpin structure; fluorescence; primer extension; hybridization; signal primer; frameshift mutation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      quenched dyes - where dyes become fluorescent when region is unpaired, useful for detection and amplification of target nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New detector oligo:nucleotide having base-paired region carrying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; Page 12; 20pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nadeau JG, Pitner BJ,
                AAV82665/c
ID AAV82665 standard; DNA; 48 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                           (BECT ) BECTON DICKINSON & CO.
                                                                                                                                       Target oligonucleotide JN5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-001406/01.
                                                                                                      25-FEB-1999
                                                                                                                                                                                                                                                                                                                                                     28-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                        30-MAY-1997;
                                                                                                                                                                                                                                                                                 EP881302-A2.
                                                                                                                                                                                                                                                                                                                    02-DEC-1998.
                                                                                                                                                                                                                                              Synthetic.
                                                                  AAV82665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Linn PC,
                                                   qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence was used in the development of a novel system, comprising an adeno-associated virus (AAV) vector containing a comprising an adeno-associated virus (AAV) vector containing a constrain DNA, and the rep 68/78 sequence of AAV, the expression of which is delayed. The components may be present in cis (in a single agent) or in trans (in separate agents).

The system is used for production of AAV vectors, particularly for gene therapy. The foreign DNA may encode a therapeutic protein, e.g. interferon, interleukin, growth factor, coagulation factor or metabolic enzyme, particularly one that increases the immunogenicity of tumour cells, and/or a diagnostic protein. The system produces AAV vectors on a large scale. It is based on the discovery that the rep68 and 78 proteins interfere with replication of AAV DNA, and that this interference is overcome by delaying
                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        System of adeno-associated viral vector and rep 68/78 sequence of this virus - expression of which is delayed until replication of viral DNA has started, provides large scale production of vectors for gene therapy
                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 11.8; DB 19; Length 34;
Pred. No. 1.1e+03;
0; Mismatches 2; Indels (
                                 Indels
                                                                                                                                                                                                                                                                                                                                 AAV; vector; rep 68/78; PCR primer; gene therapy; ss.
            Pred. No. 8.1e+02;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 34 BP; 4 A; 13 C; 9 G; 8 T; 0 other;
                                                                                                                                                                                                                                                                                                Primer for adeno-associated virus DNA.
100.08; Pic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                       AAV15506 standard; DNA; 34 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example; Page 7; 20pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78.7%;
86.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of these proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97WO-DE01333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96DE-1025188
                                                                                                                                                                                                                                                           11-JUN-1998 (first entry)
                               12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                    Adeno associated virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bogedain C, Hallek M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MEDI-) MEDIGENE GMBH.
                                                              3 cccaggtgagtc 14
                                                                                      WPI; 1998-086641/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MEDI-) MEDIGENE AG
            Best Local Similarity Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                       W09749824-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-DEC-1997.
                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                          AAV15506;
                                                                                                                                                                     AAV15506
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Schram JL;

98EP-0109682. 97US-0865675.

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Target oligonucleotides AAV82665-68 were designed to hybridise to the detector oligonucleotide of the invention. The detector oligonucleotide of the invention. The detector oligonucleotide of comprises a single-stranded target-binding region and an intramolecularly base-paired secondary structure linked to two dyes (donor and acceptor fluorophores). In the secondary structure, fluorescence of the donor is quenched, but when it is linearised or unfolded a change in some fluorescence parameter becomes detectable. A target nucleic acid is detected by hybridizing it to a detecteor oligonucleotide in which the secondary structure is 5' to the target binding region, primer extension to produce a complementary strand using the secondary structure as template, resulting in linearization or the oligonucleotide are used to detect (by primer extension and oligonucleotide are used to detect (by primer extension and hybridization) and amplify (as signal primer) target sequences, e.g. for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse PEPCK-cytosolic antisense oligonucleotide ISIS 113360.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78.7%; Score 11.8; DB 20;
86.7%; Pred. No. 1.1e+03;
ive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 48 BP; 15 A; 8 C; 10 G; 15 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    detecting frameshift mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAF62963/c
ID AAF62963 standard; DNA; 20 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 78.7
Best Local Similarity 86.7
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 TACTCAGATGAGTCT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 tacccaggtgagtct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
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Gaps

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Conservative

Local Similarity nes 13; Conserv

Best Loca Matches

Query Match

1 tacccaggtgagtct 15

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RESULT

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Sequences AAA72437, AAA72449-A72461, AAA72468 and AAA72474-A72477

represent CDNAs encoding novel plant isoflavone synthases (AAB21052 and AAB21071). Also discibsed is the soybean cytcohrone P450

concoxygenase CYP93C1, encoded by a known sequence (AAA72444, NCBI No. 2739005), which was identified in the present invention as having isoflavone synthase activity. The invention also relates to expression constructs, transformed host cells, and transgenic plants and seeds conscribing the novel CDNA sequences of the invention. The invention also encompasses methods of altering isoflavone synthase expression in a host cell, altering isoflavoned in a limit, and identifying nucleic acids encoding other plant isoflavone synthases. Isoflavone synthase catalyses cell, altering isoflavonold levels in a plant, and identifying nucleic acids encoding other plant isoflavone synthases. Isoflavone synthase catalyses cells as Ney Tole in the biosynthesis of isoflavonolds. Isoflavonolds are catas of secondary metabolites mainly produced in leguminous plants by a branch of the phenylpropanold pathway. Isoflavonolds are consumptant of the synthesis of isoflavonolds. Isoflavonolds in the defence response of legumes against phytopathogenic intermediates to the synthesis of isoflavonolds. Isoflavonolds consumption of legume sand rhizobial bacteria which eventually result in nodulation and nitrogen fixation. They have also been shown to act as artibiotics, repellents, attractants, and signal compounds, and consumption of legume isoflavonolds sis associated with health benefits in humans. The novel isoflavonolds sis associated with health benefits in humans. The novel isoflavonolds signal compounds, and consumption of legume souch as soybean, and for the production of isoflavonolds in elegumes such as soybean, and for the production of isoflavonolds in clegumes such as soybean, and for the production of isoflavonolds consumption of the invention to ampility DNA encoding soybean chalcone consumption of the invention to ampility DNA encodi
                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding isoflavonoid synthases, useful for producing transgenic plants with increased production of isoflavonoids which are involved in defense against phytopathogenic microorganisms \,
                                                                                                                                                                                                                                  Fader GM, Jung W, McGonigle B, Odell JT,
                                                                                                                                                                         (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 14; Page 52; 157pp; English.
                                                        99US-0117769.
99US-0144783.
99US-0156094.
26-JAN-2000; 2000WO-US01772
                                                                                                                                                                                                                                                                                    WPI; 2000-543395/49.
                                                        27-JAN-1999;
20-JUL-1999;
24-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ04939;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 nucleobases in length that are capable of inhibiting the expression of anotheronal pytuvate carboxykinase-cytosolic (PEPCK cytosolic). The antisense compounds are useful for inhibiting the expression of PEPCK-cytosolic in cells or tissues. They are commonly used as research reagents and in diagnostics, e.g. to elucidate the function of particular genes. They are also useful for distinguishing between functions of various members of a biological pathway and for research use. The antisense compounds are also useful prophylactically, e.g. to prevent or delay infection, inflammation or tumour formation. The present sequence is a chimeric phosphorothioate oligonucleotide with 2'-MOE wings and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present sequence is one of a number of antisense compounds of up to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antisense compound capable of modulating the expression of phosphoenol pyruvate carboxykinase-cytosolic, useful for preventing or delaying infection, inflammation or tumor formation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Soybean; chalcone reductase; phenylpropanoid pathway; isoflavone synthase; isoflavonoid biosynthesis; defence response; attractant; repellant; signal compound; antibiotic; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                       Mouse; antlinflammatory; cytostatic; antisense gene therapy; phosphoenol pyruvate carboxykinase-cytosolic; PEPCK-cytosolic; infection; inflammation; tumour formation; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 11.4; DB 22; Length 20; Pred. No. 1.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Soybean chalcone reductase PCR primer, SEQ ID NO:65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20 BP; 5 A; 6 C; 5 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Butler MM, Wyatt J, Cowsert LM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transgenic seed; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76.0%;
92.3%;
                                                                                                                                                                                                                                                                                                                     21-JAN-2000; 2000US-0488671
                                                                                                                                                                                                                                                                                                                                                                       21-JAN-2000; 2000US-0488671
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 76.0
Best Local Similarity 92.3
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 cccaggtgagtct 15
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                                                                                                                                              Mus musculus.
                                                                                                                                                                                                 US6187545-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-DEC-2000
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                                                                                                                                                                                                                                                            13-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        McKay R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA72481;
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                                                             Score 11.4; DB 21; Length 25;
Pred. No. 1.7e+03;
0; Mismatches 1; Indels C
                                                                                                                                                                                                                                                                                                     Oligonucleotide carrying mutation for factor VIII gene.
                        Sequence 25 BP; 6 A; 7 C; 5 G; 7 T; 0 other;
                                                                                                                                                                                                                                                                                                                                Human factor VIII analogue; ss.
                                                                                                                                                                                                                   AAQ04939 standard; DNA; 46 BP.
                                                                76.0%;
92.3%;
                                                                                                                                                                                                                                                                         24-OCT-1990 (first entry)
phenylpropanoid pathway).
                                                                             Best Local Similarity 92.3
Matches 12; Conservative
                                                                                                                     3 cccaggtgagtct 15
                                                                                                                                       CCCAGGTGAGTTT
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AAT AAT37933-T37946 represent the intron/exon boundaries for the human vascular endothelial growth factor (VEGF) proteins of the invention (see AAW04829, and AAW04831), which promote endothelial or mesodermal cell proliferation. VEGF is also a glycosylated cationic dimer, and is sometimes referred to as vascular permeability factor (VPF). VEGF has diverse effects, depending on the specific biological context in which it is found. VEGF is a potent endothelial cell mitogen, and directly contributes to induction of angiogenesis in vivo by promoting endothelial cell growth during normal embryonic development, wound healing, and tissue regeneration/recognistion. The VEGF proteins of the invention share the angiogenic and other properties of VEGF, but are distributed and expressed in tissues differently to VEGF. The proteins of nitibodies against the proteins can be used for inhibiting angiogenesis. The antibodies can also be used diagnostically to quantitatively detect of the invention can also be used to detect VEGF-B coding sequences. Ountification of VEGF-B in cancer biopsy specimens may be useful as an infinite of metastatic risk. VEGF-B expression in a cell can be retarded using antisense sequences direct against the VEGF coding sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Endothelial cell; proliferation; vascular endothelial growth factor; VPF; vBGF; endothelium; mesodermal cell; cationic dimer; tissue regeneration; vascular permeability factor; cell mitogen; anglogenesis; cell growth; embryonic development; wound healing; tissue reorganisation; antibody; cancer; metastatic risk; tumour cell; human; ss.
                                                                                                                           Vascular endothelial growth factor VEGF-B proteins - useful to accelerate angiogenesis in wound healing, also related nucleic acid and antibodies for cancer diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                           Olofsson B, Pajusola K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73.3%; Score 11; DB 17; I 100.0%; Pred. No. 2.9e+03; iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 other;
    (UYHE-) UNIV HELSINKI LICENSING LTD OY.
                                                                                                                                                                                                            Example 7; Page 28; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT37943 standard; cDNA; 20 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VEGF-B167 exon 5 boundary 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95US-0569063
95US-0397651
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 73.3
Best Local Similarity 100.
Matches 11; Conservative
                                             Alitalo K, Eriksson U,
                                                                                    WPI; 1996-412582/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 caggtgagtct 15
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01-MAR-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Factor VIII analogue is sufficiently mutated from the original gene that it is not recognised by blood Abs of the patient. The analogue is composed of human FVIII but carries the B-domain of human FV in place of the FVIII B-domain.

Oligonucleotides can be used to alter the profile of the blood factor without significantly altering its activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                 New hybrid DNA encoding hybrid procoagulant proteins prepd. by modifying DNA encoding human factor VIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 11.4; DB 11;
Pred. No. 1.8e+03;
); Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 46 BP; 7 A; 14 C; 12 G; 13 T; 0 other;
                                       Location/Qualifiers
24..28
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76.0%;
92.3%;
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95US-0397651.
95US-0469427.
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                                                                                                                                                                                                         89WO-0005049
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                                                                                                                                                                                                                                                                                        (GENE-) GENETICS INST INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; ; pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 76.0
Best Local Similarity 92.3
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                 Pittman DD;
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01-MAR-1995;
06-JUN-1995;
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                                                                                                                                                                31-MAY-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-SEP-1996
Synthetic
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Gaps

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AAT37933-T37946 represent the intron/exon boundaries for the human vascular endothelial growth factor (VEGF) proteins of the invention (see AAW04829, and AAW0481), which promote endothelial or mesodermal cell proliferation. VEGF is also a glycosylated cationic dimer, and is sometimes referred to as vascular permeability factor (VPF). VEGF has diverse effects, depending on the special collogical context in which it is found. VEGF is a potent endothelial cell mitogen, and directly contributes to induction of angiogenesis in vivo by promoting endothelial cell growth during normal embryonic development, wound challing, and tissue regeneration/reorganisation. The VEGF proteins of the invention share the angiogenet and other properties of VEGF, but are distributed and expressed in tissues differently to VEGF. The proteins can therefore be used to accelerate adjoigenesis in wound healing. The antibodies against the proteins can be used for inhibiting angiogenesis. The antibodies can also be used diagnostically to quantitatively detect VEGF-B. Primers complementary to the coding sequences. Countification of VEGF-B in cancer blopsy specimens may be useful as an indicator of metastatic risk. VEGF-B expression in a cell can be retarded using antisense sequences direct against the VEGF expression in tumour cells.
                                                                                                                                                                                                            Vascular endothelial growth factor VEGF-B proteins - useful to accelerate angiogenesis in wound healing, also related nucleic acid and antibodies for cancer diagnosis
                                                                                                                 Alitalo K, Eriksson U, Olofsson B, Pajusola K;
                                              (LUDW-) LUDWIG INST CANCER RES. (UYHE-) UNIV HELSINKI LICENSING LTD OY.
                                                                                                                                                                                                                                                                                                          Example 7; Page 28; 107pp; English.
95US-0469427.
                                                                                                                                                                WPI; 1996-412582/41.
06-JUN-1995;
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Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 other;

Gaps ö 73.3%; Score 11; DB 17; Length 20; 100.0%; Pred. No. 2.9e+03; Live 0; Mismatches 0; Indels Query Match 73.3 Best Local Similarity 100. Matches 11; Conservative

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Search completed: October 2, 2001, 16:18:48 Job time: 15492 sec

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APPLICANT: Monia, Brett P.
APPLICANT: Monia, Brett P.
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0389
CURRENT APPLICATION NUMBER: US/09/377,310B
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10, Application US/09377310B; Patent No. 6133031; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 taagcagctgccatt 15
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Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                  RESULT 1
US-09-377-310-30
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US-09-377-310-10
TYPE: DNA
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6.804 Million cell updates/sec
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                                                              2001, 16:03:54 ; Search time 417.38 Seconds
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Sequence 487
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Sequence 487
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Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-377-110-10

US-08-485-286-44

US-08-123-936-486

US-08-171-389-486

US-08-171-389-486

US-08-171-389-486

US-08-175-228A-486

US-08-475-228A-486

US-08-475-228A-486

US-08-475-228A-486

US-08-475-228A-486

US-08-475-228A-486

US-08-475-228A-486

US-08-482-080A-486

US-08-482-080A-558A-4

US-09-30G-876A-5

US-08-832-375-5

US-08-833-377-5

US-08-833-377-5

US-08-833-377-5
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US-08-834-655-15
US-09-363-574-15
US-08-479-614-21
US-08-479-852-12
                                                                                                                                                                                   Fotal number of hits satisfying chosen parameters:
                                                                                                                                                                   324599 segs, 94655562 residues
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                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                            - nucleic search, using sw model
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Match Length
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                                                                                                            score:
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Sequence 30, Application US/09377310B

Patent No. 6133031

Sequence 30, Application US/09377310B

APPLICANT: Monia, Brett P.

APPLICANT: Gaarde, William A.

TITLE OF INVENTION: Expression

TITLE OF INVENTION: Expression

TITLE OF INVENTION: Expression

TITLE OF INVENTION: Expression

CURRENT APPLICATION NUMBER: US/09/377,310B

CURRENT FILING DATE: 1999-08-19

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 30

LENGTH: 15
        Sedineuroe 
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US-08-479-852-64
US-08-479-852-78
US-08-462-646-12
US-08-462-646-78
US-08-462-646-78
US-08-462-646-78
US-09-013-406-12
US-09-013-406-12
US-09-013-406-92
US-09-013-406-92
US-09-013-406-92
US-09-13-406-92
US-09-13-406-92
US-09-13-406-92
US-09-13-406-93
US-08-343-682-12
US-09-198-955A-21
US-09-198-955A-21
US-09-13-404-39
US-08-951-822-13
US-09-13-404-39
US-09-13-266-7
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Mismatches
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MORGAN, ALICE ER
APPLICANT: HEY, TIMOTHY D
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Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 18 base pairs
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
                             TITLE OF INVENTION:
TITLE OF INVENTION:
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COUNTRY: USA
ZIP: 94111-3834
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                    APPLICANT:
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Sequence 45, Application US/08378761A

Sequence 45, Application US/08378761A

Patent No. 565384

GENERAL INFORMATION:

APPLICANT: WALSH, TERENCE A

APPLICANT: WALSH, TERENCE BR

TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE

TITLE OF INVENTION: USING

NUMBER OF SEQUENCES: 81

CORRESPONDENCES: 81

CORRESPONDENCES: 81

CORRESPONDENCES: 81

CORRESPONDENCES: 81

CORRESPONDENCES: 81

CORRESPONDENCE ADDRESS:

ADDRESSEE: ANDREA T. BORUCKI

STREET: 9330 ZIONSVILLE ROAD
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                                                                                       DB 3; Length 20;
                                                                                                                           0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                     Score 15; DB Pred. No. 9.8; Mismatches
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Pred. No. 72;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,761A
FILING DATE: 26-JAN-1995
CLASSIFICATION: 435
         ; OTHER INFORMATION: antisense sequence US-09-377-310-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 45, Application US/08485286
Patent No. 5646026
Patent No. 5646026 5646119
GENERAL INFORMATION:
APPLICANT: WALSH, TERENCE A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: BORUCKI, ANDREA T
REGISTRATION NUMBER: 3851
REFERENCE/CDCKET NUMBER: 3827
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 45:
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                                                                                     100.0%;
100.0%;
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93.3%;
                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14; Conservative
                                                                                                                                                              1 taagcagctgccatt 15
                                                                                                                                                                                 3 taagcagctgccatt 17
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Best Local Similarity
Matches 14; Conserva
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US-08-485-286-45/c
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US-08-378-761A-45
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STATE: IN
COUNTRY:
FEATURE:
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RIBOSOME-INACTIVATING PROTEINS, INACTIVE
PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
USING
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Patent No. 6033663
GENERAL INFORMATION: Catherine M.
APPLICANT: Ketcham, Catherine M.
TITLE OF INVENTION: Pyrophoshorylase
ITILE OF INVENTION: Pyrophoshorylase
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,286
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APPLICATION NUMBER: US/08/826,964
FILLING DATE: 09-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/378761
FILING DATE: 26-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: BORUCKI, ANDREA T
REGISTRATION NUMBER: 33651
REFERENCE-DOCKET UNBER: 38272B
TELECOMMUNICATION INFORMATION:
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                                                                                                                                 ADDRESSEE: ANDREA T, BORUCKI STREET: 9330 ZIONSVILLE ROAD CITY: INDIANAPOLIS
                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 45:
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93.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 11.8; DB 1; Length 50;
Pred. No. 5.8e+02;
0; Mismatches 2; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/171,389
      REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0175/G19P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0175/G19P3
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,070
APPLICATION NUMBER: US 08/081,070
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                                             TELEFAX: (415) 324-080
TELEFAX: (415) 324-080
INFORMATION FOR SEQ ID NO: 486:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: sin...
TOPOLOGY
                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
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86.7%;
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Best Local Similarity 86.7
Matches 13; Conservative
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; INDIVIDUAL ISOLATE:
US-08-171-389-486
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US-08-171-389-487
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Patent No. 5578444

GENERAL INFORMATION:

APPLICANT: Edwards, Cynthia A.

APPLICANT: Andrews, Beth M.

APPLICANT: Turin, Lisa M.

TITLE OF INVENTION: Sequence-Directed DNA Binding

TITLE OF INVENTION: Molecules, Compositions and Methods

WUMBER OF SEQUENCES: 641

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80.0%; Score 12; DB 3; Length 29, 100.0%; Pred. No. 4.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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ZIP: 94063
MEDIUM TYPE: FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/171,389
                                                                                                                                                    NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 014137-009910US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 base pairs
TYPE: nucleic acid
TYPE: 11near
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STREET: 505 Penobscot Drive
CITY: Redwood City
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CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-UN-1991
PRIOR APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-UN-1993
ATTORNEY/AGENT INFORMATION:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/015,241
FILING DATE: 10-ARR-1996
ATTORNEY/AGENT INFORMATION:
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Matches 12; Conservative
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US-08-171-389-486
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                                                           Human T-cell Lymphotropic virus type
III (HIV-1)
                                                                                                                                                                Score 11.8; DB 1; Length 50;
Pred. No. 5.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
TITLE OF INVENTION: Screening Assay for the Detection of NUMBER OF SEQUENCES: 640
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R:
REGISTRATION NUMBER: 4600-0075.32/G19P2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INDIVIDUAL ISOLATE: Aids-associated retrovirus;
INDIVIDUAL ISOLATE: (arv-2;proviral)
US-08-123-936-487
                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Genelabs Technologies, Inc. STREET: 505 Penobscot Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78.7%; Score 11.8;
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                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 487, Application US/08123936
; Patent No. 5726014
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                78.7%;
86.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                   Best_Local Similarity 86.7
Matches 13; Conservative
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MEDIUM TYPE: Floppy of COMPUTER: IBM PC comp
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EDNESS: single
                                                     ; INDIVIDUAL ISOLATE:
; INDIVIDUAL ISOLATE:
US-08-123-936-486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Redwood City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: RNA HYPOTHETTO:
                     OZ.
                   HYPOTHETICAL: NORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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MOLECULE TYPE:
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                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                  Length 50;
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Patent No. 5726014
GENERAL INFORMATION:
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Andrews, Beth M.
TITLE OF INVENTION: Screening Assay for the Detection of TITLE OF INVENTION: DANABINGING MODECLES
NUMBER OF SEQUENCES: 640
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                        TOPOLOGY: linear PART MA (Genomic)
HYPOTHETICAL: NO ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Aids-associated retrovirus
INDIVIDUAL ISOLATE: (arv-2;proviral)
US-08-171-389-487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0075.32/G19P2
TELEPOMUNICATION INFORMATION:
TELEPAN: (415) 324-0860
INFORMATION FOR SEQ ID NO: 486:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                Score 11.8; DB 1;
Pred. No. 5.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Genelabs Technologies, Inc. STREET: 505 Penobscot Drive CITY: Redwood City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 07/723,618
FILING DATE: 27-JUN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                 TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INPORMATION FOR SEQ ID NO: 487:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                              78.78;
86.78;
                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 86.7
Matches 13; Conservative
                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                                                                                               1 taagcagctgccatt 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 TAAGCAGCTGCTTTT 38
                                                                                                                                         STRANDEDNESS:
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US-08-123-936-486
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STATE:
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Gaps
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                                                                                                                                                                                                   GENERAL INCORMATION:
APPLICANT: Cantor, Charles R.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
APPLICANT: Turin, Lisa M.
APPLICANT: Fry, Kirk E.
TILLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 664
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 50;
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PRIOR PARTE: 00-10N 1993
APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-28P-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-30N-1991
PRIOR APPLICATION DATA:
FILING DATE: 27-30N-1993
APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-30N-1993
ATTORNEY AGENT INFORMATION:
NAME: STRATÉCTÓ, CAROL A.
REGISTRATION NUMBER: 4600-0175.21/G19P3DZ
TELECOMMUNICATION: NUNSCRMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
PPLICATION NUMBER: US/08/475,228A FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aids-associated retrovirus (arv-2; proviral)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78.7%; Score 11.8; DB 2;
86.7%; Pred. No. 5.8e+02;
ive 0; Mismatches 2;
                                                                                                                                                             Sequence 487, Application US/08475228A Patent No. 5869241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: RNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (415) 324-0880
TELEPAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 487
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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EDNESS: single
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COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
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         1 taagcagctgccatt 15
                                               24 TAAGCAGCTGCTTTT 38
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; INDIVIDUAL ISOLATE:
US-08-475-228A-487
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Best Local Similarity
Matches 13; Conserv
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US-08-475-228A-487
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                              Gaps
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Sequence 486, Application US/08475228A
Sequence 486, Application US/08475228A
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 664
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INDIVIDUAL ISOLATE: Human T-cell Lymphotropic virus type
INDIVIDUAL ISOLATE: III (HIV-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 78.7%; Score 11.8; DB 2; Length 50; Best Local Similarity 86.7%; Pred. No. 5.8e+02; Matches 13; Conservative 0; Mismatches 2; Indels
Pred. No. 5.8e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,228A
FILING DATE: 05-JUN 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/23,618
FILING DATE: 27-JUN-1991
PRIOR APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1991
PRIOR APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: STRATFORM CATOL A
RESTRATION: UNBERS: 34,444
REFERENCE/DOCKET NUMBER: 4600-0175.21/G1993D2
TILLECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Genelabs Technologies, Inc. 505 Penobscot Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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0
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TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 486:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: RNA (genomic)
    86.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
    Best Local Similarity 86.7
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 50 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
                                                                    1 taagcagctgccatt 15
                                                                                                                 24 TAAGCAGCTGCTTTT 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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                                                                                                                                                                                  RESULT 10
US-08-475-228A-486
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Sequence 487, Application US/08482080A
Patent No. 6010849
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Turin, Lisa M.
APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Molecules, Compositions and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,080A
FILING DATE: US/08/482,080A
FILING DATE: US/08/482,080A
FILING DATE: US/08/482,080A
FILING DATE: US/08/11,389
FILING APPLICATION DATA:
APPLICATION NUMBER: US 08/171,389
FILING DATE: 20-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
PRIOR APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Brady, John F.
REGISTRATION NUMBER: 39,118
REFERENCE/DOCKET NUMBER: 4600-0175.20/G19P3D1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       Genelabs Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 505 Penobscot Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (650) 324-0880
TELEFAX: (650) 324-0960
INFORMATION FOR SEQ ID NO: 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEOUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INDIVIDUAL ISOLATE: INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                               Redwood City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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RESULT 13
US-08-482-080A-487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human T-cell Lymphotropic virus type III (HIV-1)
                                                                                                                     APPLICANT: Edwards, Cynthia A. APPLICANT: Cantor, Charles R. APPLICANT: Andrews, Beth M. APPLICANT: Andrews, Beth M. APPLICANT: Fry, Kirk E. TITLE OF INVENTION: Sequence-Directed DNA Binding TITLE OF INVENTION: Molecules, Compositions and Methods NUMBER OF SEQUENCES: 664
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: ELOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,080A
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 08/171,389
FILING DATE: 12-DEC-1993
PRIOR APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION NUMBER: US 07/23,618
FILING DATE: 23-DEC-1992
PRIOR APPLICATION NUMBER: US 08/081,070
FILING DATE: 27-JUN-1991
PRIOR APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1993
APPLICATION NUMBER: US 08/081,070
FILING DATE: 23-JUN-1993
APPLICATION NUMBER: 39,118
REGISTRATION NUMBER: 4600-0175.20/G19P3D1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                    Genelabs Technologies, Inc.
                                            Sequence 486, Application US/08482080A Patent No. 6010849 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                505 Penobscot Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: RNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (650) 324-0960
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INDIVIDUAL ISOLATE: INDIVIDUAL ISOLATE:
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                   US-08-482-080A-486
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Gaps ô Length 50; Indels Aids-associated retrovirus (arv-2;proviral) Score 11.8; DB 3; Pred. No. 5.8e+02; 0; Mismatches 2; 78.7%; 86.7%; Best_Local Similarity 86.7 Matches 13; Conservative 1 taagcagctgccatt 15 24 TAAGCAGCTGCTTTT Query Match ò Q

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Gaps

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Score 11.8; DB 3; Length 50; Pred. No. 5.8e+02; 0; Mismatches 2; Indels

78.78; 86.78;

Query Match 78.7 Best Local Similarity 86.7 Matches 13; Conservative

1 taagcagctgccatt 15

24 TAAGCAGCTGCTTTT 38

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Search completed: October 2, 2001, 16:03:54 Job time: 14598 sec
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Best Local Similarity 86.7
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III (HIV-1)
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Pred. No. 5.8e+02;
0; Mismatches 2; Indels
                                                         TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 641
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence-Directed DNA Binding
Molecules, Compositions and Methods
                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12388
FILING DATE:
CLASCITTORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0175.41/G19PCTZ
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1887, Application PC/TUS9312388
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Sequence-Directed DNA in TITLE OF INVENTION: Molecules, Composition: CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17.5EP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
ATTORNEY/AGENT INFORMATION:
Sequence 486, Application PC/TUS9312388 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 486:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: RNA (genomic)
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86.78;
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Best Local Similarity 86.7
Matches 13; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
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PCT-US93-12388-486
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PCT-US93-12388-487
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                                                                                                                                                                                                             STATE: CA
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                                          APPLICANT:
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Gaps

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Indels

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Length 50;
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NAME: Fabian, Gary R.

REGISTRATION NUMBER: 33,875

REFERENCE/DOCKET NUMBER: 4600-0175.41/G19PCT2

TELEPHONE: (415) 324-0880

TELEFAX: (415) 324-0880

TELEFAX: (415) 324-0880

INFORMATION FOR SEQ ID NO: 487:

SEQUENCE CHARACTERISTICS:

LENGTH: 50 base pairs

TYPE: nucleic acid

STRANDEDNESS: single
                                                                                                                                       SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aids-associated retrovirus (arv-2;proviral)
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Pred. No. 5.8e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-193
FILING DATE: 17-SEP-193
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                               APPLICATION NUMBER: PCT/US93/12388
                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: 11near MOLECULE TYPE: RNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78.7%;
86.7%;
                                                                                                                                                                      CURRENT APPLICATION DATA:
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INDIVIDUAL ISOLATE:
PCT-US93-12388-487
Redwood City
CA
                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
                                                                                                                                                                                                                      FILING DATE:
                                     COUNTRY: US
                                                                                                                                                          SOFTWARE:
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Human T-cell lymph Aids-associated re HIV-1 TATA region

Test sequence from Test sequence from

Human T-cell lymph AIDS-associated re

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Human c-myc cDNA P Soybean chlorophyl RNA component of h Human telomerase R

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Primer #141 used i

Perfect score:

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Sequence:

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Run on:

Scoring table:

Searched:

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Database

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New antisense compounds for inhibiting focal adhesion kinase expression, especially useful for inhibiting retinal neovascularization, or for diagnosing and treating e.g. colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; focal adhesion kinase; FAK; signal transduction; cancer; embryonic development disorder; angiogenic disorder; wound healing; antisense; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human focal adhesion kinase antisense seguence #28.
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                                    AAT64199
AAV65660
AAX17486
AAX17487
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AAX77812
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AAT10302
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  99US-0377310.
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 (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Monia BP, Gaarde WA;
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AAC65562;
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 RESULT
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PCR primer for PG1
PCR primer for hum
Human GDP-fucose p
Human GDP-fucose p
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Human flt1 VEGF re
HIV-1 promoter fra
HIV-1 TATA region.
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Human focal adhesi
                                                                                                (without alignments)
10.740 Million cell updates/sec
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                                                                                   Search time 876.95 Seconds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /SIDSB/gcgdata/geneseq/geneseq/Na1999.Dar: */SIDSB/gcgdata/geneseq/geneseq/na1999.Dar: */SIDSB/gcgdata/geneseq/geneseqn/Na1990.Dar: */SIDSB/gcgdata/geneseq/geneseqn/Na1991.Dar: */SIDSB/gcgdata/geneseq/geneseqn/Na1992.Dar: */SIDSB/gcgdata/geneseq/geneseqn/Na1994.Dar: */SIDSB/gcgdata/geneseq/geneseqn/Na1995.Dar: */SIDSB/gcgdata/geneseqn/Na1995.Dar: */SIDSB/gcgdata/geneseqn/Na1995.Dar: */SIDSB/gcgdata/geneseqn/Na1999.Dar: */SIDSB/gcgdata/geneseqn/Na2000.Dar: */SIDSB/gcgdata/geneseqn/Na2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                /SIDS8/gcgdata/geneseq/geneseqn/NA1983.DAT:*/SIDS8/gcgdata/geneseqn/geneseqn/NA1984.DAT:*/SIDS8/gcgdata/geneseqn/geneseqn/NA1985.DAT:*/SIDS8/gcgdata/geneseqn/geneseqn/NA1986.DAT:*/SIDS8/gcgdata/geneseqn/geneseqn/NA1987.DAT:*/SIDS8/gcgdata/geneseqn/geneseqn/NA1987.DAT:*/SIDS8/gcgdata/geneseqn/geneseqn/NA1987.DAT:*/SIDS8/gcgdata/geneseqn/geneseqn/NA1988.DAT:*
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                                                                                                                                                                                                                                                     854978
           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                               Potal number of hits satisfying chosen parameters:
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                                                                                   2, 2001, 16:18:47;
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Maximum Match 100%
Listing first 45 summaries
                                                           - nucleic search, using sw model
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AAX36327
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AAA64261
AAT96994
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Gapop 10.0 , Gapext 1.0
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Human clone 28-1 t Human KM-102-deriv KHCV cDNA fragment Human biallelic po Human IL-8 recepto PCR primer PRDSI u

M. alpina delta-6 Sequence at juncti Maize polymorphic

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AAX36327 standard; DNA; 22
    1 taagcagctgccatt 15
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meningioma;
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                                          The present invention describes a number of phosphorothioate antisense sequences to the human focal adhesion Kinase (FAK) protein. This protein is involved in integrin-mediated signal transduction, and is implicated in cancer, particularly colon, breast and oral tumours, embryonic development disorders, angiogenic disorders and wound healing. The antisense sequences, including the one shown here, can be used in the treatment of all of these.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a number of phosphorothicate antisense sequences to the human focal adhesion kinase (FAK) protein. This protein is involved in integrin-mediated signal transduction, and is implicated in cancer, particularly colon, breast and oral tumours, embryonic development disorders, angiogenic disorders and wound healing. The antisense sequences, including the one shown here, can be used in the treatment of all of these.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antisense compounds for inhibiting focal adhesion kinase expression, especially useful for inhibiting retinal neovascularization, or for diagnosing and treating e.g. colon cancer
                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; focal adhesion kinase; FAK; signal transduction; cancer; embryonic development disorder; angiogenic disorder; wound healing; antisense; phosphorothloate; ss.
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                                                                                                                                                                                                                                                                                                 Length 15;
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27;
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                                                                                                                                                                                                                                                                                                                                              Mismatches
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Pred. No.
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Claim 15; Column 25; 30pp; English.
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                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAC65542;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
AAC65542
  8 \times 999999988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCR primers AAX36327-28 were used to amplify human FAK cDNA, in the course of the invention. The specification describes a method for altering the tumorigenicity or malignancy of brain cancer cells by changing the activity of glycosyltransferase in the cell so that glycosylation of cellular proteins is modified. The method is applied to glicom or meningiona, for prevention or treatment of brain tumours. Measuring the level of glycosyltransferase expression in brain cells is used to detect or predict their tumorigenicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                      brain cancer cell; protein glycosylation; glioma; brain tumour; FAK; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Altering tumorigenicity and malignancy of brain cancer cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 22 BP; 4 A; 7 C; 5 G; 6 T; 0 other;
                                                  Sense primer used to amplify human FAK cDNA
                                                                                                  Human; tumorigenicity; glycosyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCR primer for PG1 gene exon border.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3; Page 34; 83pp; English.
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100.0%;
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21-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                            (NEUR-) NEUROTHERAPEUTICS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA201016/c
ID AA201016 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 taagcagctgccat 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-327411/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 TAAGCAGCTGCCAT
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les 14; Conserv
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Gaps

; 0

100.0%; Score 15; DB 22; Length 20; 100.0%; Pred. No. 28; 0; Indels ive 0; Mismatches 0; Indels

15; Conservative

Best_Local Similarity Matches 15; Conserv

Ouery Match

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fibrononectin collagen-binding domain. The amplified sequence was used to construct a collagen-binding physiologically active polypeptide. This polypeptide comprises a peptide from fibronectin ligated to a physiologically active peptide. The polypeptides are used in an agent for enabling topical retention or sustained release of a physiological active peptide active peptide or physiological activity-imparting agent. They may be used in gene therapy and in tissue regeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This primer is used for the PCR amplification of guanosine 5-diphospho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Guanosine 5-diphospho- beta L-fucose pyrophosphorylase; human; GDPFPP; carbohydrate; donor substrate; GDP-fucose; PCR primer; ss.
                                                                                                                                                                              Collagen-binding active polypeptide for use in an agent for enabling topical retention or sustained release of a physiologically active peptide or physiological activity-imparting agent comprises a fibronectin peptide -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding GDP-fucose pyro:phosphorylase - useful to synthesise specific carbohydrate structures e.g. to investigate role of carbohydrate(s) in cell surface recognition
                                                                                                                                                                                                                                                                                                                        PCR primers AAA64261-62 were used to amplify cDNA encoding a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human GDP-fucose pyrophosphorylase (GDPFPP) amplifying 5' primer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 12.4; DB 21;
Pred. No. 8.2e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 49 BP; 12 A; 16 C; 11 G; 10 T; 0 other;
                                                                                                                                                                                                                                                                                   Example 1; Page 124; 135pp; English.
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AAT96994/c
ID AAT96994 standard; DNA; 29 BP.
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92.9%;
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  99JP-0041913.
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Best Local Similarity 92.9
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 taagcagctgccat 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31 TAAACAGCTGCCAT 18
                                                                                                    Kitajima
                                                                                                                                          WPI; 2000-565375/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (KETC/) KETCHAM C M.
                                                            (TERU ) TERUMO CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NPI; 1997-512414/47.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9737682-A1.
19-FEB-1999;
01-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-APR-1998
                                                                                                    Ishikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-0CT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a mammalian PG1 gene and protein, and a set of PG1 biallelic markers. The PG1 polynucleotide and biallelic markers are used in a hybridisation assay, a sequencing assay, or in an allele-specific amplification assay for determining the identity of a nucleotide at a PG1-related biallelic marker. The methods can be used to detect and to assass the risk of developing cancer or prostate cancer. Early-stage diagnosis of prostate cancer relies on prostate specific antigen (PBA) dosage. However, the effectiveness of this is limited due to discriminate between malignant and non-malignant affections of the organ. A need exists for both a reliable diagnostic procedure which would enable early-stage diagnosis, and for preventative and curative treatments of the disease. The PG1 gene can be used for detection of prostate cancer, and the risk of developing it in the cuture, and can also be used to determine therapies for the disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fibrononectin; collagen-binding domain; sustained release; gene therapy; physiologically active polypeptide; topical retention; PCR primer; tissue regeneration; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCR primer for human fibrononectin collagen-binding domain cDNA.
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0
                                                                                                                                                                                                                                                                                                                                                                                 a prostate cancer associated gene and biallelic markers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 27;
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                                                                                                                                                                                                                                                                                                      Cohen D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82.7%; Score 12.4; DB 20; 92.9%; Pred. No. 7.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 27 BP; 6 A; 4 C; 6 G; 11 T; 0 other;
                                                                                                                                                                                                                                                                                                      Bougueleret L, Chumakov I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 8; Page 261; 385pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA64261 standard; DNA; 49 BP.
                                                                                                                                                           98WO-IB02133
                                                                                                                                                                                               980S-0099658
970S-0996306
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                                                                                                                                                                                                                                                                                                                                       WPI; 1999-405178/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                      from it
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                                                                                                                                                                                                                                                         (GEST ) GENSET
                                                                                                                                                                                                                                                                                                 Blumenfeld M,
                                       Homo sapiens.
                                                                             WO9932644-A2
                                                                                                                                                         22-DEC-1998;
                                                                                                                                                                                                                    22-DEC-1997;
                                                                                                                                                                                                 09-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                   01-JUL-1999
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                  Synthetic
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AAA64261;

AAA64261/c

Query Match

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derived

use of

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Gaps

BP; 6 A; 6 C; 10 G; 7 T; 0 other;

Sequence 29

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beta L-fucose (GDP-fucose) pyrophosphorylase (GDPFPP) cDNA. Cells can be genetically engineered to contain the GDPFPP nucleic acids and produce the protein. GDPFPP enzymes can be used to synthesise carbohydrate molecules of defined structures, useful in investigating the role of carbohydrates as recognition elements on cell surfaces. They are especially useful in producing donor substrates (e.g. GDP-fucose) in reactions of a glycosyl transferase (e.g. fucosyltransferase) with the substrate, an acceptor sugar and a divalent metal cation to allow formation of glycosylic linkages adding a saccharide to a substrate saccharide. The proteins can also be used to produce antibodies or antisera useful to characterise, detect and isolate proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A 5' primer (AAT997584) and a 3' primer (AAT997585) were used in the PCR amplification of human GDP-fucose pyrophosphorylase (GDPFPP) cDNA (see AAT97583) from Epstein-Barr virus-transformed B lymphoblastoid cell line JY, and were designed to incorporate EcoRV sites at the 5' and 3' termin of the amplified sequence. The amplified GDPFPP CDNA was subsequently incorporated into expression vectors. Recombinant human GDPFPP was expressed in COS, NSO and Spodoptera frugiperda Sf9 cells. The claimed enzyme (see AAW36811) is useful in the synthesis of carbohydrate structures.
                                                                                                                                                                                                              cross-reacting with the GDPFPP protein.
Note: The specification refers to claimed GDPFPP nucleotide and amino acid sequences, neither of which are given in the specification.
                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GDP-fucose pyrophosphorylase and related coding sequences - useful to synthesise GDP-fucose as substrate for producing specific carbohydrate structures, e.g. to study cell surface recognition
                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GDP-fucose pyrophosphorylase; GDPFPP; human; oligosaccharide; carbohydrate; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                   Length 29;
                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human GDP-fucose pyrophosphorylase cDNA 5' PCR primer.
                                                                                                                                                                                                                                                                                                                                                                    1.3e+03;
                                                                                                                                                                                                                                                                                                                                                   80.0%; Score 12; DB 18;
                                                                                                                                                                                                                                                                                          Sequence 29 BP; 6 A; 6 C; 10 G; 7 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                            100.0%; Preu. ...
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Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           3 agcagctgccat 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                27 AGCAGCTGCCAT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-512415/47.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT97584;
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                                                                                                                                                                                                                                                                                                    Human; variant thrombospondin 1; variant thrombospondin 4; SNP; polymorphism; vascular disease; coronary artery disease; forensics; myocardial infarction; atherosclerosis; stroke; venous thromboembolism; pulmonary embolism; paternity test; ds.
                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         McCarthy JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids comprising single nucleotide polymorphisms, useful in applications such as forensics, paternity testing, medicine, genetic analysis and phenotype correlations to diseases such as diabetes and atherosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= a
/standard_name= "single nucleotide polymorphism"
                               ö
Length 29;
                               Indels
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              Pred. No. 1.3e+03;
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Score 12; DB 18;
                                                                                                                                                                                                                                                                          Human gene single nucleotide polymorphism #19.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 21 BP; 6 A; 7 C; 4 G; 4 T; 0 other;
         100.0%; Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (WHED ) WHITEHEAD INST BIOMEDICAL RES. (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers replace(11,T)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Examples; Page 48; 242pp; English.
                                                                                                                                                                            AAF95258 standard; DNA; 21 BP.
80.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-SEP-2000; 2000WO-US24503.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0153357.
                                                                                                                                                                                                                                          06-JUN-2001 (first entry)
                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gargill M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-226749/23.
                                                                                   27 AGCAGCTGCCAT 16
                                                             3 agcagctgccat 14
Query Match
Best Local Similarity
Matches 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lander ES,
                                                                                                                                                                                                            AAF95258;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Variation
                                                                                                                                                            AAF95258/C
                                                               δλ
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HIV-1 promoter fragment used as a target sequence.

(first entry)

16-DEC-1998

AAV65645;

BP.

AAV65645 standard; DNA; 30

AAV65645 RESULT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes nucleic acid molecules which modulate the synthesis, expression and/or stability of a mRNA encoding 1 or more receptors of vascular endothelial growth factor (VEGF). A patient (preferably human) having a condition associated with the level of the fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour be treated by administering the nucleic acid molecule or the expression vector to the patient. AAX67275 to AAX75752 represent specific examples of nucleic acid molecules from the present invention.
                                                                                                                                                                                                                                                                                                         Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage; tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease; flms-like tyrosine kinase 1; kinase insert domain containing receptor;
                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene expression angiogenesis,
                                                 ö
                   Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid molecule modulating VEGF receptor(s) gene exp
mRNA stability – useful for treating e.g. tumour angiogen
psoriasis, rheumatoid arthritis, etc., in a human patient
                                                 Indels
Score 11.8; DB 22,
7.4 No. 1.6e+03;
2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ä
                                                                                                                                                                                                                                                                             Human flt1 VEGF receptor hammerhead ribozyme #665.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stinchcomb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 27 BP; 9 A; 4 C; 9 G; 4 U; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pavco P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 9; Page 66; 218pp; English.
                                                 ó;
                                                                                                                                                                                     BP.
                 78.78;
86.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96US-0584040.
95US-0005974.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96WO-US17480
                                                                                                                                                                                    AAX67939 standard; RNA; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CHIR ) CHIRON CORP. (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                      foetal liver kinase 1; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escobedo J, McSwiggen J,
            Query Match 18.7
Best Local Similarity 86.7
Matches 13; Conservative
                                                                              1 taagcagctgccatt 15
                                                                                                         17 TAGGCAGCTGCGATT
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                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-OCT-1996;
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26-OCT-1995;
                                                                                                                                                                                                                                              28-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                  AAX67939;
                                                                                                                                                                        AAX67939/c
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This represents a promoter fragment of the HIV-1 genome that is used as a target sequence. The invention provides polyamide DNA-binding ligands for modulating expression of cellular and viral genes. One method comprises identifying a unique target DNA sequence adjacent to the binding site of a minor groove transcription factor protein (MGTFP), choosing a polyamide having subnanomolar affinity for the target DNA and treating the target DNA with the polyamide as transcription inhibiting replication of a pathogen by administering a transcription-inhibiting replication of a pathogen by administering a transcription-inhibiting replication of a pathogen by replacing a transcription-inhibiting polyamide; (2) improving binding affinity of polyamide, selected for an identified viral DNA target by replacing a carboxamide binding pair (CBP) that does not include N-methylimidazole carboxamide (IM) with a CBP comprising paired beta-alanine (beta) residues; (3) inhibiting binding of the zinc finger protein TFIIIA to
                                                                                                                    Polyamide; DNA-binding ligand; modulation; gene expression; CBP; IM; minor groove transcription factor protein; MGTFP; TFILIA; adenocarcinoma; transcription inhibitor; pathogen; binding affinity; zinc finger protein; carboxamide binding pair; N-methylimidazole carboxamide; bacteria; fungi; S. Tibosomal RNA gene; internal control region; virus; protozoa; HIV-1; human immune deficiency virus; cancer; DNA capture; genomic sequencing; her-2/neu oncogene; gene transcription; DNA cleavage; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modulating expression of genes with poly:amide(s) specific for region near the binding site for transcription factor - for inhibiting replication of pathogen, especially human immune deficiency virus and for treating cancers associated with expression
                                                                                                                                                                                                                                                                                                                                        /*tag= a
/note= "six basepair sequence bound by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "six basepair sequence bound by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DE;
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                                                                                                                                                                                                                                                                                                                                                                                                              b
"TFIID binding site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gottesfeld JM,
                                                                                                                                                                                                                                                                   Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                            polyamide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polyamide"
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97US-0038384.
97US-0038394.
97US-0853022.
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of the her-2/neu oncogene
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/note=
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                                                                                                                                                                                                                                                                                                                     misc_binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9835702-A1
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14-FEB-1997;
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                                                                                                                                                                                                                                                                                                                                                                                               TATA_signal
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Gaps

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Indels

Length 27;

Score 11.8; DB 18; Pred. No. 1.6e+03; 0; Mismatches 2;

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78.7%; ilarity 86.7%; Conservative (

Query Match Best Local Similarity Matches 13; Conserv

taagcagctgccatt 15

õ g

15 TCATCAGCTGCCATT

9

86.78;

Best Local Similarity

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the SS ribosomal RNA gene internal control region; (4) for treating adenocarcinoma of ovary, endometrium, breast, fallopian tubes and cervix with the polyamide are also provided. Method (1) is applied to viruses, bacteria, fungi and protozoa, especially human immune deficiency virus (HIV)-1, both therapeutically and for treating blood cells in vitro. Method (4) is especially used against cancers that overexpress the her-2,new oncogene. The polyamide can also be used for diagnosis of disease, very generally as therapeutic agents for any disease involving cellular or viral gene transcription, for genomic sequencing, for DNA capture and for DNA cleavage (oxidative or by light). The polyamide has excellent specificity and very high affinity for the target DNA, which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TATA modulating factor, TMF; transcription; TATA box; promoter; HIV-1; human immunodeficiency virus-1; short arm; human chromosome 3; p12-p21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents the TATA region of the HIV-1 LTR from -46 to -1. This region is bound by TATA modulating factor (TMF). TMF is a protein of mol. wt. 123-130 kD which activates transcription in most genes, esp. in human immundeficiency virus-1 (HIV-1) by binding to the TATA box region of the promoter. TMF is encoded by the short arm of human chromosome 3 in the region p12-p21 which is often involved in translocations in patients having lung and other types
                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New protein cellular factor - capable of binding double stranded HIV-1 tata region and activating gene expression of HIV-LTR
                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                             Score 11.8; DB 19; Length 30; Pred. No. 1.7e+03;
                                                                                                                                                                                                   are specific for particular genes, and are cell permeable
                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                         Sequence 30 BP; 7 A; 6 C; 7 G; 10 T; 0 other;
                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Page 48; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immunodeficiency virus-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAQ49401 standard; cDNA; 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93WO-US03077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translocation; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TEXA ) UNIV TEXAS SYSTEM
                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                   taagcagctgccatt 15
                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1993-336836/42.
                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HIV-1 TATA region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wu F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-APR-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ49401;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The test sequences may also be randomly generated. DNA:protein interaction may be used for screening purposes, e.g. the Herpes Simplex Virus (HSV) origin of replication and UL9 (see AAQ69851-52, AAQ69865 and AAQ69891).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A DNA protein-binding assay is provided, useful for screening libraries of synthetic or biological cpds. for their ability to bind DNA test sequences. The assay is versatile in that any number of test sequences can be tested by placing the test sequence adjacent to a defined protein-binding screening sequence. Binding of mols. to these test sequences changes the binding characteristics of the protein mol. to its cognate binding sequence. When such a binds the test sequence, the equilibrium of the DNA:protein complexes is disturbed, generating changes in the concentration of free DNA probe.
                    Gaps
                                                                                                                                                                                                                                                                                     Human T-cell lymphotropic virus type III (HIV-I), target region.
                    ö
                                                                                                                                                                                                                                                                                                                       DNA protein-binding assay; test sequence; screening sequence; promoter; target; TATA box; Herpes Simplex Virus; HSV; origin of replication; UL9; transcription factor; TFIID: ds.
                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Turin LM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence-directed DNA-binding molecules - useful in
Pred. No. 1.7e+03;
); Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 50 BP; 9 A; 14 C; 13 G; 14 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fry KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pharmaceuticals and as molecular reagents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Edwards CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 28; Page 455; 587pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GENE-) GENELABS TECHNOLOGIES INC
                  ;
0
                                                                                                                                                                                 BP.
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                                                                                                                                                                               AAQ69736 standard; DNA; 50
                                                                                                                                                                                                                                                  06-MAR-1995 (first entry)
                  13; Conservative
                                                      15
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                                                      1 taagcagctgccatt
                                                                                         22 taagcagctgctttt
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                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                  AAQ69736;
                  Matches
                                                                                                                                             RESULT 12
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Gaps

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Length 50; Indels

Score 11.8; DB 15; Pred. No. 1.8e+03;); Mismatches 2;

78.78; 86.78;

Query Match 78.7 Best Local Similarity 86.7 Matches 13; Conservative

taagcagctgccatt 15

δλ

78.7%; Score 11.8; DB 14; Length 46;

Query Match

Sequence 46 BP; 8 A; 12 C; 11 G; 15 T; 0 other;

Duplex DNA; target region; binding characteristic; DNA binding protein; TFIID; transcription factor; binding site; inhibition; enhance; cancer; inherited genetic disorder; ds.

Human lymphotropic virus type III.

US5578444-A.

26-NOV-1996,

Human T-cell lymphotrophic virus type-III (HIV-1) TFIID binding site.

(first entry)

17-MAR-1997

AAT64198;

AAT64198 standard; DNA; 50 BP.

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RESULT 14
                    AAT64198
                                                                        factors (e.g. TFIID), where the target region is typically selected from DNA sequences adjacent to the binding site for the eucaryotic transcription factor. Numerous exemplary test sequences are given: the sequences in AAO69251-731 and AAO69850 correspond to promoter targets (typically, TATA box-contg. sites) for human genes and the sequences in AAO69732-849 correspond to promoter targets for viral genes. The test sequences may also be randomly generated. DNA:protein interaction may be used for screening purposes, e.g. the Herpes Simplex Virus (HSV) origin of replication and UL9 (see AAO69851-52, AAO69865 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A DNA protein-binding assay is provided, useful for screening libraries of synthetic or biological cpds. for their ability to bind DNA test sequences. The assay is versatile in that any number of test sequences can be tested by placing the test sequence adjacent to a defined protein binding screening sequence. Binding of mols. to these test sequences changes the binding characteristics of the protein mol. to its cognate binding sequence. When such a mol. binds the test sequence, the equilibrium of the DNA.protein complexes is disturbed, generating changes in the concentration of free DNA probe. One application of this method is to eucaryotic general transcription
                                                                                                                                                                                                                                                   DNA protein-binding assay; test sequence; screening sequence; promoter; target; TATA box; Herpes Simplex Virus; HSV; origin of replication; UL9; transcription factor; TFIID: ds.
                                                                                                                                                                                                                 AIDS-associated retrovirus (arv-2; proviral), target region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Turin LM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence-directed DNA-binding molecules - useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 50 BP; 8 A; 13 C; 13 G; 16 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fry KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pharmaceuticals and as molecular reagents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Edwards CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 28; Page 455; 587pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GENE-) GENELABS TECHNOLOGIES INC.
                                                                                                        AAQ69737 standard; DNA; 50 BP.
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                                                                                                                                                                             06-MAR-1995 (first entry)
24 taagcagctgctttt 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cantor CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1994-234711/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                        20-DEC-1993;
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                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAQ69891).
                                                                                                                                            AAQ69737;
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Altering binding characteristics of DNA binding proteins to duplex DNA - by attaching specific small cpd. to target region close to the protein's binding site, useful in treatment of viral disease, cancer

Turin LM;

Fry KE,

Cantor CR, Edwards CA,

Andrews BM,

WPI; 1997-020402/02.

(GENE-) GENELABS TECHNOLOGIES INC.

93US-0123936

27-JUN-1991; 23-DEC-1992;

17-SEP-1993;

20-DEC-1993;

93US-0171389. 91US-0723618. 92US-0996783.

91US-0723618

27-JUN-1991;

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The sequences given in AAT63713-4312 represent duplex DNA's which act as target regions in the method of the invention. The method for altering the binding characteristics of a DNA-binding protein to duplex DNA comprises contacting the duplex DNA with a small molecule which binds sequence-specifically to a target region, where, when the small collection is bound to the target region, it is adjacent to, but not conclapping by more than 4 bp, a binding site for a DNA-binding protein. The small molecule is added at a concentration effective to alter the binding of the DNA binding site on the duplex DNA. The binding of the small molecule may inhibit or compounds isolated using this method are potentially useful as the method is suitable for trement of any disease which involves a specific DNA sequence, or inherited genetic disorders etc. The method is suitable for screening large biological or chemical libraries and allows determination of sequence-specific and relative affinities of known DNA-binding agents for different DNA sequences. The design of these duplex DNA's allows a single DNA:protein interaction to be used for screening sequence-specific or preferential, DNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to be used for screening sequence-specific, or preferential, DNA binding proteins that recognise almost any possible sequence (see also AAT49539-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78.7%; Score 11.8; DB 18;
llarity 86.7%; Pred. No. 1.8e+03;
Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 50 BP; 9 A; 14 C; 13 G; 14 T; 0 other;
Claim 6; Column 347-348; 264pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 taagcagctgccatt 15
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Indels

78.7%; Score 11.8; DB 15; 86.7%; Pred. No. 1.8e+03; iive 0; Mismatches 2;

Query Match 78.7 Best Local Similarity 86.7 Matches 13; Conservative

1 taagcagctgccatt 15

24

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Length 50;

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as target regions in Anion 19713-1912 represent dupter DNA succes as target regions in the method of the invention. The method for altering the binding characteristics of a DNA-binding protein to duplex DNA somprises contexting the duptex DNA with a small molecule which binds sequence-specifically to a target region, where, when the small molecule is bound to the target region, it is adjacent to, but not overlapping by more than 4 bp, a binding site for a DNA-binding protein. The small molecule is added at a concentration effective to alter the binding of the DNA binding protein, pref. TFIID, to its binding site on the duplex DNA. The binding of the Small molecule may inhibit or enhance the binding of the DNA-binding protein to its binding site. The compounds isolated using this method are potentially useful as therapeutic agents for treatment of any disease which involves a specific DNA sequence, e.g. cancer, or inherited genetic disorders etc. The method is suitable for screening large biological or chemical libraries and allows determination of sequence-specific and relative affinities of known DNA-binding agents for different DNA sequences.

The design of these duplex DNA's allows a single DNA-brotein interaction to be used for screening sequence-specific, or preferential, DNA binding proteins that recognise almost any possible sequence (see also AAT49539-
                                                                                                                                                                                               Duplex DNA; target region: binding characteristic; DNA binding protein; TFIID; transcription factor; binding site; inhibition; enhance; cancer; inherited genetic disorder; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequences given in AAT63713-4312 represent duplex DNA's which act
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Altering binding characteristics of DNA binding proteins to duplex DNA - by attaching specific small cpd. to target region close to the protein's binding site, useful in treatment of viral disease, cancer
                                                                                                                                                           Aids-associated retrovirus proviral arv2 TFIID binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Turin LM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 50 BP; 8 A; 13 C; 13 G; 16 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fry KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 6; Column 347-348; 264pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Edwards CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GENE-) GENELABS TECHNOLOGIES INC.
                                       AAT64199 standard; DNA; 50 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                93US-0171389.
91US-0723618.
92US-0996783.
93US-0123936.
                                                                                                                                                                                                                                                                                                                                                                                                           91US-0723618
                                                                                                                                                                                                                                                                                   Aids-associated retrovirus
                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cantor CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-020402/02.
                                                                                                                                                                                                                                                                                                                                                                                                         27-JUN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                20-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-JUN-1991;
23-DEC-1992;
                                                                                                                     17-MAR-1997
                                                                                                                                                                                                                                                                                                                           US5578444-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Andrews BM,
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                                                                               AAT64199;
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RESULT 1
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13; Conservative

Matches

Local Similarity

Query Match

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Search completed: October 2, 2001, 16:18:48 Job time: 15492 sec

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Sequence 23, Application US/09377310B
| Fatent No. 6133031
| GENERAL INFORMATION:
| APPLICANT: Monia, Brett P. |
| APPLICANT: Gaarde, William A. |
| TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase |
| TITLE OF INVENTION: Expression |
| FILE REFERENCE: ISPH-0389 |
| CURRENT APPLICATION NUMBER: US/09/377,310B |
| CURRENT FILING DATE: 1999-08-19 |
| NUMBER OF SEQ ID NOS: 43 |
| SOFTWARE: Patentin Ver. 2.0 |
| SEQ ID NO.23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Monia, Brett P.
APPLICANT: Geard, William A.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0389
CURRENT APPLICATION NUMBER: US/09/377,310B
CURRENT PILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 15; DB 3;
100.0%; Pred. No. 8.6;
ive 0; Mismatches 0
US-08-171-718-51
US-08-46-580-50
US-08-478-087-51
US-08-905-359A-4
US-09-35-556-4
US-08-643-21-72
PCT-US95-03731-50
US-09-011-745-18
US-08-09-011-745-18
US-08-188-969
                                                                                                                                                                                                         PCT-US93-00977-84
US-09-344-579-40
                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-377-310-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 15; Conserv
    RESULT 1
US-09-377-310-23
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US-09-377-310-3
 SEQ ID NO 3
LENGTH: 20
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Sequence 5, Appli
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Sequence 10, Appl
Patent No. 5190871
                                                                                                    (without alignments)
6.804 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 23,
                                                                                       2001, 16:03:53 ; Search time 417.38 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18, Sequence 6, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11,
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Sequence 856
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Sequence
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          14.5
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                      /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/pcTuS_COMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-488-551B-802
US-09-315-886C-5
US-09-275-680-11
US-09-428-219-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-377-310-3
US-09-282-996-18
US-08-732-612-11
US-08-161-015-17
US-08-445-2898-25
US-08-4859-998-85
US-08-33-57-8
PCT-US92-08634-8
US-08-31-57-8
US-08-31-01-2
US-08-31-01-2
US-08-271-880A-50
US-08-249-215-50
                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                 324599 segs, 94655562 residues
             GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                               - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Match Length
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length: 50
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Perfect score:
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Minimum DB Maximum DB

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ZIP: 20006-1812
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US-08-732-612-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: MORBEY, MOHAMAD A.
TITLE OF INVENTION: METHODS FOR PRODUCTION OF RECOMBINANT
TITLE OF INVENTION: PLASMIDS
TITLE OF INVENTION: PLASMIDS
TOTHER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVE., NW
CITY: WASHINGTON
STRATE: DC
                                                                                        Length 20;
                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                            Sequence 18, Application US/09282996
Patent No. 6143502
GENERAL INFORMATION:
APPLICANT: Gentramen, Guido
APPLICANT: Gesteland, Raymond F.
APPLICANT: Gesteland, Raymond F.
TILLE OF INVENTION: Dual-Luciferase Reporter System
FILE REFERENCE: T9864. NP
CURRENT FILING DATE: 1999-03-31
EARLIER FILING DATE:
NUMBER OF SEQ ID NOS: 18
SOFTWARE: WordPerfect 8.0
SEQ ID NO 18
LENGTH: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                        DB 3;
                                                                                     Query Match 100.0%; Score 15; DE Best Local Similarity 100.0%; Pred. No. 8.6 Matches 15; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 13.4; D
Pred. No. 63;
0; Mismatches
                ; OTHER INFORMATION: antisense sequence US-09-377-310-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/732,612
FILING DATE: 16-OCT-1996
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Primer fsAZ2
US-09-282-996-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89.3%;
93.3%;
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Best Local Similarity 93.3
Matches 14; Conservative
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CLASSIFICATION:
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US-08-732-612-6
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FEATURE:
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Patent No. 5922583
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MORSEY, MOHAMAD A.
TITLE OF INVENTION: METHODS FOR PRODUCTION OF RECOMBINANT
TITLE OF INVENTION: PLASMIDS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVE., NW
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 16-OCT-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 11.8; DB 2;
Pred. No. 4.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                          /note= "downstream primer designated murF2"
ATTORNEY/AGENT INFORMATION:

NAME: MURASHIGE, KATE H.

REGISTRATION NUMBER: 29,959

REFERENCICE/DOCKET NUMBER: 29311-20006.21

TELECOMMUNICATION INFORMATION:

TELEFAX: (202) 887-1500

TELEFAX: (202) 887-1503

TELEFAX: 90-4030 MRSNPOERSWSH

INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:

TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29311-20006.21
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NAME: MURASHIGE KATE H.
REGISTRATION NUMBER: 29.159
REFERENCE/COCKET NUMBER: 2931.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEY 90-4030 MRSNPOSESWSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78.7%;
86.7%;
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CCATION: 1..31
OTHER INFORMATION: /note=
COTHER INFORMATION: designalus-08-732-612-6
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1..39
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Best Local Similarity 86.7
Matches 13; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
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Gaps
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Pred. No. 7.5e+02;
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APPLICANT: Chenchik, Alex
APPLICANT: Chenchik, Alex
APPLICANT: Jokhadze, George
APPLICANT: Bibliashvilli, Robert
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1375
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & ALchardson, P.C.
STREET: 2200 Sand Hill Road, Suite 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: Windows95
SOFRWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: oligonucleotide primer US-08-859-998-856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09096/002001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/859,998
FILING DATE: 21-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                  RD00003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 856, Application US/08859998 Patent No. 5994076
   NAME: Bade, Annette L.
REGISTRATION NUMBER: 37,029
REFERENCE/DOCKET NUMBER: RD00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-231-5520
TELEFAX: 310-816-4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37,620
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TELECOMMUNICATION:
TELEPHONE: 415-322-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                              76.0%;
92.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Field, Bret E.
REGISTRATION NUMBER: 37,8
                                                                                                                              TELEFAX: 310-810-400: 20 INFORMATION FOR SEQ ID NO: 20 SEQUENCE CHARACTERISTICS: LENGTH: 22 base pairs TYPE: nucleic acid TYPE: nucleic acid TYPE: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 76.0 Best Local Similarity 92.3 Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                         linear
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
US-08-859-998-856/c
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US-08-445-289B-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY:
STATE:
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| Sequence 25, Application US/08445289B
| Patent No. 5693467
| APPLICANT: Hu, Mendong APPLICANT: Hu, Mendong APPLICANT: Lee, Sunmin TITLE OF INVENTION: A Mycoplasma PCR Testing System Using A TITLE OF INVENTION: Set of Mixed and Single Sequence Primers
                                                                                                                                                           Length 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 18;
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US-09-161-015-17/C
US-09-161-015-17/C
Patent No. 5965370
GENERAL INFORMATION:
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF RhoG EXPRESSION
FILE REFERENCE: RTS-0015
CURRENT APPLICATION NUMBER: US/09/161,015A
CURRENT FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 17
                                                                                                                                                                                                                2; Indels
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                                                                                                                                                    Score 11.8; DB 2;
Pred. No. 4.6e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 11.4; DB 2;
Pred. No. 7.5e+02;
0; Mismatches 1;
   /note= "downstream primer designated murF4"
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STREET: 12301 Parklawn Drive
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Antisense Oligonucleotide US-09-161-015-17
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ZIP: 20852
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

"THER: IBM PC compatible
"THER: TOWN:

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FILING DATE: 19-MAY-1995
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                                                                                                                                                    78.7%;
86.7%;
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                                                                                                                                                    Query Match 78.7
Best Local Similarity 86.7
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 76.0
Best Local Similarity 92.3
Matches 12; Conservative
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NUMBER OF SEQUENCES: 2'
CORRESPONDENCE ADDRESS:
ADDRESSEE: American
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 cgggctcacagtg 14
||||| ||||||||
17 CGGCGCACAGTG 5
; OTHER INFORMATION:
; OTHER INFORMATION:
US-08-732-612-11
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Smith, Richard K.

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RESULT
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                                          Gaps
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                                                                                                                                                                                                                 Sequence 8, Application US/07959946
Patent No. 5408038
GENERAL INFORMATION:
APPLICANT: Smith, Richard K.
APPLICANT: Young, Stephen G.
APPLICANT: Young, Stephen G.
APPLICANT: Units, Linda K.
APPLICANT: Units, Linda K.
TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a TITLE OF INVENTION: Dan Native Epitope and Recombinant Antigens NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
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  Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/07/959,946
FILING DATE: 19921008
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,706
FILING DATE: 18-70N-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Dressler, Goldsmith, Shore, Sutker & ADDRESSEE: Milnamow, Ltd.
STREET: 180 No. 5408038th Stetson, Suite 4700
CITY: Chicago
STATE: 111inois
COUNTRY: USA
73.3%; Score 11; DB 2; Le
100.0%; Pred. No. 1.2e+03;
:1ve 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMEDUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/08333577 Patent No. 5786206 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (312)616-5400
TELEFAX: (312)616-5460
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: DNA (genomic)
US-07-959-946-8
Query Match 73.3
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11; Conservative
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Best Local Similarity
                                                                               4 ggctcacagtg 14
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                                                                                                    11 GCTCACAGTG 1
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APPLICANT: Smith, Richard K.
APPLICANT: Koduri, Raju
APPLICANT: Young, Stephen G.
APPLICANT: Turing, Linda K.
APPLICANT: Curtiss, Linda K.
TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
TITLE OF INVENTION: Pan Native Epitope and Recombinant Antigens
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                    TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a TITLE OF INVENTION: Pan Native Epitope and Recombinant Antigens NUMBER OF SEQUENCES: 20 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                           ADDRESSE: Dressler, Goldsmith, Shore, Sutker & ADDRESSE: Milnamow, Ltd.
STREET: 180 No. 5786206th Stetson, Suite 4700 CITY: Chicago STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Dressler, Goldsmith, Shore, Sutker & ADDRESSEE: Milnamow, Ltd.
STREET: 180 North Stetson, Suite 4700
CITY: Chicago
STATE: 1111nois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/333,577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.2e+03;
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100.0%; Pred. No. 1.2e+0
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALTERATION NUMBER: 29,381
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 29,381
TELEPHONE: (312)616-5400
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDUIW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 8, Application PC/TUS9208634
; GENERAL INFORMATION:
APPLICANT: Koduri, Raju
APPLICANT: Young, Stephen G.
APPLICANT: Witztum, Joseph L.
APPLICANT: Curtiss, Linda K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: DNA (genomic) US-08-333-577-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 gctcacagtgg 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
PCT-US92-08634-8/c
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APPLICANT: Dalrymple, Michael A
APPLICANT: Prunkard, Donna E
APPLICANT: Foster, Donald C
TITLE OF INVENTION: Production of Fibrinogen in Transgenic
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72.0%; Score 10.8; DB 1; Length 24; 85.7%; Pred. No. 1.6e+03; Live 0; Mismatches 2; Indels
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TITLE OF INVENTION: Methods and Composition for Treating
TITLE OF INVENTION: Tumor Cells
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gray Cary Ware & Freidenrich
STREET: 401 "B" Street, Suite 1700
                                                                                                                                                                                                                                                                        ZIP: 98105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Rolease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/206,176
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31-64
REFERENCE/DOCKET NUMBER: 93-15
TELECOMMUNICATION INFORMATION:
TELEPRONE: 206-548-2329
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHRACTENISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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FILING DATE: January 10, 1995
                                                                                                                                                                  ADDRESSEE: ZymoGenetics, Inc.
STREET: 4225 Roosevelt Way, N.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 2, Application US/08371001
; Patent No. 5783683
; GENERAL INFORMATION:
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Best Local Similarity 85.7
Matches 12; Conservative
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MEDIUM TYPE: Floppy
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CLASSIFICATION: 435
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                                                                                                                                                                                                                                    STATE: WA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
US-08-371-001-2
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STATE:
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Patent No. 5968826
GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
APPLICANT: Condon, Tom P.
APPLICANT: Cowsert, Lex M.
TITLE OF INTENTION: ANTISENSE MODULATION OF INTEGRIN 4 EXPRESSION
FILE REFERENCE: ISPH-013.
CURRENT APPLICATION NUMBER: US/09/166,203A
CURRENT FILING DATE: 1998-10-05
SEQ ID NO 9
LENGTH: 18
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                     OPERATING SYSTEM: PCT-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SORTWARE: PATENTIN BATA:
APPLICATION NUMBER: PCT/US92/08634
FILING DATE: 19921009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72.0%; Score 10.8; DB 2;
85.7%; Pred. No. 1.6e+03;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION UNDER:
ILING DATE: 18-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: NUCLEIC ACID
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTHER INFORMATION; antisense sequence US-09-166-203-9
       IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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%Sequence 10, Application US/08206176
%Patent No. 5639940
%GENERAL INFORMATION:
APPLICANT: Garner, Ian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: DNA (genomic)
PCT-US92-08634-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 73.3%
Best Local Similarity 100.0
Matches 11; Conservative
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Best Local Similarity 85.7
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Garner, Ian
APPLICANT: Cottingham, Ian R.
APPLICANT: Temperley, Simon M.
APPLICANT: Temperley, Simon M.
APPLICANT: Sprecher, Condy A.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Prunkard, Donna E.
TITLE OF INVENTION: PROTEIN C PRODUCTION IN TRANSGENIC
TITLE OF INVENTION: ANIMALS
NUMBER OF SOUGHNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-POS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/756,506
                                                                    ALIGNALIA TOURING THE CONTROL OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: Other Nucleic Acid
US-08-371-001-2
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CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A
REGIGSTRATION NÜMBER: 37,438
REFRENCE/CDOCKET NÜMBER: 95-21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
TELEFAX: 206-442-6678
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 72.0
Best Local Similarity 85.7
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-756-506-9/c
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Query Match
72.0%; Score 10.8; DB 2; Length 24;
Best Local Similarity 85.7%; Pred. No. 1.6e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 cgggctcacagtgg 15
| | | | | | | | | | |
| Db 24 CTGGCTCACAGAGG 11
Search completed: October 2, 2001, 16:03:54
Job time: 14598 sec
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